# **ADDENDUM TO FINAL REPORT**

Lower Deschutes River Macroinvertebrate & Periphyton Study

**Additional Analyses** 

Prepared for: Portland General Electric Company

> Prepared by: T. Nightengale, A. Shelly R2 Resource Consultants, Inc. 15250 NE 95th Street Redmond, Washington 98052

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## **SUMMARY**

On April 1, 2016, the final report of the "Lower Deschutes River Macroinvertebrate and Periphyton Study Report" was filed with FERC by Portland General Electric (PGE) and the Confederated Tribes of the Warm Springs Reservation of Oregon for the Project. On May 23, 2016, the Oregon DEQ sent a letter to PGE regarding the results of the Lower Deschutes River Macroinvertebrate and Periphyton Study prepared for PGE by R2 Resource Consultants, Inc. (R2) (R2 2016). In the letter, Oregon DEQ acknowledged that the work reported "fills the basic expectations of the 401 Condition," but also believed the work had "serious shortcomings in the analysis of the macroinvertebrate data at several levels." Attached to the letter was a memo from Mr. Shannon Hubler of Oregon DEQ which outlined his concerns regarding the analysis and interpretation of the macroinvertebrate data collected for the study, and listed several recommendations.

The main purpose of this addendum to the 2016 "Lower Deschutes River Macroinvertebrate and Periphyton Study" was to address the concerns and recommendations of Oregon DEQ. The efforts documented in this addendum were conducted specifically to address the recommendations proposed by Mr. Hubler: to format pre- and post-SWW data sets into a single, consistent, and compatible flat file for the required analyses; to conduct an independent review of the taxonomic consistency between pre- and post-SWW datasets; and, to conduct additional analyses that will first standardize all samples to a 500-count subsampling effort, recalculate all metrics accordingly, and then run comparative univariate and multivariate analyses between the standardized pre- vs. post-SWW data and results.

The independent review by River Continuum Concepts (RCC) looked at baseline samples available from the first year of study (1999 and 2000). Unfortunately, a sample-by-sample review of the taxonomic efforts and accuracy was not possible. The unexpected presence of additional debris and specimens made it impossible to separate the original specimens from the additional ones that were unaccounted. Therefore, it was concluded that the samples found were not in the same condition as they were when originally analyzed. However, the exercise provided a broader assessment of the taxonomy employed on the baseline samples, which allowed RCC and R2 greater confidence when determining appropriate Optimal Taxonomic Units (OTUs) for comparison between the pre- and post-SWW data sets.

With the OTU list finalized, the final flat file was created, and the recommended analyses to apply standard subsampling effort adjustments and ultimately run univariate and multivariate tests on the resulting data sets. To obtain representative and compatible 500-count subsamples from greater subsampling efforts, we examined three different approaches in order to achieve simulated 500-count subsamples, and evaluated the potential biases that may occur. The primary advantage to conducting these simulations was that it provided comparable samples with equal subsampling efforts that allowed for statistical comparisons of taxa richness metrics. Results were similar, regardless of the simulation method. Final results indicated a slight increase in overall taxa richness, possibly attributed to a combination of more Trichoptera taxa, Diptera taxa, and non-insect taxa in the post-SWW period. EPT taxa richness as a whole did not significantly change, but Plecoptera alone registered a small average decrease in taxa post-

SWW, as did counts of Sensitive taxa. These decreases were small, but significant, highlighting that the macroinvertebrate communities have changed over the 12 years between studies. It is important to note that these changes in taxa richness are not large, though.

Univariate statistical comparisons between pre- and post-SWW metric results produced very similar outcomes, regardless of which simulation estimate method was used. The significant changes noted in the analyses of this addendum are also generally in agreement with those presented and discussed in the 2016 report. The exception is the tolerance-base metrics, which utilized the ATI scoring to assign "tolerant" and "sensitive" designations to taxa, and the FSBI, which became the measurement of sediment tolerance, each replacing the more subjective assignments previously used (Hafele and Mulvey 1998; OWEB 1999). LME results show that tolerances and the relative abundance of tolerant taxa increased in the post-SWW Spring periods, but remained unchanged in the Fall periods. These results are further supported by LME tests on community compositions, with a significant average 20-percent decrease in Chironomidae relative abundances, and a corresponding significant average 20-percent increase in the more tolerant non-insect taxa. Results generated by these additional analyses clearly indicate that number of changes in the macroinvertebrate community have occurred during the time from 2001 to 2013. Results also suggest that macroinvertebrate community in the Spring now favors more tolerant macroinvertebrate taxa.

Finally, the addendum addresses the multivariate analysis proposed as part of the Final Study Plan. Each of the NMDS test runs completed, with and without reference sites or onceoccurring taxa, produced the same basic trends and relationships that were shown and discussed in the 2016 report. NMDS biplots clearly show a distinct longitudinal community pattern, shifting from non-insect taxa predominating sample sites 1, 1S, and 3 immediately downstream of the Project, to aquatic insect taxa further downstream at sites 5 through 10. Each NMDS test run revealed an apparent shift from pre- to post-SWW period communities as well, with a larger shift apparent in the Spring, again highlighting the LME test results. This spatial separation is especially noticeable when reference sites are removed from analysis. However, it is also important to note that even within the reference sites, which are not affected by the SWW operations, there is a separation of pre- and post-SWW data points. This is even true of data at Site ME, on the Metolius River, where a small, but noticeable temporal separation can be seen. Thus, it is not unreasonable to conclude that the temporal shift in the benthic community could be due to changes unrelated to SWW over the 12 years between the two studies. These changes might include, for example, climate change and changes in land use practices in the upper basins of the Deschutes and Crooked rivers.

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## INTRODUCTION

In June of 2005, a new license was issued by the Federal Energy Regulatory Commission (FERC) for the Pelton Round Butte Hydroelectric Project (FERC No. 2030). Article 416 in this license requires the Joint Licensees to "conduct water quality monitoring pursuant to the Water Quality Management and Monitoring Plan (WQMMP) approved by the Oregon Department of Environmental Quality (Oregon DEQ) and the Confederated Tribes of the Warm Springs Reservation Water Control Board (CTWS WCB) as part of the water quality certifications issued by those agencies and attached to the license as Appendices A and B, respectively." One of the requirements for the Clean Water Act Section 401 Certification Conditions included in the WQMMP was that a macroinvertebrate and periphyton monitoring study be conducted following the implementation of selective water withdrawal (SWW) at the Round Butte Dam facility. During relicensing, a macroinvertebrate study was conducted in 1999-2001 to establish the baseline data to which comparisons could be made after the implementation of selective water withdrawal (Kvam et al. 2001, 2002). Section 6.2.6 of the WQMMP directs that the study be repeated (i.e., two Spring and two Fall sampling events) once a new equilibrium has been reached, starting three years after implementation of selective water withdrawal using the same methods and locations. Selective water withdrawal was initiated in late 2009. Post-SWW sampling was conducted in October of 2013, April/May of 2014, October of 2014, and April of 2015.

On April 1, 2016, the final report of the "Lower Deschutes River Macroinvertebrate and Periphyton Study Report" was filed with FERC by Portland General Electric (PGE) and the Confederated Tribes of the Warm Springs Reservation of Oregon for the Project. On May 23, 2016, the Oregon DEQ sent a letter to PGE regarding the results of the Lower Deschutes River Macroinvertebrate and Periphyton Study prepared for PGE by R2 Resource Consultants, Inc. (R2) (R2 2016). In the letter, Oregon DEQ acknowledged that the work reported "fills the basic expectations of the 401 Condition," but also believed the work had "serious shortcomings in the analysis of the macroinvertebrate data at several levels." Attached to the letter was a memo from Mr. Hubler of Oregon DEQ which outlined his concerns regarding the analysis and interpretation of the macroinvertebrate data collected for the study, and listed several recommendations.

PGE responded to those recommendations in a June 30, 2016 letter. In that letter, PGE acknowledged the Oregon DEQ comments, and agreed with Oregon DEQ that the macroinvertebrate report submitted to FERC meets the requirements of the 401 certification. PGE further stated that while they already met the conditions of the License with the final report filed April 1, they were also committed to conducting the best science so that regulators and stakeholders would have full confidence in the data provided, and therefore would address the recommendations made by Mr. Hubler. This addendum to the 2016 macroinvertebrate report is a summary of the additional work completed as per those requested Oregon DEQ recommendations.

# STUDY GOALS & OBJECTIVES

As was stated in the Lower Deschutes River Macroinvertebrate and Periphyton Study Report (R2 2016), the primary goal of the study was to provide a more comprehensive understanding of the ecosystem changes downstream from the Pelton Round Butte Project following the implementation of selective water withdrawal. The report was successful in revealing the overall spatial and seasonal trends in the benthic communities both above the Project and in the Lower Deschutes River below the Project. However, differences in field and laboratory methodologies complicated the pre-SWW versus post-SWW analytical comparisons that were to be made, especially involving metrics and analyses dependent upon taxa richness. As such, the recommendations listed by Mr. Hubler in his internal memo sent on May 16, 2016 largely focus on issues caused by these differences. The recommendations listed in the memo were as follows:

- All datasets, pre- and post-, need to be in consistent electronic format.
- Oregon DEQ should request an independent review of the taxonomic consistency between pre- and post- datasets
  - An independent taxonomy lab should examine preserved samples and verify identifications.
  - An independent review of taxonomic consistency across all samples should be completed.
- Oregon DEQ should request further analyses:
  - Subsample the data accordingly to make pre- and post- datasets comparable.
  - Recalculate all metrics (including updated, published tolerances).
  - Do a full multivariate comparison of pre- and post- SWW macro data.
- Oregon DEQ should request all the data from this study, for verification purposes.

As noted in PGE's June 30, 2016 response to Oregon DEQ, these recommendations have been addressed, and served as the basic objectives of the additional analysis efforts to be summarized in this addendum to the 2016 Lower Deschutes River Macroinvertebrate and Periphyton Study Report. Those objectives are:

- 1) Format pre- and post-SWW data sets into a single, consistent, and compatible flat file suitable for the required analyses and available for verification purposes;
- Conduct an independent review of the taxonomic consistency between pre- and post-SWW datasets using the the services of the taxonomic laboratory utilized for the post-SWW samples; and,
- 3) Conduct additional analyses by a) subsampling to a standardized 500-count effort, b) recalculating all metrics (including new tolerance metrics), and c) running comparative pre- vs. post-SWW univariate and multivariate analyses.

# SAMPLING SITES

### Post-SWW Sampling 2013-2015

The post-SWW sampling was based on the sampling effort conducted during the second year of baseline studies (Table 1). Sample sites included the 7 downstream sites where baseline analyses were completed in both years during the baseline study (1, 1S, 3, 5S, 7S, 9, and 10). Two additional downstream sites (Sites 12 and 13) were sampled at the request of reviewers in order to provide additional lower river reference sites well-removed from the area of SWW effects (Figure 1). Sample Site 12 (Sandy Beach) was added – this site was sampled during the first baseline year but not in the second. A new site was also selected downstream in the vicinity of Mack's Canyon (Site 13); however, this site has no pre-SWW comparison. The three above-Project reference sites (ME, DE, and CR) located above Lake Billy Chinook were also included for identifying any long-term changes in conditions independent of SWW effects.

			River	Pre-SWW		Post-SWW		Post-SWW
	Site	Depth	Mile	Yr 1	Yr 2	Yr 1	Yr 2	Sample type
	1	Deep	99.9	4+4=8	4+4=8	1+1=2 <sup>b</sup>	1+1=2 <sup>b</sup>	Composite
	1S	Shallow	99.9	4+4=8	4+4=8	4+4=8	4+4=8	Replicate
ರ	3	Deep	99	4+4=8	4+4=8	4+4=8 <sup>c</sup>	4+4=8 <sup>c</sup>	Replicate
oje	5s	Shallow	96	4+4=8	4+4=8	1+1=2 <sup>b</sup>	1+1=2 <sup>b</sup>	Composite
∧ PI	7s	Shallow	90.4	4+4=8	4+4=8	4+4=8	4+4=8	Replicate
	9	Deep	85	4+4=8	4+4=8	4+4=8	4+4=8	Replicate
ä	10	Deep	84	4+4=8	4+4=8	1+1=2 <sup>b</sup>	1+1=2 <sup>b</sup>	Composite
	12	Deep	45.5	4+4=8		1+1=2 <sup>bd</sup>	1+1=2 <sup>bd</sup>	Composite
	13	Deep	23.9			1+1=2 <sup>bd</sup>	1+1=2 <sup>bd</sup>	Composite
e	ME	Deep	Metolius R.	4+4=8	4+4=8	1+1=2 <sup>b</sup>	1+1=2 <sup>b</sup>	Composite
Po Vo	DE	Deep	Deschutes R.	4+4=8	4+4=8	1+1=2 <sup>b</sup>	1+1=2 <sup>b</sup>	Composite
A	CR	Deep	Crooked R.	0+4=8 <sup>a</sup>	4+4=8	1+1=2 <sup>b</sup>	1+1=2 <sup>b</sup>	Composite
	Total	Sites		11ª	10	12	12	
	Total	Samples		84	80	48	48	

Table 1.	Summary of macroinvertebrate sample	sites and	samples	collected	in pre- vs.	post-SWW
	study periods.					

<sup>a</sup> Crooked River sample was not included in first sample season.

<sup>b</sup> 500-count composite kick samples.

<sup>c</sup> Replicates also serve as control for gravel augmentation analysis.

<sup>d</sup> Value of replicated sampling at new site would be limited by lack of pre-SWW baseline data for comparison.



Figure 1. Sampling site locations for the Lower Deschutes Macroinvertebrate and Periphyton study.

## **Field Sampling**

Field sampling methods established in the baseline study were emulated during the post-SWW sampling. The baseline study collected 4 samples per site as per Oregon DEQ protocol, but unlike the protocol, samples were not composited for analysis. At four sites (1s, 3, 7s, and 9), this approach was maintained in post-SWW sampling, and four replicate kick samples were collected for macroinvertebrates (Table 1), which provided replicate samples to facilitate statistical comparisons. Each replicate kick sample consisted of one, two-foot square area

(consistent with the baseline). Lab analyses of these samples were based on a 300-count invertebrate subsample for each replicate sample (e.g., 4 per site).

At the request of the reviewers, composited kick samples were collected at the remaining eight sampling sites (1, 5s, 10, 12, 13, and the three reference sites) (Table 1). The composited kick sample consisted of the aggregate of four, two-foot square areas for consistency with the baseline sampling protocol.<sup>1</sup> Lab analyses were based on a 500-count invertebrate subsample for each site.

<sup>&</sup>lt;sup>1</sup> Oregon DEQ protocol has been changed from four, two-foot squares to eight, one-foot squares in order to reduce potential confounding effects of patchy habitat distributions. However, the Fish Committee recommended maintaining a consistent protocol to the baseline study for the post-SWW analysis.

## **METHODS**

#### **Formatting Data Sets**

All pre-SWW data from the baseline study from 1999-2001 was found in a series of spreadsheet files in a final format with total sample abundance of each taxon present in a. For the initial year (1999-2000), all samples were fully sorted and all specimens in a sample were identified and counted, therefore this information was complete. For the second year (2001), samples were subsampled using a 300-specimen fixed count; however, the final format did not indicate what the original 300-count subsample was, nor what fraction of the sample was processed in order to obtain the 300-plus subsample total. Additional archived data files were located that recorded the subsampling fraction of each sample from the Spring and Fall 2001 efforts, allowing for the conversion from its current format back to count data, and to further cross-check all conversions.

The baseline count data was then put in a format similar to post-SWW data from 2013-2015, so all datasets were compatible. This original count matrix format was necessary for the taxonomic validation effort, providing the independent laboratory with original count data for its validation assessment, as well as for making taxonomic adjustments to the taxa list and the assignment of Optimal Taxonomic Units (OTUs). Following the final assignments of OTUs, the data matrix was converted to a flat file database format using the Excel Query Editor and Pivot Table functions, with one line per taxon with a non-zero count for each sample at each site for each collection period, for a total of 7,200 data entries. This final format was necessary for simulating 500-count subsampling efforts later on in the analysis process, and subsequent metric calculations, which were performed using the statistical program R.

#### Independent Taxonomic Review

One of the comments made by Mr. Hubler in his Oregon DEQ internal memo sent on May 16, 2016 concerned the 2016 report's suggestion that the substantial pre- vs. post-SWW (selective water withdrawal) differences reported for oligochaetes may be due to poor preservation of pre-SWW samples, and/or an artifact of different taxonomists counting them differently. He maintained that such differences in processing and identification would then require all pre-SWW data to be re-assessed by the second (current) taxonomist, and inquired if any of the pre-SWW samples were retained. Additionally, Mr. Hubler noted that the datasets provided in the report's appendices showed a taxonomic inconsistency within the Oligochaeta families; namely that the family Tubificidae in the baseline data set was now included in the family Naididae in the post-SWW data set. He states, "Given the switch between labs for pre- and post-datasets, it is imperative that the datasets are rectified for taxonomic consistency." Therefore, one of the recommendations was that "Oregon DEQ should request an independent review of the taxonomic consistency between pre- and post- datasets," specifically that:

1) "An independent taxonomy lab should examine preserved samples and verify identifications" and

2) "An independent review of taxonomic consistency across all samples should be completed."

At the beginning of the post-SWW study, R2 had searched its storage areas for any archived samples or records of possible archiving of samples from the previous baseline study, but was unable to locate any of the samples. At that time, it was believed that all samples had been discarded, as is common practice with archived samples after a period of at least 5 years (Miller and Judson 2011; Plotnikoff and White 1996; USEPA 1995; Woodard et al. 2012). However, upon this request from Oregon DEQ and authorization by PGE, R2 initiated a more thorough search and on June 1, 2016 located what appeared to be the preserved samples from the first year of the baseline study (Fall 1999 and Spring 2000); no samples from the second year (2001) were found. However, R2 found no documentation regarding the existence of these archived samples, nor did any documents (chain-of-custody forms, notes, memos) describing the contents of the samples accompany them. The samples were found stored in snap-lid or screwlid prescription bottles; we also discovered additional vials containing the chironomid larvae from the 1999 samples. Sample bottles were examined for external and internal labeling, and overall condition; most still contained trace amounts of preservative liquid, but many were only moist, and a total of seven were completely desiccated. Therefore, at the time of discovery, both the source of the samples and the condition of their contents were questionable.

The samples were then inventoried and site labels were compared to those listed in the data and the report (Kvam et al. 2001). The site designations for the Spring 2000 samples matched those in the report, but the Fall 1999 samples appeared to be missing Sites 11 and 12, and contained extra site designations not noted in reports or data files (specifically, Sites 5A, 5B, 6A, and 6B). Without documentation, R2 initially assumed that these were additional sample sets, perhaps shallow and deep sets, for those sites. However, subsequent discovery of the field notes for the Fall 1999 trip revealed that the initial field collection efforts in October 1999 used a different site nomenclature. With this clarification, all of the samples could be matched to the site designations of the recorded data. A total of 131 samples were found corresponding to 4 samples per sampling trip at each the 17 sites; with the exception of Crooked River, which was not sampled in 1999, and had only 3 samples in 2000. At that time, the located samples ostensibly represented the same samples that had been analyzed previously.

To address Oregon DEQ's recommendation regarding taxonomy of the pre-SWW samples, R2 retained the laboratory used for the post-SWW study, River Continuum Concepts (RCC), to analyze the located samples. The objective of the analysis was to evaluate and compare the identifications resulting from the new analysis with those listed in the report. In accordance with Oregon DEQ's request, an initial nine (9) samples were selected for laboratory analysis to make a preliminary assessment of the utility of completing a more comprehensive re-analysis.

R2 selected sets of samples from the first year corresponding to the sites sampled for the post-SWW study in 2013-2015. This included samples from sites 1, 1S, 3, 5, 7, 9, 10, 12, DE, ME, and CR. Sample contents in snap-lid bottles were transferred to Nalgene bottles with screw-on caps to prevent sample loss during shipping. Sample lids were sealed with electrical tape, and double- or triple-bagged, as required by 49 CFR 173.4b for Scientific Research Specimens. R2 shipped 79 samples to the RCC laboratory. Additionally, R2 compiled all data from both the pre-SWW study (baseline study) and post-SWW study for reference when determining which of the shipped samples to select for the initial round of examinations.

R2 and RCC reviewed the taxonomy lists for the pre- and post-SWW sampling efforts, and flagged samples from Fall 1999 and Spring 2000, which either displayed high taxa richness (thus maximizing the number of taxa to assess), or contained commonly misidentified taxa warranted additional verification (e.g., oligochaetes, limpet snails, leuctrid stoneflies, elmid beetle larvae, and others). A total of nine samples (roughly 10-percent, rounded up) were selected for examination (Table 2), following the final work plan for these additional analyses proposed by R2. The laboratory counted all specimens present, and identified them generally to the same taxonomic levels used for the samples collected at the same sites in 2013-2015.

Table 2.List of the nine samples selected from the 1999 and 2000 baseline study samples for<br/>taxonomic evaluation.

Year	Month	Site	Sample Selected	Reason for Selection			
1999	Oct	DE	4	High taxa richness; Megaleuctra, Prodiamesa recorded			
1999	Oct	ME	2	Variety of EPT taxa; Moselia recorded			
1999	Oct	ME	4	High richness			
1999	Oct	1S	3	High oligochaete abundance (polychaete validation)			
1999	Oct	11	2	Initially believed to be Site 9, due to original labels			
2000	Мау	1S	1	High abundances of Amiocentrus, Fossaria/Galba, Orthocladiinae			
2000	May	3	3	High taxa richness			
2000	May	7S	4	High taxa richness			
2000	Мау	12	4	High taxa richness; diverse elmids, Psephenidae, high chironomid abundances			

Minor differences in condition or abundance are expected to occur when re-examining older samples due to sample degradation over time, or damage to specimens in the initial identification process. To minimize the influence on the similarity comparisons, several presence-absence similarity indices (Jaccard, Sørensen-Dice, and Ochiai) were applied by the laboratory to describe the overall agreement of the sample's current taxonomy with historic records (Ludwig and Reynolds 1988). Presence-absence indices should be less susceptible to shifts in abundance that may have occurred over time. These metrics range from 0 to 1, with 1 indicating identical compositions of historic data with a current re-assessment of the sample. Values of zero would occur when the two evaluations shared zero common taxa.

The laboratory also calculated the Bray-Curtis Index, a measure of similarity commonly used by ecologists (Legendre and Legendre 1998), as a secondary abundance-based similarity index. However, this metric is more prone to be affected by changes in abundance of each taxon, and therefore was not considered in regards to any decision threshold. Discussions with Oregon

DEQ set a preliminary threshold of 95-percent similarity in taxa identifications as the criteria of success. Based on these criteria, if the average similarity of the nine samples is less than 95-percent, or if any one sample is less than 85-percent similar, an additional 10-percent of the samples would need to be examined, and again assessed until either success is achieved as indicated by the above criteria, or all available baseline samples are processed.

### **Operational Taxonomic Units**

Upon initial review of the baseline samples, RCC identified specific taxonomic groups that were potentially misidentified but were underrepresented in the initial sample set. This included a closer look at Ephemerellidae mayflies, stoneflies from Leuctridae and Capniidae, craneflies (family Tipulidae), and limpets and snails. Careful review of an additional 6 samples was conducted specifically for those groups only. Results were used in developing a proposed set of OTUs to allow the optimal comparison with the historic dataset

R2 and RCC then created an overall taxonomic listing compiled from all samples, pre- and post-SWW. By basing the comparisons on the current taxonomic levels from the post-SWW study, results highlighted a number of potential differences between the two studies' data sets. Taxonomic adjustments were made using the information gathered from the resorted baseline samples, as well as RCC's professional judgement on a number of taxa or family groups where it was determined that there was not enough reliable information to support the lower level taxonomic identification. Ultimately, R2 and RCC adopted an OTU list to apply to the entire data set, which makes the baseline data comparable with the 2013-2015 study period.

#### **Data Analysis**

#### **Metrics**

Key biotic metrics included several identified in the Oregon DEQ's Level 3 protocol (Hafele and Mulvey 1998; OWEB 1999). At the request of Oregon DEQ, several tolerance metrics were replaced with peer-reviewed metrics. The modified Hilsenhoff Biotic Index (HBI) was replaced with the recommended peer-reviewed Assemblage Tolerance Index (ATI). Subsequently, other tolerance metrics (sensitive taxa and percent tolerant taxa) were also modified and based on the ATI score, instead of utilizing those defined by Hafele and Mulvey (1998). In addition, sediment tolerance was measured using the Fine Sediment Biotic Index (FSBI), instead of classifying taxa as tolerance or sensitive as defined by Hafele and Mulvey (1998). The following metrics were used in the analyses:

**Abundance** – The total number of individuals collected in a given sample. Density is calculated as the number of individuals per unit area (i.e.,  $m^2$ ). Density values could be calculated from the samples because each kick was obtained from a standardized sampling area (0.186 m<sup>2</sup>, or 2 ft<sup>2</sup>).

**Taxa Richness** – The total number of macroinvertebrate taxa present in each sample. This metric generally increases with increasing water quality and/or habitat diversity and is used as a relative measurement of the health of the benthic invertebrate community.

*Mayfly, Stonefly, and Caddisfly Richness* – The number of distinct taxa within the insect orders Ephemeroptera (mayflies), Plecoptera (stoneflies), and Trichoptera (caddisflies) were determined, often termed 'EPT taxa richness.' These orders are regarded to be relatively sensitive to pollution. Following Oregon DEQ Level 3 protocols (Hafele and Mulvey 1998; OWEB 1999), EPT taxa richness values were calculated separately rather than jointly for mayflies, stoneflies, and caddisflies. The separate taxa richness values generally increase with increasing water quality. Consequently, this is a widely used indicator of overall stream health.

**Community Composition** – The relative abundance of major taxonomic groups provides information on a stream community's structure and the relative contribution of the populations to the total fauna (Barbour et al. 1999). Eight major taxonomic groups were used to describe the community structure in our analysis: Ephemeroptera, Plecoptera, Trichoptera, Coleoptera (beetles), Chironomidae (midges), Diptera (true flies other than midges), Other Insects, and Non-insects. Composition measures of certain taxonomic groups are often used as indicators of impairment in streams. For example, Chironomid (midge) relative abundance can be used as a general indicator of organic or sediment pollution and impairment and provides a measure of invertebrate community balance (Barbour et al. 1999). Samples that have a disproportionate number of Chironomidae may indicate environmental stress, as midge larvae are often tolerant to sedimentation and nutrient enrichment.

**Assemblage Tolerance Index Index** – The Assemblage Tolerance Index (ATI) is used to portray the tolerance of the benthic invertebrate community to overall human disturbance as a single value (Whittier and Van Sickle 2010). Tolerance values range from 1 to 10, with 1 describing very little or no tolerance to overall human disturbance and 10 describing a very high tolerance. The ATI is calculated as:

#### $ATI = \sum x_i t_i / n$

Where  $x_i$  is number of individuals within a given taxon,  $t_i$  is the tolerance value for this taxon, and n the total number of organisms in a sample.

**Sensitive Taxa** – This is the number of taxa in each sample that are known to be very sensitive to stream disturbance. For comparability of post-SWW samples with baseline study results, the tolerance ratings were determined for each taxonomic group based upon the taxa's ATI score. Those taxa with a tolerance value of 3 or less are classified as "sensitive" taxa.

**Percent Tolerant Taxa** – This is the percentage of all invertebrates present in a sample that are considered to be tolerant to disturbance. In contrast to metrics that describe the presence of sensitive species, tolerant species are likely to be found at all sites, including the most pristine or undisturbed sites. For comparability of post-SWW samples with baseline study results, the tolerance ratings were determined for each taxonomic group based upon the taxa's ATI score. Those taxa with a tolerance value of 7 or greater are classified as "tolerant" taxa.

**Percent Dominant Taxon** – This metric is the percent contribution of the numerically most dominant taxon to the total number of invertebrates present in a sample. A community

dominated by one species may indicate high levels of nutrient enrichment (high invertebrate density levels), or the presence of toxic contaminants (low invertebrate density levels).

**Fine Sediment Biotic Index** – The FSBI is a regional, stressor-specific biomonitoring index to assess fine sediment (<2 mm) impacts on macroinvertebrate communities in northwestern US streams (Relyea et al. 2012). Taxa which exhibit some sensitivity to fine sediment are classified into four categories with weighted scores: extremely (20), very (15), moderately (10), and slightly sensitive (5). The FSBI score is calculated by summing the sensitive taxa found in a stream, with lower scores indicating more fine sediment influence. Rare taxa and taxa identified at coarse taxonomic levels, including Chironomidae and most non-insect taxa, are excluded from the FSBI.

*Functional Feeding Group Classification* – Each aquatic invertebrate taxon was placed in one of six functional feeding groups, which identify the trophic status (i.e., food requirements) of a particular taxon. The functional feeding group categories that were employed in our analysis were: 1) grazers (or scrapers), which feed on attached algae or periphyton; 2) shredders, which feed on coarse particulate organic matter (CPOM) such as leaves; 3) collectors, which feed on fine particulate organic matter (FPOM) deposits; 4) filter feeders, which feed on FPOM within the water column; 5) predators; and 6) omnivores, which feed on a variety of materials. Invertebrate functional food groups were determined from the literature, including classifications provided for invertebrate genera by the EPA (Barbour et al. 1999). The percent of organisms belonging to each functional feeding group reflects the type of food base that may be determining the composition of invertebrate taxa in a river or stream. For example, a high grazer to filter feeder ratio is indicative of an aquatic ecosystem in which periphyton is the most abundant source of food for the invertebrate community (Klemm et al. 1990). In contrast, a low grazer to filter feeder ratio is indicative of an aquatic ecosystem where FPOM is the most important source of energy to the aquatic invertebrate community.

#### Compositing and Equalizing Sampling Effort

The first step in the re-analysis was to manually composite all individual samples for any sites where individual samples were collected, and to expand all subsampled samples to estimated full counts. This process puts all samples into equivalent units and allows for comparisons. These samples comprise the best estimates available for abundance metrics for each site/period combination. However, metrics based on richness are not comparable across samples when they are based on different subsample totals. Three potential processes for estimating sample metrics with these different sampling designs are:

 Full composite: Use the full-composite sample metric values for all metrics that do not depend on the number of observed taxa. Use the expected number of observed taxa under an exact 500-count subsample (rarefied estimate) for metrics requiring this estimate.

- 2) **Single 500-count**: Select a single random sample of exactly 500 organisms from all samples that were not already 500 subsample composites, and treat this simulated sample as though it was the observed sample.
- 3) 500-count simulation: Simulate the laboratory process used to conduct 500-count subsamples all samples that were not already 500-count subsample composites. The average result from 1000 simulations is a good approximation of the most likely outcome if 500-count subsamples were done in the lab.

When trying to estimate abundance of a single taxa in a sample, the best estimate of that number would come from a complete count or the highest subsampling level available. This is also true, then, of any metric dependent on abundance, including total abundance, all relative abundance metrics, and indices based on abundance (e.g., FSBI). If different samples have differing levels of precision, this can be a violation of assumptions for statistical comparisons that assume equal variance. However, using a less accurate result based on simulating a subsample is more likely to impact conclusions. In this report, the full composite results are considered the true sample results for all abundance-based metrics. When statistical comparisons are performed, results for the three methods described above are presented, and differences discussed.

Estimates of taxa richness (and all richness-dependent metrics) based on incomplete sample counts are biased estimates of total taxa richness in a full sample, with the amount of bias related to the number of species truly present in the sample and the percent of the total number of invertebrates that are counted. Thus, samples with a different proportion of total invertebrates actually counted differ in the amount of bias (Chao and Jost 2012). Although it doesn't completely equalize the bias, the common method for standardizing richness metrics based on different sampling levels is to estimate the number of taxa expected under equal sampling effort at the lowest sampling effort used.

For each sample, we provide three estimates for taxa richness and richness-based metrics: 1) based on the statistical expectation from an exact 500 count (rarefaction estimate); 2) based on a single simulated exact 500-count sample (single 500-count); and 3) the average number of taxa observed in 1000 simulated 500-count subsamples (simulation; counts greater than 500, but within 20-percent of the target count, based on a simulated laboratory process). Of these, the simulation result provides the most realistic and stable estimate for a 500-count subsample as performed by a processing laboratory. A single simulation (like any sample) could be less than or greater than this result, but this mean estimate gives the best representation of the sample (using all sample information in the full sample) at a reduced sampling effort. The rarefaction estimate is also an estimate of the mean that uses all of the sample information available, but it is based on an exact 500 count which rarely, if ever, actually happens in practice. Thus, these results are biased low compared to actual 500-count subsample results performed by a laboratory. Although it is provided here for completeness, a single simulated

500-count subsample is not recommended for comparisons because it is adding an unnecessary source of variability to the process – simulation variance – and could provide errant results.

<u>Rarefaction Estimate</u> – To estimate expected richness metrics for a 500-count subsample composite based on exactly 500 specimens for each sample, we used the "rarefy" function in the vegan package for R (Oksanen et al. 2017; R Core Team 2016). The "rarefy" function provides the expected value and standard error of a multinomial random variable sampled from a known distribution with an exact 500 count. To use this function, unidentified OTUs first had to be re-portioned into identified OTUs based on proportions of OTUs observed in each group (see Appendix A for OTU information). For example, Unidentified Baetidae were assigned to one of the four baetid OTUs that were observed in the study, depending on the proportion of each OTU observed at the site. These expanded, reportioned counts were also rounded to be integers as a requirement for the function.

The "rarefy" function cannot provide a direct estimate of expected richness of subgroups of taxa (e.g., EPT taxa richness) because the subsampling level is not controlled at the subgroup level. However, if the subgroup comprises a small proportion of the entire sample, we can assign all OTUs outside of the subgroup to a single new OTU, run the rarefy function on this new set of OTUs, assume the "other" OTU is observed in all samples, and subtract one from the estimated rarefied subgroup taxa richness.

<u>Single 500-Count</u> – To generate a single, random sample with an exact 500 count, we used the "rrarefy" function in vegan (Oksanen et al. 2017), on the expanded (but not reportioned) data set. Thus, unidentified OTUs can arise in the random realization. Note that there is no estimate for total abundance based on this single 500-count sample generated by the simulation (the original sample total abundance was used for this estimate in all cases.) Also, there was one sample at the DE site (Spring 2000) that was not rarefied nor randomized at the 500 count because only 394 total specimens were counted in this sample.

<u>500-Count Simulation</u> – The rarefy estimation of expected counts of each OTU under an exact 500 count does not account for the inherent variability in counts which results from actual subsampling processes in the lab. Because lab processes vary and are often adapted depending on sample characteristics, it is not possible to emulate exact methods. However, we can simulate a process that is similar to what the lab would do under the standard practice for a 500-count subsample. We simulated the lab process that would be conducted with a Caton tray (Caton 1991), beginning with spreading the sample as evenly as possible in a tray with 30 divisions. A random 1/30th portion is selected from the tray, and placed in a dish subdivided into 4 subsections, thus sampling 1/120<sup>th</sup> at a time until a count of 500 is reached. The final section is completed in its entirely, thus producing a result usually exceeding 500. The following were the steps in the simulation process:

1) Generate a random subsample size for each (site/season) sample by first dividing the sample estimated total abundance (expanded count) into 120 "cells" using a random

realization of a multinomial random variable with the probability of landing in each cell having a mean of 1/120 = 0.0083. Because the actual probability for landing in each cell depends on how well the sample was mixed and the size and composition of the bugs in the sample, we added random variability to the cell probabilities based on a truncated normal distribution, allowing the probabilities to range from 0.001 to 0.02. This added variability was found to provide reasonable average and variability in rates of total counts in a 500-count subsampling process. The random subsample size is then found by randomly summing cell sizes until 500 is reached and exceeded.

- 2) Sample the required number of invertebrates randomly without replacement from the site/season sample, and estimate all metrics.
- 3) Repeat steps 1 and 2 1000 times, saving all metrics.

The simulations were run on the expanded (but not reportioned) data for only pre-and post-SWW sites for which site/period samples were not already 500-count subsample composites.

The full list of metrics were estimated on the full composite samples, the single 500-count sample, and each of 1000 simulated samples. For statistical comparisons based on the full composite samples, the taxa richness metrics were based on the results of rarefy. For statistical comparisons based on the single 500-count samples, total abundance was not tested, as it could not be estimated directly from this sample. Statistical comparisons based on simulations used the average of 1000 simulated metrics for each site/period sample.

#### Univariate Statistical Comparisons

Statistical analyses have been performed where sample replication was sufficient to allow for statistical comparisons. The analyses were run on a select subset of the calculated benthic metrics. Only those sites below the Project that were consistently sampled in both studies (Sites 1, 1S, 3, 5S, 7S, 9, and 10) were included in comparisons of pre- and post-SWW metrics.

Statistical comparisons were based on linear mixed models (LME; also known as repeated measures analyses of variance [ANOVA]). The model was first run on all data, including season and period as the fixed effects (the repeated measures are on site) with years as the replicates at each site. If there was evidence of interaction between period and site (post-LME ANOVA F-test p-value < 0.10; indicating that pre-post results may differ by season), the seasons were individually evaluated. P-values for pre- to post-SWW comparisons are reported for interpretation.

The analysis was run on three different data sets, as follows.

 Full Composite: Metrics calculated for full composite samples for each site (Appendix II Tables 1 through 8). For this data set, the taxa richness metrics for all replicate sample composites are based on the rarefaction estimate for a 500-count subsample (i.e., using vegan function "rarefy"). Results from samples already subsampled to a 500-count level are retained for this data set, to avoid theoretical bias. This is the most accurate data for abundance metrics, based on most complete data. However, the FSBI index cannot be estimated using the rarefaction function, and is not included in this analysis.

- 2) 500-count Simulations: The second data set is metrics calculated on the average of 1000 500-count simulations. All metrics were estimated for these simulations, but note that abundance metrics may be less accurate than for the full composite sample. Richness metrics for this data set are more realistic than the rarefaction results because they are based on variable counts greater than 500.
- 3) **Single 500-count**: This is a single simulation of an exact 500 count sample. It is likely to be both less accurate and less precise than the other two methodologies for all metrics. It is included only for completeness.

Several EPT macroinvertebrate taxa of particular interest to salmonids were also examined for significant changes from pre- to post-SWW periods. These taxa include the Giant Salmonfly (*Pteronarcys*), Golden Stone (*Hesperoperla*), net-spinning hydropsychid caddisflies (*Hydropsyche* and *Cheumatopsyche*), saddle-cased caddisflies (*Glossosoma* spp.), spiny crawler mayflies (*Ephemerella* sp. and *Serratella* sp.), flatheaded mayflies (*Rhithrogena* and *Epeorus* sp.), *Antocha* sp. craneflies, Oligochaetes, and *Vorticifex* snails. The same LME model was also applied to expanded sample abundance for these 12 important individual taxa.

#### Multivariate Community Analysis

Multivariate analysis of species composition data is used to evaluate overall differences in community composition across sites using visual comparisons in a reduced number of dimensions. Non-metric multidimensional scaling (NMDS) was used to evaluate multivariate distances among samples during the Spring and Fall season separately. The function "metaMDS" in the vegan package in R (Oksanen et al. 2017; R Core Team 2016) was used to conduct the following steps for each NMDS analysis.

- 1) Transform the counts using square root transformation and Wisconsin double standardization if reasonable. The Wisconsin double standardization transforms the counts to relative abundances both across sites and across species, by dividing each data value by the species maximum and the site maximum.
- 2) Calculate the Bray-Curtis dissimilarities among samples.
- 3) Perform NMDS with multiple random starts and return the solution with the lowest stress value. Stress is a measure of goodness-of-fit for the NMDS.
- 4) Rotate the selected NMDS solution so that the largest variance of scores is on the first component axis.

- 5) Scale the solution using half-change scaling.
- 6) Calculate the species scores (average of site scores weighted by the species abundance at each site) and expand the species scores to have equal variance to site scores for plotting together.

The NMDS results are based on the **full composite** samples for all sites with pre- and post-SWW data. Although these composites are based on differing subsampling levels, the standardizations used for the NMDS analysis adjusted for most impacts of the differing sampling levels. Some bias is still possible, based on species richness differences across unequally sampled sites. To evaluate the possibility of such bias, the multivariate analysis was also run on the **single 500-count** simulation used for univariate analyses. Because there are many possible compositions of random 500 counts from the larger composite samples, a single selection of exactly 500 organisms could have different characteristics from the complete sample. Therefore, differing results between these two (real unequal versus random equal sampling) would indicate uncertainty in conclusions, but neither result could be interpreted as superior.

Rare species can sometimes have undue influence on multivariate analyses based on reduced dimensionality. To evaluate the impact of rare species, multivariate analyses were also run without OTUs that occurred in only one or two samples.

Statistical testing of multivariate results (e.g., is the pre- to post-SWW change in community composition statistically significant?) is usually done via permutations. The compositing of all individual samples for this report has resulted in a small dataset with only samples collected in different years comprising replicates of pre- and post-SWW conditions at each site. There are only three ways to permute the four years of samples into two groups, so no statistical test via permutations is sensible. Instead, the final two NMDS axes estimated for full composite samples without reference sites were statistically tested for changes from pre- to post-SWW using a paired t-test. The pre- to post- change in each axis was also tested for correlation with longitudinal location relative to the project, using Spearman's rank correlation coefficient applied to distance from the project versus the magnitude of the change.

## RESULTS

### Independent Taxonomic Review

The re-examination of the nine samples presumably from the first year of the baseline study revealed a number of deviations from the original data sets that proved problematic for successful comparisons. Seven of the nine samples evaluated returned more individuals than were originally recorded in the data, and many of these contained significant amounts of extraneous detritus (Figure 2). Several samples also included a number of empty snail shells, calling into question whether these were counted as specimens or included for other reasons.

Counted portions of processed invertebrates are expected to be generally "clean," containing only counted and identified specimens with minimal debris, and should generally have the approximate number of specimens reported in the data, with an allowable shortage due to degradation over time (desiccation, biodegradation, physical losses), or possible unrecorded removals for voucher specimens. Instead, seven samples contained 2.6-percent (31) to 24.4percent (372) more specimens than the recorded data indicated, with an overall average of 12percent (128) extra specimens (Figure 3). The remaining two samples returned shortages of 31 and 124 specimens, accounting for 92.4-percent and 88.3-percent of the recorded totals, respectively.



Figure 2. Detritus found in a picked baseline sample 1S-3 from the Deschutes River, Fall 1999.



Figure 3. Abundance of the re-sorted samples expressed as a percentage of the original taxonomist's assessment of the sample.

Given these differences, comparisons of the taxonomy for each sample, based on the current taxonomic levels from the post-SWW study, scored well below the 95-percent similarity threshold (Figure 4). For the Jaccard Index (JI), the nine sample scores ranged from 0.38 to 0.73, averaging 0.56. For the Ochiai Index, which is similar to the Jaccard but based on Harmonic averages, scores were higher, ranging from 0.55 to 0.85, and averaging 0.71. For the Sørensen-Dice Index, which is similar to the Jaccard but based on geometric averages, scores ranged from 0.55 to 0.84, averaging 0.71.

The Bray-Curtis Index scored closer to 90-percent for most sites than the other indices, ranging from 0.27 to 0.91 and averaging 0.75, but exceeded 90-percent for only the one sample (Figure 4). The Bray-Curtis Index generally scored higher than the presence-absence indices because the dominant taxa were usually correctly identified. However, occasionally, this was not the case. For instance, the sample selected from Site 3 had many snails (approximately 400) that represented a different species than what had been originally reported, along with 224 flatworms (Planariidae) that were unaccounted for in the sample. This difference resulted in a reduced Bray-Curtis Index of similarity.

Because most of the examined samples containing extra specimens returned multiple differences, it is impossible to qualify whether those differences came from specimens originating from the original counted specimens (i.e., a specimen was misidentified), or



Figure 4. Similarity index scores for the unadjusted taxonomic data, based on the current taxonomic levels from the post-SWW study.

whether it is a new specimen that the original taxonomist never saw and therefore could not have identified. In this type of comparison, it is generally assumed that both taxonomists are examining the same specimens. In this case, this assumption may be inaccurate, for at least part of some of the samples. Re-identifying old samples often raises more questions than can be answered because the results are never identical and the secondary investigator never sees exactly what the initial investigator saw. The condition of the samples invariably degrades over years and decades. This was certainly a factor in this case, as most samples, when discovered, had little to no preservative remaining, and several samples were desiccated or degraded

Additionally, specimens are sometimes removed for consultation or workshops and don't get returned to the original sample, and the removals are not documented. This possibility certainly exists for the 1999 and 2000 samples because some of the missing taxa are often large and conspicuous. For example, the original taxonomist found *Pteronarcys* sp., in a sample from DE in 1999, but RCC did not find them. These specimens were not likely to be misidentified by either party and should have been readily apparent. The fact that *Pteronarcys* were not present in the taxonomic review dataset indicates something within the sample has changed. Perhaps they were large pristine specimens moved to a reference collection, or instead, they were small immature specimens which had degraded beyond recognition; it is unknown.

Many of the differences found were often differences in the assignment of specimens to different taxonomic levels based on procedures followed by individual taxonomists. For example, many of the immature Perlodidae of 1999-2000 were correctly identified to family level. However, the current laboratory was able to identify some of them to genus level based

on modern knowledge of some inner mouth parts. This alone would cause enough differences in taxonomic determinations to affect the similarity indices, even though both taxonomists were correct. In fact, the response of the Jaccard Index for just one error (two deviant taxa) suggests that 95-percent agreement cannot occur in the range of richness observed in with the samples examined, even if only one odd species is in disagreement (Figure 5). Therefore, this criterion for the Jaccard Index was generally not attainable with the baseline samples examined. The 95-percent threshold is attainable for one error using the Sørensen-Dice Index, but only with samples containing  $\geq$ 21 taxa.



Figure 5. A simulation showing the effect of one error (2 deviant taxa) on the Jaccard Index and Sørensen-Dice Index with differing taxa richness levels for a sample.

For these reasons, R2 and RCC concluded that the samples found were not in the same condition as they were when originally analyzed. With the unexpected presence of additional debris and specimens, it was impossible to separate the original specimens from the additional ones that were unaccounted. However, the exercise provided some insight into the identifications made by the original taxonomist proved useful in determining appropriate OTUs required for the planned statistical comparisons of the pre-versus post-SWW samples. Therefore, R2 and RCC proposed that no further samples be evaluated, and the evaluation of the baseline samples focus on a results-oriented analysis to derive optimized OTUs for comparison between the two Deschutes River datasets (Kvam et al. 2001; R2 2016), and not a cycle of re-examining each taxon, due to the identified differences and related uncertainty.

This assessment was provided in a TM to PGE and Oregon DEQ for review and comments. In a March 6, 2017 communication from Mr. Hubler, and a March 7, 2017 meeting with Oregon DEQ regarding the TM, it was recommended that no further identification work be done, and that

the information gathered be used to rectify the differences between the pre- and post-SWW taxa lists to produce a common list of optimized OTUs.

### **Operational Taxonomic Units**

The combination of all taxa from the pre- and post-SWW studies resulted in 228 different taxa designations. Several of these designations had considerable overlap, with mostly unidentifiable family-level identifications (often termed parent-level) existing alongside finer genus or species level identifications (children level). We also found several taxa listed that had no counts attributed to them; these were automatically removed.

Using the information from the independent taxonomic review stage, R2 and RCC adopted a final list of 109 OTUs to use for the complete data set. The final list of OTU can be viewed in Table 1 of Appendix I. A total of 12 parent-level taxa (11 at the family level, 1 at the order level) were retained due to a large number of immature or damaged specimens in those groups, with the understanding that further steps in the analysis would be apportioning these parent levels into the children levels.

RCC's professional judgement was applied to a number of taxa or family groups where it was determined that there was not enough reliable information to support the lower level taxonomic identification. We had high confidence that specimens of the mayfly *Drunella doddsi* were consistently identified correctly; however, other *Drunella* species are difficult to identify if specimens are damaged or immature, so they were grouped into the *Drunella "not doddsi"* OTU group. We made multiple attempts to confirm Leuctridae specimens identified in the pre-SWW samples, but found none. Leuctrid stoneflies are typically found in smaller springs and tributaries, so it was highly unlikely such taxa were present. Instead, RCC noted that Leuctridae and Capniidae stoneflies are commonly confused during identification, with they were able to confirm. Therefore, Lecutridae were reclassified with Capniidae as an OTU. Other decisions made for OTUs:

- Pre-SWW samples displayed a large amount of Unidentified Perlodidae. This is a difficult family to identify to genus level, especially with immatures and damage specimens. The OTU was left at Perlodidae (family level).
- Pre-SWW samples were inconsistent with identifications of *Rhyacophila* to the species or species group levels. The OTU was left at *Rhyacophila* sp.
- Pre-SWW samples were inconsistent with identifications of Limnephilidae to the genus level. Family level is more reliable.
- Pre-SWW samples were inconsistent with identifications of Elmidae to the genus level. Family level is more reliable.
- Pre-SWW samples were inconsistent with identifications of Empididae to the genus level. Family level is more reliable.

- Pre-SWW samples were inconsistent with identifications of Oligochaeta families. Taxa were combined into one "Oligochaeta" OTU.
- Pre-SWW samples were inconsistent with identifications of Hirudinea (leech) families. Taxa were combined into one "Hirudinea" OTU.
- Unable to locate or identify any pre-SWW specimens of limpets (Ancylidae, *Ferrissia*, *Fisherola nuttalli*). Taxa were combined into a "Limpet" OTU group.
- In the 1999 samples, snails identified as *Fossaria/Galba* were primarily *Juga newberryi*.
- In the 2000 samples, snails identified as *Fossaria/Galba* were primarily *Fluminicola* spp.

#### **Recalculated Metrics**

Following the application of OTUs to all datasets, metrics were recalculated using the three different subsampling approaches discussed in the Methods section "Compositing and Equalizing Sampling Effort." Metric summary results for pre-SWW and post-SWW collections can be viewed in Appendices II through IV. Each Appendix provides metric results for one of the three approaches.

For the purposes of this addendum, results are limited to metrics that are new (ATI and FSBI) or were calculated differently from the 2016 report (taxa richness, EPT richness, sensitive taxa). Additional figures of the new or changed metrics for pre-SWW and post-SWW collections are included in Appendix V for further reference.

#### Taxa Richness

Taxa richness measures were estimated in three different ways: rarefaction estimate, single 500-count estimate, and the 500-count simulation estimate. The three estimates were compared to the original total richness for the composited samples reported in the 2016 report (Figures 6 and 7; Appendix V Figures 1-4). When comparing estimates, it is important to note that total taxa richness estimates differed by effort, depending on the year of sample collection. Samples from 1999 and 2000 reflected a total sample sort effort, therefore all taxa from the combined 4 samples were part of the taxa richness estimates. Samples from 2001 collections were based on the combination of 4 samples with 300-count subsamples, averaging around 1,200 specimens. Samples in 2013-2015 were either 500-count composites of 4 samples or the combination of 4 samples, as in 2001.

Estimates of total taxa richness during the first year of the pre-SWW study (1999 and 2000) showed a noticeable reduction in number of taxa counted from full sampling efforts in all three methods. Differences in total taxa from full sorted samples ranged from 0 to 16 less taxa and averaged from -9.35 taxa for simulation estimates to -9.75 taxa for the rarefaction estimates. All three estimation methods returned similar results, and maintained the same spatial trends as the total sort data, with lower taxa richness immediately below the dam, and gradually



Figure 6. Comparison of 4 different taxa richness estimates at sites in the lower Deschutes River downstream from the re-regulation dam and three reference sites for the pre-SWW period of 1999-2001. Error bars provided for the rarefaction estimates represent ±1 standard error of the rarefaction mean.



Figure 7. Comparison of 4 different taxa richness estimates at sites in the lower Deschutes River downstream from the re-regulation dam and three reference sites for the post-SWW period of 2013-2015. Error bars provided for the rarefaction estimates represent ±1 standard error of the rarefaction mean.
increasing downstream (Figure 6). Estimates from 2001 displayed less of a reduction, with taxa counts reduced from 1 to 8.9 taxa, and averaging from -5.3 taxa for single 500-counts to 5.9 for rarefaction estimates. Again, all three estimate methods present similar taxa richness estimates and follow the spatial trends of the combined replicate estimates closely (Figure 6).

Post-SWW sampling was conducted with 500-count composites at 8 of the 12 sites, with only 4 sites (1S, 3, 7S, and 9) maintaining separate replicates that were combined for a composite estimate. These four sites exhibited more variability in taxa richness among the estimation methods used (Figure 7). Sites 1S, 3, 7S, and 9 had 0 to 11 taxa less, and averaged from -5.4 taxa for single 500-count estimation to -7.6 taxa for rarefaction estimates. Original composite taxa richness estimates were used in place of simulation estimates at these 8 sites, as is evidenced by the overlap for those sites (Figure 7). When these 500-counts results from the lab were adjusted to a single-500-count or based on rarefaction methods, taxa richness for those sites was reduced from 0-7 taxa, with an average of -3.125 taxa for single 500-count estimation, and -3.8 taxa for rarefaction estimation. Application of these methods to total taxa estimates based on 500-count lab samples produces results that are theoretically biased, because the total taxa estimates are biased low depending on the subsampling level. For example, if the lab 500-count is estimated to be ¼ of the total sample, there is undoubtedly taxa that were in the sample that were not observed. These unobserved taxa, then, cannot be considered by the rarefaction estimation, and the rarefaction result is biased low. Rarefaction estimation produced the lowest estimates in taxa richness among the 4 estimates examined (Figure 7).

Despite differences in taxa richness estimates among the three estimation methods, all approaches maintained the same spatial trends as the total sort data. As was seen in 2016 report results, taxa richness during both seasons showed lower numbers of taxa immediately downstream from the Project (Sites 1 and 1S), with a gradual increase in taxa numbers downstream to Site 9 and 10 (Figures 7 and 8). Taxa richness decreases slightly at Sites 10 and 12, with an increase again at Site 13 in Fall sampling. For the upstream reference sites, taxa richness at the ME reference site was generally higher than the DE and CR sites for all visits, with the exception of Spring 2001 (Figures 6 and 8), and Fall 2014 (Figures 7 and 8), when DE taxa richness was equal to or exceeded ME taxa richness.

EPT Richness and Sensitive Taxa Richness also show similar results amongst the different estimation methods and the original full composite results (Appendix V Figures 1-4). Plotting the results of EPT and sensitive richness using results from simulation estimations, spatial trends are similar to those seen for total taxa richness (Figures 9 and 10). For the upstream reference sites, the ME reference site recorded higher numbers of sensitive taxa all other sites during all 8 collection periods (Figure 10).



Figure 8. Taxa Richness in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies using simulation estimation results.



Figure 9. EPT Taxa Richness in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies using simulation estimation results.



Figure 10. Sensitive Taxa Richness in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies using simulation estimation results.

#### **Tolerance Measures and Indices**

Tolerance metrics differed little among the different 500-count estimation methods. ATI metric score results differed 0.1 or less among the data sets. Percent tolerant taxa results differed by less than 1-percent between full and simulated estimations, but the single 500-count estimates differed from other data sets by up to 5-percent for some samples likely due to the single random selection. Likewise, FSBI scores varied by up to 30 points between the simulation and single 500-count estimate data sets, highlighting the difference of averaging 1000 simulation samples versus selecting a single random 500-count result.

ATI metric scores at the lower Deschutes River sites were generally 6.0 or less, with increased scores at the sites immediately downstream of the Re-regulating Dam in the Spring (Figure 11). During the pre-SWW period, ATI scores at lower river sites averaged 5.44 in the Fall, and 4.53 in the Spring. Reference site ATI scores were similar in both seasons, averaging 3.95 in the Fall and 3.81 in the Spring. For the post-SWW period, ATI scores in the lower river in the Fall remained similar to pre-SWW levels, averaging 5.67. However, Spring ATI scores in the lower river increased slightly, averaging 5.26. For reference site during the 2013-2015 period, ATI scores remained unchanged at the ME site, ranging from 3.16 to 3.8, similar to pre-SWW scores. Scores at DE and CR showed increases from the pre-SWW period, especially at CR, which recorded ATI scores of greater than 7 in the Spring periods (Figure 11).

Percent tolerant taxa (the relative abundance of those taxa with ATI scores of 7 or greater) shows that the contribution of tolerant taxa is generally greater in the Fall than in the Spring period. Pre-SWW levels for lower river sites averaged 46.6-percent in the Fall, and 16.7-percent in the Spring. Post-SWW levels for lower river sites in the Fall were similar to pre-SWW, averaging 46.0-percent (Figure 12). Average post-SWW contributions of tolerant taxa at lower river sites in the Spring increased to 30.4-percent. For the upstream reference sites, the relative abundance of tolerant taxa remained low at ME, with a slight pre- to post-SWW increase in the Spring (average of 2-percent vs. 6.5-percent); however, DE and CR both showed post-SWW increases in percent tolerant taxa, especially at CR in post-SWW Spring sampling, with recorded relative abundances of approximately 80-percent tolerant taxa (Figure 12).

The FSBI results generated by the simulation estimation method generally show trends similar to taxa richness metrics, with scores at the lowest levels immediately downstream of the Reregulating Dam (Sites 1 and 1S), and gradually increasing downstream to Site 10, with lower scores at Sites 12 and 13 (Figure 13). Pre- to Post-SWW comparisons in FSBI scores for lower river sites indicate that scores in the Fall dropped slightly from an average of 68.8 to 60.0; in the Spring, the average FSBI dropped from 89.5 pre-SWW to 75.2 post-SWW (Figure 13). For reference sites above the Project, ME displayed the highest scores, ranging from 135 to 160 during the pre-SWW period, and from 135 to 137.5 during the post-SWW period, indicating the presence of many sediment sensitive taxa in the Metolius River. FSBI scores at DE and CR were markedly lower than ME, with DE ranging from 75-100, and CR scoring 50 or less (Figure 13).



Figure 11. Assemblage Tolerance Index (ATI) scores in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies. Lower scores indicate healthy stream conditions.



Figure 12. Relative abundances of benthic invertebrate taxa classified as "tolerant" (ATI >7) in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies.



Figure 13. Fine Sediment Biotic Index (FSBI) scores in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies. Higher scores indicate more sediment-sensitive taxa present. Results based on simulation estimation data set.

### Pre-SWW vs. Post-SWW Univariate Comparisons

The LME analysis for each metric modeled annual site-specific results as a function of "season" and "pre-" versus "post-SWW" groups. The model used "site" as a random effect, and "years" within periods as replicates. Statistical results for the three data sets analyzed are included in Tables 3 through 5 and summarized briefly below. The discussion focuses on results for full composite samples for metrics not based on taxa richness (Table 3), and for average simulation results for metrics based on taxa richness (Table 4), but results were similar for the three methods, and all are provided for reference. The p-values in the tables are for ANOVA F-tests conducted on the LME model. Statistical results for pre- versus post-SWW abundance estimates for 12 individual taxa of interest are provided in Table 6. Additional graphs depicting density, taxa richness metrics, and tolerance metrics are included for reference in Appendix V Figures 5-11.

#### Density

Univariate analysis of total density estimates indicates a statistically significant increase of approximately 12,000 individuals/m<sup>2</sup> in the post- versus pre-SWW years for the Fall sampling period only (Table 3; Appendix V Figure 5). Of the individual taxa tested, the net-spinning caddisflies *Hydropsyche* sp. and *Cheumatopsyche* sp., spiny mayfly *Ephemerella* sp., and saddle-cased caddisfly *Glossosoma* sp. each had corresponding significant increases in density only for the Fall period (Table 6). Oligochaetes also contributed significantly to increased densities (more than 2,000/m<sup>2</sup>) in both Fall and Spring seasons for the post-SWW period. The cranefly *Antocha sp.* was confirmed to be significantly less abundant (decrease of 18/m<sup>2</sup> in the Fall and 180/m<sup>2</sup> in the Spring) during the post-SWW period. For the prominent stoneflies in the lower Deschutes River, the perlid stonefly *Hesperoperla pacifica* showed a significant post-SWW decrease (ca. 75/m<sup>2</sup>) limited to the Spring period (Table 6), whereas the giant stonefly, *Pteronarcys californica*, showed no significant pre- to post-SWW changes in either season, although an average Fall increase of approximately 33/m<sup>2</sup> was notable (*p-value=0.052*). Additional analyses showed no significant changes in mayflies *Epeorus sp.*, *Rhithrogena sp.*, *Serratella tibialis*, or the abundant planorbid snail *Vorticifex* sp.

#### Taxa Richness

Univariate analyses for taxa richness measures, using the simulation estimation data set, revealed statistically significant increases of total taxa in both seasons (2.6 in the Fall, 3 in the Spring) in the post-SWW period (Table 4; Appendix V Figure 6). Other estimation methods also indicated significant increases of 1 to 2.5 taxa (Tables 3 and 5). EPT taxa richness showed no significant change (Table 4; Appendix V Figure 7). LME tests on the individual components of the EPT taxa richness showed a significant decrease in Plecoptera taxa (average 0.5 taxa), but no significant changes were detected for Ephemeroptera or Trichoptera taxa. Sensitive taxa richness was found to have decreased an average of 1.5 taxa in the post-SWW period (Table 4; Appendix V Figure 8).

Table 3.Results of statistical comparisons (LME-test) between Pre- and Post-SWW metrics for<br/>Spring and Fall sampling within 7 sites below the Project (Sites 1, 1S, 3, 5S, 7S, 9, and 10),<br/>using full composites for all metrics based on abundance. Taxa Richness metrics for<br/>replicate samples are rarefaction estimates for a 500-count subsample.

	Aver (Post-SWW - Differ	rage – Pre-SWW) ence <sup>1</sup>	ANOVA Linear Mixed Effects p-values				
Metric	Fall	Spring	Interaction	Combined Seasons	Fall	Spring	
Density (#/m2)	11761	1320	0.0001		0.00003	0.38	
Percent Dominant (single taxon)	-6.30	-11.5	0.35	0.0023			
Percent Tolerant Taxa	0.377	15.0	0.022		0.94	0.0003	
ATI Index	0.294	0.784	0.047		0.16	0.000004	
Richness Metrics		•					
Taxa Richness	1.40	2.53	0.33	0.00131			
Number of EPT Taxa	-1.13	-0.563	0.49	0.041			
Number of Ephemeroptera Taxa	-0.910	-0.696	0.68	0.0031			
Number of Plecoptera Taxa	0.736	0.689	0.90	0.0006			
Number of Trichoptera Taxa	-0.952	-0.557	0.41	0.0029			
Number of Sensitive Taxa	-1.67	-1.90	0.75	0.00001			
<b>Community Composition</b>							
Percent Mayflies	-1.72	-1.98	0.94	0.33			
Percent Caddisflies	2.88	-2.32	0.17	0.88			
Percent Chironomids	-3.93	-19.9	0.0066		0.18	0.0006	
Percent Other Diptera	1.22	4.46	0.29	0.067			
Percent Coleoptera	-1.88	0.733	0.12	0.49			
Percent Plecoptera	-1.84	-2.08	0.73	0.000001			
Percent Non-Insects	5.69	21.0	0.047		0.32	0.0002	
Functional Feeding Groups							
Percent Collector-Filterers	7.48	6.13	0.78	0.008			
Percent Collector-Gatherers	4.61	-5.49	0.076		0.20	0.24	
Percent Omnivores	0.776	0.582	0.95	0.67			
Percent Parasites	0.558	1.67	0.026		0.010	0.0007	
Percent Predators	0.0877	-0.278	0.65	0.81			
Percent Scrapers	-13.2	-2.08	0.11	0.029			
Percent Shredders	-0.357	-0.522	0.61	0.0088			

<sup>1</sup>Average differences are provided for magnitude reference, but they are not directly being compared in the statistical analysis.

Table 4.Results of statistical comparisons (LME-test) between Pre- and Post-SWW metrics for<br/>Spring and Fall sampling within 7 sites below the Project (Sites 1, 1S, 3, 5S, 7S, 9, and 10),<br/>using average of 1000 500-count simulations.

	Aver (Post-SWW - Differ	rage – Pre-SWW) ence <sup>1</sup>	ANOVA Linear Mixed Effects p-values					
Metric	Fall	Spring	Interaction	Combined Seasons	Fall	Spring		
Density (#/m2)	11957	1261	0.00009		0.000002	0.43		
Percent Dominant (single taxon)	-6.40	-11.6	0.35	0.0020				
Percent Tolerant Taxa	0.371	15.0	0.023		0.95	0.0003		
ATI Index	0.294	0.784	0.048		0.16	0.000004		
FSBI Index	-9.53	-19.1	0.092		0.045	0.00002		
Richness Metrics								
Taxa Richness	2.59	2.95	0.77	0.00005				
Number of EPT Taxa	-0.681	-0.676	1.00	0.098				
Number of Ephemeroptera Taxa	-0.365	-0.228	0.76	0.20				
Number of Plecoptera Taxa	-0.582	-0.528	0.83	0.0001				
Number of Trichoptera Taxa	0.266	0.080	0.72	0.50				
Number of Sensitive Taxa	-1.20	-1.80	0.46	0.0004				
Community Composition								
Percent Mayflies	-1.70	-1.96	0.94	0.34				
Percent Caddisflies	2.90	-2.32	0.17	0.88				
Percent Chironomids	-3.95	-19.9	0.0065		0.18	0.0006		
Percent Other Diptera	1.23	4.47	0.29	0.067				
Percent Coleoptera	-1.88	0.732	0.12	0.49				
Percent Plecoptera	-1.83	-2.08	0.72	0.000001				
Percent Non-Insects	5.67	21.0	0.047		0.32	0.0002		
Functional Feeding Groups					-			
Percent Collector-Filterers	7.50	6.14	0.78	0.0082				
Percent Collector-Gatherers	4.62	-5.48	0.076		0.20	0.24		
Percent Omnivores	0.765	0.584	0.96	0.67				
Percent Parasites	0.562	1.67	0.026		0.0093	0.0007		
Percent Predators	0.103	-0.288	0.63	0.82				
Percent Scrapers	-13.2	-2.11	0.11	0.029				
Percent Shredders	-0.356	-0.520	0.61	0.0091				

<sup>1</sup>Average differences are provided for magnitude reference, but they are not directly being compared in the statistical analysis.

Table 5.Results of statistical comparisons (LME-test) between Pre- and Post-SWW metrics for<br/>Spring and Fall sampling within 7 sites below the Project (Sites 1, 1S, 3, 5S, 7S, 9, and 10),<br/>using single 500-count sample.

	Ave (Post-SWW Diffe	rage – Pre-SWW) rence <sup>1</sup>	ANOVA Linear Mixed Effects p-values				
Matria	[all	Series	Interaction	Combined	[all	Caring	
	Fall	Spring		Seasons	Fall	Spring	
Percent Dominant (single taxon)	-6.30	-11.0	0.40	0.0034	0.01	0.0001	
Percent Tolerant Taxa	0.586	15.9	0.018		0.91	0.0001	
All Index	0.286	0.831	0.033		0.18	0.000003	
FSBI Index	-12.5	-26.4	0.044		0.016	0.00002	
Richness Metrics						1	
Taxa Richness	1.43	1.00	0.80	0.16			
Number of EPT Taxa	-0.857	-2.00	0.27	0.0078			
Number of Ephemeroptera Taxa	-0.286	-0.857	0.39	0.089			
Number of Plecoptera Taxa	-0.857	-0.500	0.28	0.00015			
Number of Trichoptera Taxa	0.286	-0.643	0.13 0.56				
Number of Sensitive Taxa	-1.43	-2.79	0.19	0.00014			
Community Composition	-						
Percent Mayflies	-1.39	-2.23	0.83	0.37			
Percent Caddisflies	2.47	-2.84	0.19	0.93			
Percent Chironomids	-4.09	-20.9	0.0042		0.18	0.0003	
Percent Other Diptera	1.29	4.76	0.24	0.042			
Percent Coleoptera	-2.40	1.56	0.025		0.096	0.090	
Percent Plecoptera	-1.33	-2.03	0.37	0.000076			
Percent Non-Insects	5.71	21.7	0.037		0.32	0.0001	
Functional Feeding Groups		1	T			1	
Percent Collector-Filterers	6.96	5.77	0.81	0.014			
Percent Collector-Gatherers	4.77	-4.59	0.11	0.97			
Percent Omnivores	0.100	0.614	0.88	0.83			
Percent Parasites	0.429	1.34	0.073		0.088	0.0032	
Percent Predators	0.643	-0.171	0.35	0.59			
Percent Scrapers	-12.6	-2.61	0.15	0.031			
Percent Shredders	-0.343	-0.357	0.97	0.083			

<sup>1</sup>Average differences are provided for magnitude reference, but they are not directly being compared in the statistical analysis.

Table 6.Results of statistical comparisons (LME-test) between Pre- and Post-SWW expanded<br/>individual taxa counts for Spring and Fall sampling within 7 sites below the Project (Sites<br/>1, 1S, 3, 5S, 7S, 9, and 10) for 12 taxa based on full composites.

	Ave (Post-SW SWW) Di	rage /W – Pre- ifference <sup>1</sup>	ANOVA Linear Mixed Effects p-values					
Таха	Fall	Spring	Interaction	Combined Seasons	Fall	Spring		
Antocha (ANTO)	-17.8	-177	0.0005		0.0001	0.0004		
Cheumatopsyche (CHEU)	373	1.91	0.013		0.012	0.91		
Epeorus (EPEO)	58.7	61.9	0.96	0.071				
Ephemerella (EPLL)	692	-338	0.0065		0.017	0.14		
Glossosoma (GLOSS)	680	47.1	0.029		0.024	0.33		
Hesperoperla pacifica (HEPA)	23.1	-75.5	0.028		0.45	0.031		
Hydropsyche (HYPS)	2232	-152	0.00007		0.00003	0.45		
Oligochaeta (OLIGO)	2937	2170	0.20	<0.000001				
Pteronarcys californica (PTCA)	32.5	-38.4	0.038		0.052	0.099		
Rhithrogena (RHIT)	-64.9	-19.8	0.67	0.42				
Serratella (SERR)	-4.73	13.7	0.074		0.090	0.17		
Vorticifex (VORT)	608	14.1	0.47	0.45				

<sup>1</sup>Average differences are provided for magnitude reference, but they are not directly being compared in the statistical analysis. Units are count/m<sup>2</sup>.

#### Tolerance Measures and Indices

LME analyses revealed significant pre- versus post-SWW differences for tolerance metrics. Comparisons indicated a statistically significant increase in ATI scores for Sites 1-10 (average increase of 0.78) in the lower Deschutes River during the post-SWW Spring collection, but no significant change in the Fall collection (Table 3; Appendix V Figure 9). The relative abundance of Tolerant Taxa also increased significantly in the post-SWW Spring collection (absolute change of 15-percent from post-SWW minus pre-SWW) (Table 3; Appendix V Figure 10). Univariate analysis revealed a significant decrease in FSBI scores in the post-SWW years for both seasons (Table 4; Appendix V Figure 11).

#### Community Composition/Functional Feeding Groups

For the relative abundance of major taxa at Sites 1-10 in the lower Deschutes River, there were no significant differences detected between pre- and post-SWW sampling in either season for Percent Mayflies, Caddisflies, Other Dipterans, or Coleoptera taxa groups. For Percent Plecoptera, both post-SWW Fall and Spring collection efforts showed a significant overall decrease of about 2-percent compared with pre-SWW percentages (Table 3). For the Spring periods, Percent Chironomids significantly decreased by about 20-percent. In contrast, Percent Non-insects show a significant increase in Spring collections, with a post-SWW minus pre-SWW difference of about 20-percent, suggesting an equivalent replacement of chironomids in the Spring, post-SWW periods.

For the functional feeding groups, the overall average relative abundances between pre- and post-SWW estimates at Sites 1-10 did not differ significantly for Omnivores, Predators, or Collector-Gatherers. Percent Scrapers and percent Shredders both significantly decreased for the post-SWW period in both seasons, while Parasites and Collector-Filterers increased in both seasons (Table 3).

#### Multivariate Community Analysis

The multivariate NMDS results for Fall sampling with all data are displayed in Figure 14 (full composite sample) and Figure 15 (single exact 500-count simulation). The two figures show similar results overall, most noticeably revealing a clear and consistent spatial arrangement of sites along the X axis (NMDS 1). Sites immediately downstream of the Re-regulation Dam (Sites 1, 1S, and 3) are positioned in a grouping to the right. Shifting to the left, lower river sites further downstream (Sites 5S through 10) are grouped together. The upstream reference sites DE and ME are positioned separately to the left, whereas CR is separated downward from the downstream sites. These biplots indicate that those sites are grouping due to similar taxa (OTUs), or communities. These groupings support similar findings discussed in the 2016 report as well, which detailed different taxonomic compositions below the Project, further downstream, and in the reference sites above the Project.

Examining the Y-axis (NMDS 2), most sites can be seen with a separation the pre- to post-SWW periods, with post-SWW collections shifting down and to the right, but with considerable overlap in the communities in both time frames. Because the reference sites have markedly different communities, additional NMDS tests were run to examine the multivariate results with the reference sites removed (Figures 16 and 17). By removing the reference sites, and focusing on the Lower Deschutes River sites alone, the overlap is reduced, somewhat clarifying the pre- to post-SWW shift, as well as further separating the site groupings. Site 5 is now separating itself from the downstream site grouping, suggesting it has a slightly different community composition. The NMDS on the single 500-count data with reference sites removed (Figure 17) gives results similar to the full composite data set (Figure 18), but reverses NMDS axis 1, which happens often with multivariate analyses.

As an additional investigation, rare taxa (those taxa that only occurred in a single sample) were removed to see if they were responsible for any bias in the NMDS biplots. As is seen in Figures 18 and 19, removing rare taxa does not perceptibly change the results in the biplots.



Figure 14. NMDS results for full composite samples collected during the Fall sampling period at all sites. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 15. NMDS results for single 500-count rarified sample collected during the Fall sampling period at all sites. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 16. NMDS results for full composite samples collected during the Fall sampling period without reference sites. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 17. NMDS results for a single 500-count simulated sample from data collected during the Fall sampling period without reference sites. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 18. NMDS results for full composite samples collected during the Fall sampling period without reference sites and without rare OTU found in only one sample. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 19. NMDS results for a single 500-count simulated sample from data collected during the Fall sampling period without reference sites and without rare OTU found in only one sample. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes. For Fall sampling, the NMDS 1 axis is strongly associated with the spatial relationship among the sites and their communities. The OTUs that are positively correlated with Axis 1 for the full composite data set without references (Figure 16), thus being taxa found immediately below the Project, include MICRA and SIMU, as well as non-insect taxa NEMER, GALBA, VORT, JUGA, GAMM, FLUMIN, and PLAN (refer to Appendix I Table 1 for OTU codes). The OTUs that are negatively correlated with this axis, being taxa more prevalent downstream, include ACENT, SERR, PERLO, DRUN, RHIT, PARA, ANTO, PETRO, ELMID, TRICO, LEUC, and HEPA. The NMDS2 axis is strongly associated with the temporal pattern, with a downward shift in the post-SWW period. The OTUs that are positively correlated with this axis, being more prevalent in post-SWW samples, include ANTO, TIPULA, VORT, and HYPT (Figure 16). The OTUs that are negatively correlated with this axis, being more prevalent in post-SWW samples, include OLIGO, ACARI, HYPS, NEMA, EPLL, EPEO, GLOSS, EMPID, and CHEU.

For the Fall season, the average change in NMDS1 was 0.24 units (Table 7). This is the average across 7 sites of the average post NMDS1 value (across 2 years) minus the average pre NMDS1 value (across 2 years). The 95-percent confidence interval on the change was (0.074, 0.41), which does not include zero, indicating a significant positive change in the NMDS1 axis from pre- to post-project. The change was not significantly correlated with relative location in the river (p-value = 0.48). The average change in NMDS2 was -0.46 units. The 95-percent confidence interval on the change was (-0.59, -0.33), which does not include zero, indicating a significant negative change in the NMDS2 axis from pre- to post-project. The change was not significantly correlated with relative location a significant negative change in the NMDS2 axis from pre- to post-project. The change was not significantly correlated with relative location in the significantly correlated with relative location in the river (p-value = 0.48).

Season	Metric	Site 1	Site 1S	Site 3	Site 5S	Site 7S	Site 9	Site 10
Spring	Post NMDS1 – Pre NMDS1	-0.58	-0.085	-0.13	-0.34	-0.24	-0.26	-0.19
	Post NMDS2 – Pre NMDS2	0.42	0.73	0.42	0.56	0.27	0.38	0.45
Fall	Post NMDS1 – Pre NMDS1	0.33	0.21	-0.11	0.23	0.47	0.23	0.31
	Post NMDS2 – Pre NMDS2	-0.51	-0.62	-0.31	-0.65	-0.30	-0.45	-0.38

 Table 7.
 Average pre- to post- changes in combined multivariate axes formed using non-metric multidimensional scaling.

The multivariate NMDS results for Spring sampling with all data are displayed in Figure 20 (full composite sample) and Figure 21 (single exact 500-count simulation). There is some difference in these figures, with the single exact 500-count data swapping axes, possibly indicating that the sampling differences may be causing biased results. As with the Fall samples, the NMDS Axis 1 for full composites shows clear and consistent longitudinal separations of the sites along

the river continuum, with sites immediately below the Project to the right, and sites downstream in the lower river to the middle, and the reference sites to the left (Figure 20). NMDS Axis 2 defines the temporal differences, with pre-SWW being positive (upper) and post-SWW being negative (lower). With the single 500-counts, it is NMDS Axis 2 which shows more influence with the spatial relationships among the sites and their communities and NMDS Axis 1 that highlights the pre- versus post-SWW differences (Figure 21).

Again, the reference sites group separately from the other sites, meaning they have markedly different communities, so additional NMDS tests were run on Spring samples with the reference sites removed for each data set (Figures 22 and 23). This greatly clarifies the pre- to post-SWW shift, and clearly shows the different spatial community types along the river continuum similarly in both the full composite and single 500-count sample results, although it does flip the trends left to right, and upper to lower. As an additional investigation, rare taxa (those taxa that only occurred in a single sample) were removed to see if they were responsible for any bias in the NMDS biplots. Removing rare taxa does not perceptibly change the relationships in the biplots for Spring sampling (Figures 24 and 25).

For Spring sampling, the NMDS 1 axis is strongly associated with the spatial relationship among the sites and their communities. The OTUs that are negatively correlated with Axis 1 using the full composite sample data set with reference sites removed (Figure 22), thus being taxa found immediately below the Project, include non-insects PLAN, GAMM, OLIGO, and NEMA, and snails PHYSA, FLUMIN, VORT, JUGA, and GALBA, as well as the dipteran SIMU (refer to Appendix I Table 1 for OTU codes). The OTUs positively correlated with Axis 1, thus located in sites further downstream, include 16 EPT taxa such as EPLL, DRUN, PERLO, CHEU, HYPS, CAUD, HEPA, HNEL, EPEO, ACENT, and RHIT.

The NMDS2 axis is strongly associated with the temporal pattern, with a downward shift in the post-SWW period (the NMDS1 axis shift is much smaller). The OTUs that are positively correlated with this axis, and thus are more prevalent in post-SWW samples, MASP, ACENT, SERR, EPEO, LEUC, GALBA, CHIRO, ACARI, NEMA, and OLIGO. The OTUs that are negatively correlated with this axis, and thus are more prevalent in pre-SWW samples, include ORTHO, PHYSA, ANTO, DIAM, VORT, and HEPA.

For the Spring season, the average change in NMDS1 was -0.26 units (Table 7). The 95-percent confidence interval on the change was (-0.41, -0.11), which does not include zero, indicating a significant negative change in the NMDS1 axis from pre- to post-project. The change was not significantly correlated with relative location in the river (p-value = 0.94). The average change in NMDS2 was 0.46 units. The 95-percent confidence interval on the change was (0.33, 0.60), which does not include zero, indicating a significant positive change in the NMDS2 axis from pre- to post-project. The change was not significantly correlated with relative location in the river (p-value = 0.40).



Figure 20. NMDS results for full composite samples collected during the Spring sampling period at all sites. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 21. NMDS results for single 500-count rarified sample from data collected during the Spring sampling period at all sites. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 22. NMDS results for full composite samples collected during the Spring sampling period without reference sites. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 23. NMDS results for a single 500-count simulated sample from data collected during the Spring sampling period without reference sites. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 24. NMDS results for full composite samples collected during the Spring sampling period without reference sites and without rare OTU found in only one sample. Left plot has polygons connecting locations, and right plot adds polygon showing overall preversus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.



Figure 25. NMDS results for a single 500-count simulated sample from data collected during the Spring sampling period without reference sites and without rare OTU found in only one sample. Left plot has polygons connecting locations, and right plot adds polygon showing overall pre- versus post-SWW spatial location in two dimensions. Refer to Appendix I Table 1 for OTU codes.

## DISCUSSION

The main purpose of this addendum to the 2016 "Lower Deschutes River Macroinvertebrate and Periphyton Study" was to address the concerns and recommendations of Oregon DEQ in its May 23, 2016 letter to PGE. The efforts documented in this addendum were conducted specifically to address the recommendations proposed by Mr. Hubler in his memorandum attached to the May 23rd letter: to format pre- and post-SWW data sets into a single, consistent, and compatible flat file for the required analyses; to conduct an independent review of the taxonomic consistency between pre- and post-SWW datasets; and, to conduct additional analyses that will first standardize all samples to a 500-count subsampling effort, recalculate all metrics accordingly, and then run comparative univariate and multivariate analyses between the standardized pre- vs. post-SWW data and results.

The independent review by River Continuum Concepts (RCC) looked at baseline samples from the first year of study (1999 and 2000). Unfortunately, a sample-by-sample review of the taxonomic efforts and accuracy was not possible. The unexpected presence of additional debris and specimens made it impossible to separate the original specimens from the additional ones that were unaccounted. Therefore, it was concluded that the samples found were not in the same condition as they were when originally analyzed. However, the exercise provided a broader assessment of the taxonomy employed on the baseline samples, which allowed RCC and R2 greater confidence when determining appropriate OTUs for comparison between the pre- and post-SWW data sets.

One taxonomic issue requires some additional discussion, as the increased abundances of Oligochaeta in post-SWW samples, and the initial explanations given in the 2016 report were likely a factor in the Oregon DEQ letter and recommendations for independent review of the baseline samples. In Mr. Hubler's memorandum, oligochaetes are listed specifically as a discussion point of concern. In the 2016 report, R2 suggested that these substantial differences reported for Oligochaetes might have been due to poor preservation of pre-SWW samples, and/or an artifact of different taxonomists counting them differently. Additionally, Oregon DEQ noted the inconsistency of taxonomy concerning Tubificidae in pre-SWW data and Naididae in post-SWW data. As was correctly noted, these two Oligochaete families are no longer separate, with Tubificids having been moved into the family Naididae in 2008, as subfamily Tubificinae (Erséus et al. 2008). However, Mr. Hubler makes the assumption that all Naididae are now the same as Tubificinae, known as extremely tolerant to organic pollution, and that all Naididae identified in post-SWW samples are reclassified, pollution-tolerant Tubificinae. While he correctly notes that tubificids were relatively rare in the pre-SWW dataset, Mr. Hubler then states that they were common and highly abundant in the post-SWW dataset. He continues: "A dramatic increase in tubificids is a strong indication of degraded water quality post-SWW, one that is not captured due to taxonomic inconsistency."

First, it is important to note that the occurrence of Tubificidae in the pre-SWW was rare. In fact, they were identified in a total of 9 samples out of the 166 samples collected from 1999-2001, for a total of 26 individuals (range of 1-9 per sample). The follow up taxonomic review by RCC

was unable to verify this identification. Secondly, no Naididae identified in the post-SWW samples were Tubificinae. There were identified as *Nais* spp., from the subfamily Naidinae.

*Nais* spp. adults are small oligochaete worms, typically 2-10 mm in length, and are known to generally reproduce asexually for most of the year, particularly when environmental conditions are favorable (Krieger and Stearns 2010; Parish 1981). Asexual reproduction usually involves the budding-off of zooids or by fragmenting; in general, naidid abundances are greatest during the summer months when higher temperatures and a plentiful food stimulates growth rates and asexual reproduction (Learner et al. 1978). Naidids commonly colonize river beds with coarse substrates, but abundances are promoted with deposition of fine sediment such as sand, or increased aquatic vegetation beds. Large seasonal fluctuations in density have been observed for many naidid species from a variety of habitats, with most researchers observing late summer to early autumn peaks (Smith 1985). Learner et al. (1978) noted that the response of naidid species to different kinds of pollution varies, but generally organic enrichment in rivers with coarse substrates can result "in a considerable (ten- to twenty-fold) increase in naidid abundance" with densities reaching 200,000/m<sup>2</sup>.

The presence and life history of *Nais* spp. could explain why oligochaete abundances suddenly increased ten-fold between pre-SWW and post-SWW periods of study. It is possible that warmer temperatures brought about by SWW operations could have favored an increase in naidid abundances, but it is also unclear as to exactly when *Nais* spp. populations appeared in the Deschutes basin after 2001, or if they were present and just not detected. It is also not clear when the larger increases in abundance started to occur. The 12-year gap in information from 2001 to 2013 prevents us from determining many changes in occurrences in the macroinvertebrate populations in the Lower Deschutes River. Regardless, by 2013, Naidinae were ubiquitous in the system, both above (at reference sites DE and CR) and below the Project. Their absence or lower numbers in the Metolius River is understandable, given that river is spring-fed and exhibits colder stream temperature year-round, which would be unfavorable to naidids.

It is also important to note that many *Nais* spp. appear to be relatively intolerant of organic enrichment. Chapman and Mitchell (1986) found that the naidid *Nais communis* was consistently less tolerant than the tubificids tested for the effects of pollutants (Hg, NaPCP) and environmental factors (pH, temperature, salinity). Therefore, it is not necessarily accurate to equate the *Nais* spp. observed in post-SWW samples with the extremely tolerant Tubificinae taxa.

With the OTU list finalized, the final flat file was created, and the recommended analyses to apply standard subsampling effort adjustments and ultimately run univariate and multivariate tests on the resulting data sets. In order to obtain representative and compatible 500-count subsamples from greater subsampling efforts, we examined three different approaches in order to achieve simulated 500-count subsamples, and evaluated the potential biases that may occur. The primary advantage to conducting these simulations was that it provided comparable samples with equal subsampling efforts that allowed for statistical comparisons of taxa richness metrics. Results were similar, regardless of the simulation method. Final results indicated a slight increase in overall taxa richness, possibly attributed to a combination of more Trichoptera taxa, Diptera taxa, and non-insect taxa in the post-SWW period. EPT taxa richness as a whole did not significantly change, but Plecoptera alone registered a small average decrease in taxa post-SWW, as did counts of Sensitive taxa. These decreases were small, but significant, highlighting that the macroinvertebrate communities have changed over the 12 years between studies. It is important to note that these changes in taxa richness are not large, though.

Univariate statistical comparisons between pre- and post-SWW metric results produced very similar outcomes, regardless of which simulation estimate method was used. The significant changes noted in the analyses of this addendum are also generally in agreement with those presented and discussed in the 2016 report. The exception is the tolerance-base metrics, which utilized the ATI scoring to assign "tolerant" and "sensitive" designations to taxa, and the FSBI, which became the measurement of sediment tolerance, each replacing the more subjective assignments previously used (Hafele and Mulvey 1998; OWEB 1999). LME results show that tolerances and the relative abundance of tolerant taxa increased in the post-SWW Spring periods, but remained unchanged in the Fall periods. These results are further supported by LME tests on community compositions, with a significant average 20-percent decrease in Chironomidae relative abundances, and a corresponding significant average 20-percent increase in the more tolerant non-insect taxa. Results generated by these additional analyses clearly indicate that number of changes in the macroinvertebrate community have occurred during the time from 2001 to 2013. Results also suggest that macroinvertebrate community in the Spring now favors more tolerant macroinvertebrate taxa.

Finally, the addendum addresses the multivariate analysis proposed as part of the Final Study Plan. Each of the NMDS test runs completed, with and without reference sites or onceoccurring taxa, produced the same basic trends and relationships that were shown and discussed in the 2016 report. NMDS biplots clearly show a distinct longitudinal community pattern, shifting from non-insect taxa predominating sample sites 1, 1S, and 3 immediately downstream of the Project, to aquatic insect taxa further downstream at sites 5 through 10. Each NMDS test run revealed an apparent shift from pre- to post-SWW period communities as well, with a larger shift apparent in the Spring, again highlighting the LME test results. This spatial separation is especially noticeable when reference sites are removed from analysis. However, it is also important to note that even within the reference sites, which are not affected by the SWW operations, there is a separation of pre- and post-SWW data points. This is even true of data at Site ME, on the Metolius River, where a small, but noticeable temporal separation can be seen. Thus, it is not unreasonable to conclude that the temporal shift in the benthic community could be due to changes unrelated to SWW over the 12 years between the two studies. These changes might include, for example, climate change and changes in land use practices in the upper basins of the Deschutes and Crooked rivers.

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Lower Deschutes Macroinvertebrate & Periphyton Study

# APPENDIX I – MACROINVERTEBRATE OPTIMAL TAXONOMIC UNITS (OTU) AND TOLERANCE VALUES

Appendix I Table 1.

List of Optimized Taxonomic Units (OTUs) designated for taxa listed for both the pre-SWW (1999-2001) and post-SWW (2013-2015) studies. Taxa Codes (for multivariate plots), Functional Feeding Group (FFG) assignments, Assemblage Tolerance Index (ATI) scores, and Fine Sediment Biotic Index (FSBI) scores are also provided.

		TAXA					TAXA	AXA					
Phylum	Class	Subclass	Order	Family	Subfamily	Tribe	Taxon or Taxa Included from Pre- and Post-SWW Lists	Designated OTU	INDEX #	CODE	FFG	ΑΤΙ	FSBI
Arthropoda	Insecta		Ephemeroptera	Baetidae			Unidentified Baetidae	Unidentified Baetidae	1	BAET	CG	4.5	5
Arthropoda	Insecta		Ephemeroptera	Baetidae			A. insignificans, A. turbida	Acentrella sp.	2	ACENT	CG	6.1	5
Arthropoda	Insecta		Ephemeroptera	Baetidae			Baetis bicaudatus	Baetis bicaudatus	3	BABI	CG	0.8	5
Arthropoda	Insecta		Ephemeroptera	Baetidae			Baetis tricaudatus	Baetis tricaudatus	4	BATR	CG	2.9	0
Arthropoda	Insecta		Ephemeroptera	Baetidae			Diphetor hageni	Diphetor hageni	5	DIHA	CG	2.8	0
Arthropoda	Insecta		Ephemeroptera	Ephemerellidae			Unidentified Ephemerellidae	Unidentified Ephemerellidae	6	EPHE	CG	1.6	5
Arthropoda	Insecta		Ephemeroptera	Ephemerellidae			Attenella sp.	Attenella sp.	7	ATTE	CG	2.9	10
Arthropoda	Insecta		Ephemeroptera	Ephemerellidae			Caudatella sp.	Caudatella sp.	8	CAUD	CG	0.4	15
Arthropoda	Insecta		Ephemeroptera	Ephemerellidae			Drunella doddsi	Drunella doddsi	9	DRDO	SC	0.6	15
Arthropoda	Insecta		Ephemeroptera	Ephemerellidae			Drunella sp., D. coloradensis/flavilinea, D.spinifera	Drunella sp. (not doddsi)	10	DRUN	CG	1	15
Arthropoda	Insecta		Ephemeroptera	Ephemerellidae			Ephemerella sp.	Ephemerella sp.	11	EPLL	CG	2.2	0
Arthropoda	Insecta		Ephemeroptera	Ephemerellidae			Serratella tibialis	Serratella tibialis	12	SERR	CG	1.8	5
Arthropoda	Insecta		Ephemeroptera	Heptageniidae			Unidentified Heptageniidae	Unidentified Heptageniidae	13	HEPT	SC	2.7	0
Arthropoda	Insecta		Ephemeroptera	Heptageniidae			Cinygmula sp.	Cinygmula sp.	14	CINY	SC	4.2	5
Arthropoda	Insecta		Ephemeroptera	Heptageniidae			Epeorus sp., E. longimanus	Epeorus sp.	15	EPEO	SC	0.8	10
Arthropoda	Insecta		Ephemeroptera	Heptageniidae			Heptagenia, Nixe, Ecdyonurus, Leucrocuta	Heptagenia/Nixe/Ecdyonurus/Leucrocuta	16	HNEL	SC	6.8	0
Arthropoda	Insecta		Ephemeroptera	Heptageniidae			Rhithrogena sp.	Rhithrogena sp.	17	RHIT	SC	0.8	15
Arthropoda	Insecta		Ephemeroptera	Leptophlebidae			Paraleptophlebia sp., P. bicornata, P. temporalis	Paraleptophlebia sp.	18	PARA	CG	2.8	0
Arthropoda	Insecta		Ephemeroptera	Ameletidae			Ameletus sp.	Ameletus sp.	19	AMEL	CG	0.9	0
Arthropoda	Insecta		Ephemeroptera	Leptohyphidae			Tricorythodes sp.	Tricorythodes sp.	20	TRICO	CG	5.7	0
Arthropoda	Insecta		Megaloptera	Sialidae			Sialis sp.	Sialis sp.	21	SIAL	PR	3.7	0
Arthropoda	Insecta		Odonata				Odonata	Odonata	22	ODON	PR		0
Arthropoda	Insecta		Plecoptera	Capniidae			Unidentified Capniidae, Paracapnia, Utacapnia Unidentified Leuctridae, Megaleuctra, Moselia	Capniidae	23	CAPN	SH	2.3	0
Arthropoda	Insecta		Plecoptera	Chloroperlidae			Unidentified Chloroperlid, Plumiperla, Sweltsa	Chloroperlidae	24	CHLORO	PR	1.5	0
Arthropoda	Insecta		Plecoptera	Neumouridae			Unidentified Nemourid, Malenka, Zapada	Nemouridae	25	NEMO	SH	2	0
Arthropoda	Insecta		Plecoptera	Perlidae			Unidentified Perlid	Unidentified Perlid	26	PERL	PR	1.8	0
Arthropoda	Insecta		Plecoptera	Perlidae			Claassenia sabulosa	Claassenia sabulosa	27	CLSA	PR	1.8	20
Arthropoda	Insecta		Plecoptera	Perlidae			Doroneuria sp.	Doroneuria sp.	28	DORO	PR	1.2	15
Arthropoda	Insecta		Plecoptera	Perlidae			Hesperoperla pacifica	Hesperoperla pacifica	29	HEPA	PR	2.2	15
Arthropoda	Insecta		Plecoptera	Perlodidae			Unidentified Perlodid, Cultus, Isoperla, Osobenus, Skwala	Perlodidae	30	PERLO	PR	2	0
Arthropoda	Insecta		Plecoptera	Peltoperlidae			Yoraperla sp.	Yoraperla sp.	31	YORA	SH	0.8	5
Arthropoda	Insecta		Plecoptera	Pteronarcyidae			Pteronarcys californica	Pteronarcys californica	32	PTCA	SH	3.2	10
Arthropoda	Insecta		Hemiptera	Corixidae				Corixidae	33	CORX	PR		0
Arthropoda	Insecta		Trichoptera				Unidentified Trichoptera	Unidentified Trichoptera	34	TRICH	UNK	4.4	0
Arthropoda	Insecta		Trichoptera	Apataniidae			Pedomoecus sp.	Pedomoecus sp.	35	PEDO	SC	0	10
Arthropoda	Insecta		Trichoptera	Brachycentridae			Unidentified Brachycentrid	Unidentified Brachycentrid	36	BRACH	CF	3.1	0
Arthropoda	Insecta		Trichoptera	Brachycentridae			Amiocentrus sp.	Amiocentrus sp.	37	AMIO	CG	2.7	5
Arthropoda	Insecta		Trichoptera	Brachycentridae			Brachycentrus sp.	Brachycentrus sp.	38	BRACHY	CF	4.5	0
Arthropoda	Insecta		Trichoptera	Brachycentridae			Micrasema sp.	Micrasema sp.	39	MICRA	SH	2.2	0
Arthropoda	Insecta		Trichoptera	Glossosomatidae			Unidentified Glossosomatidae	Unidentified Glossosomatidae	40	GLOS	SC	2	0
Arthropoda	Insecta		Trichoptera	Glossosomatidae			Glossosoma sp.	Glossosoma sp.	41	GLOSS	SC	1.1	10
Arthropoda	Insecta		Trichoptera	Glossosomatidae			Protoptila sp.	Protoptila sp.	42	PROTO	SC	4.3	5
Arthropoda	Insecta		Trichoptera	Helicopsychidae			Helicopsyche sp.	Helicopsyche sp.	43	HELICO	SC	3.6	0
Arthropoda	Insecta		Trichoptera	Hydropsychidae			Unidentified Hydropsychidae	Unidentified Hydropsychidae	44	HYPSY	CF	7.1	0
Arthropoda	Insecta		Trichoptera	Hydropsychidae			Arctopysche grandis	Arctopysche grandis	45	ARGR	CF	1.6	15
			and the second se	1									
										TAXA			
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Phylum	Class	Subclass	Order	Family	Subfamily	Tribe	Taxon or Taxa Included from Pre- and Post-SWW Lists	Designated OTU	INDEX #	CODE	FFG	ΑΤΙ	FSBI
Arthropoda	Insecta		Trichoptera	Hydropsychidae			Cheumatopsyche sp.	Cheumatopsyche sp.	46	CHEU	CF	9.1	0
Arthropoda	Insecta		Trichoptera	Hydropsychidae			Hydropsyche sp.	Hydropsyche sp.	47	HYPS	CF	5.7	0
Arthropoda	Insecta		Trichoptera	Hydroptilidae			Unidentified Hydroptilidae	Unidentified Hydroptilidae	48	HYPTI	PH	5.7	0
Arthropoda	Insecta		Trichoptera	Hydroptilidae			Hydroptila sp.	Hydroptila sp.	49	НҮРТ	SC	5.7	0
Arthropoda	Insecta		Trichoptera	Hydroptilidae			Leucotrichia sp.	Leucotrichia sp.	50	LEUC	SC	3.4	0
Arthropoda	Insecta		Trichoptera	Hydroptilidae			Ochrotrichia sp.	Ochrotrichia sp.	51	OCHR	CG	3	0
Arthropoda	Insecta		Trichoptera	Lepidostomatidae			Lepidostoma sp.	Lepidostoma sp.	52	LEPID	SH	2.2	0
Arthropoda	Insecta		Trichoptera	Limnephilidae			Unidentified Limnephilidae, Dicosmoecus, Eocosmoecus, Onocosmoecus	Limnephilidae	53	LIMNE	SH	1.8	0
Arthropoda	Insecta		Trichoptera	Psychomiidae			Psychomyia sp.	Psychomyia sp.	54	PSYCHO	CG	4.8	0
Arthropoda	Insecta		Trichoptera	Rhyacophilidae			Rhyacophila sp., Rhyacophila Alberta Gr., Rhyacophila angelita, Rhyacophila Arnaudi, Rhyacophila Betteni Gr., Rhyacophila Coloradensis Gr., Rhyacophila Hyalinata Gr., Rhyacophila Brunnea Gr., Rhyacophila narvae, Rhyacophila Sibirica Gr.	Rhyacophila sp.	55	RHYA	PR	1.2	0
Arthropoda	Insecta		Trichoptera	Uenoidae			Neophylax sp.	Neophylax sp.	56	NEOP	SC	1.2	10
Arthropoda	Insecta		Trichoptera	Uenoidae			Oligophlebodes sp.	Oligophlebodes sp.	57	OLIGPH	SC	1.1	20
Arthropoda	Insecta		Trichoptera	Philopotamidae			Dolophilodes sp.	Dolophilodes sp.	58	DOLO	CG	1.4	10
Arthropoda	Insecta		Lepidoptera	Pyralidae			Petrophila sp.	Petrophila sp.	59	PETRO	SC	4	10
Arthropoda	Insecta		Lepidoptera	Crambidae			Crambidae	Crambidae	60	CRAM	PH	4	0
Arthropoda	Insecta		Coleoptera	Elmidae			Ampumixis, Cleptelmis, Dubiraphia, Heterlimnius, Lara, Microcylloepus, Narpus, Optioservus, Zaitzevia	Elmidae	61	ELMID	CG	5.1	0
Arthropoda	Insecta		Coleoptera	Psephenidae			Psephenus sp.	Psephenus sp.	62	PSEPH	SC	2.9	0
Arthropoda	Insecta		Coleoptera	Dytiscidae			Dytiscidae	Dytiscidae	63	DYTIS	PR		0
Arthropoda	Insecta		Diptera	Blephariceridae			Blephariceridae	Blephariceridae	64	BLEPH	SC	0.8	0
Arthropoda	Insecta		Diptera	Ceratopogoniidae			Dasyhelea sp.	Dasyhelea sp.	65	DASY	CG	4.6	0
Arthropoda	Insecta		Diptera	Ceratopogoniidae			Palpomyia/Bezzia complex	Palpomyia/Bezzia complex	66	PABEZ	PR	6.8	0
Arthropoda	Insecta		Diptera	Ceratopogoniidae			Probezzia sp.	Probezzia sp.	67	PROBZ	PR	7.7	0
Arthropoda	Insecta		Diptera	Chironomidae			Unidentified Chironomidae pupae	Unidentified Chironomidae pupae	68	CHIRPUP	CG	5.8	0
Arthropoda	Insecta		Diptera	Chironomidae	Chironominae	Chironomini	Chironomini	Chironomini	69	CHIRO	CG	7.7	0
Arthropoda	Insecta		Diptera	Chironomidae	Chironominae	Tanytarsini	Tanytarsini	Tanytarsini	70	TANYT	CF	5.2	0
Arthropoda	Insecta		Diptera	Chironomidae	Tanypodinae		Tanypodinae	Tanypodinae	71	TANYP	PR	6.7	0
Arthropoda	Insecta		Diptera	Chironomidae	Diamesinae		Diamesinae	Diamesinae	72	DIAM	CG	2.2	0
Arthropoda	Insecta		Diptera	Chironomidae	Prodiamesinae		Prodiamesinae	Prodiamesinae	73	PRODIAM	CG	5.4	0
Arthropoda	Insecta		Diptera	Chironomidae	Orthocladiinae		Orthocladiinae	Orthocladiinae	74	ORTHO	CG	4.7	0
Arthropoda	Insecta		Diptera	Tanyderidae			Protanyderus sp.	Protanyderus sp.	75	PROTANY	UNK	1	0
Arthropoda	Insecta		Diptera	Dixidae			Dixa sp.	Dixa sp.	76	DIXA	CG	2.1	0
Arthropoda	Insecta		Diptera	Athericidae			Atherix sp.	Atherix sp.	77	ATHRX	PR	5.1	5
Arthropoda	Insecta		Diptera	Empididae			Clinocera, Chelifera, Hemerodromia, Neoplasta, Oreogeton, Roederiodes	Empididae	78	EMPID	PR	4	0
Arthropoda	Insecta		Diptera	Ephydridae			Ephydridae	Ephydridae	79	EPHYD	CG	10	0
Arthropoda	Insecta		Diptera	Simuliidae			Simulium sp.	Simulium sp.	80	SIMU	CF	6.1	0
Arthropoda	Insecta		Diptera	Stratiomyidae			Stratiomyidae	Stratiomyidae	81	STRAT	CG	3.3	0
Arthropoda	Insecta		Diptera	Tipulidae			Unidentified Tipulidae	Unidentified Tipulidae	82	TIPUL	SH	3.3	0
Arthropoda	Insecta		Diptera	Tipulidae			Antocha sp.	Antocha sp.	83	ANTO	CG	2.5	5
Arthropoda	Insecta		Diptera	Tipulidae			Dicranota sp.	Dicranota sp.	84	DICRA	PR	3.3	0
Arthropoda	Insecta		Diptera	Tipulidae			Hexatoma sp.	Hexatoma sp.	85	HEXA	PR	3.3	0
Arthropoda	Insecta		Diptera	Tipulidae			Limnophila sp.	Limnophila sp.	86	LIMNO	PR	2.4	0
Arthropoda	Insecta		Diptera	Tipulidae			Tipula sp.	Tipula sp.	87	TIPULA	SH	5.5	0
Nemertea							Nemertea	Nemertea	88	NEMER	PR	6	0

										TAXA			
Phylum	Class	Subclass	Order	Family	Subfamily	Tribe	Taxon or Taxa Included from Pre- and Post-SWW Lists	Designated OTU	INDEX #	CODE	FFG	ATI	FSBI
Platyhelminth	Rhabditophora		Tricladida	Planariidae			Planariidae	Planariidae	89	PLAN	ОМ	1.9	0
es													
Nematoda							Nematoda	Nematoda	90	NEMA	PA	5.3	0
Annelida	Clitellata	Hirudinea					Hirudinea	Hirudinea	91	HIRUD	PR	7.7	0
Annelida	Clitellata	Oligochaeta					Haplotaxidae, Lumbricidae, Lumbriculidae, Naididae, Tubificidae	Oligochaeta	92	OLIGO	CG	7.9	0
Annelida	Polycheata		Sabellida	Fabriciidae			Manayunkia speciosa	Manayunkia speciosa	93	MASP	CF	8	0
Mollusca	Gastropoda			Limpets			Ancylidae, Ferrissia sp., Fisherola nuttalli	Limpets	94	LIMPET	SC	7.1	0
Mollusca	Gastropoda			Lithoglyphidae			Fluminicola sp., Lymnaeidae, Lymnaea sp.	Fluminicola sp.	95	FLUMIN	SC	7.5	0
Mollusca	Gastropoda			Hydrobiidae			Potamopyrgus antipodarum	Potamopyrgus antipodarum	96	ΡΟΤΑ	SC	7.5	0
Mollusca	Gastropoda			Lymnaeidae			Fossaria, now Galba sp.	Galba sp.	97	GALBA	SC	5.2	0
Mollusca	Gastropoda			Physidae			Physa/Physella sp.	Physa/Physella sp.	98	PHYSA	SC	7.5	0
Mollusca	Gastropoda			Planorbidae			Unidentified Planorbidae	Unidentified Planorbidae	99	PLANO	SC	7.1	0
Mollusca	Gastropoda			Planorbidae			Planorbella sp.	Planorbella sp.	100	PLANORB	SC	7.1	0
Mollusca	Gastropoda			Planorbidae			Vorticifex sp.	Vorticifex sp.	101	VORT	SC	7.1	0
Mollusca	Gastropoda			Semisulcospiridae			Juga newberryi	Juga newberryi	102	JUGA	SC	4.1	0
Mollusca	Bivalvia	Heterodonta	Veneroida	Sphaeriidae			Sphaeriidae	Sphaeriidae	103	SPHAE	CF	6.7	0
Arthropoda	Malacostraca		Amphipoda	Gammaridae			Gammarus sp.	Gammarus sp.	104	GAMM	ОМ	5.8	0
Arthropoda	Malacostraca		Amphipoda	Hyalellidae			Hyalella azteca	Hyalella sp.	105	HYAL	CG	7.9	0
Arthropoda	Malacostraca		Decapoda	Astacidae			Pacifasticus sp.	Pacifasticus sp.	106	PACIF	ОМ	4	0
Arthropoda	Malacostraca		Isopoda	Asellidae			Asellidae	Asellidae	107	ASEL	CG	7.7	0
Arthropoda	Ostracoda						Ostracoda	Ostracoda	108	OSTRA	CG	6.7	0
Arthropoda	Arachnida	Acari	Trombidiformes				Acari, Hydracarina	Acari	109	ACARI	PR	4.3	0

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## APPENDIX II – FULL COMPOSITE SUMMARY METRICS BY PERIOD & SITES

Appendix II Table 1.Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October1999 (Fall). Abundance metrics are estimated from four composited full-count replicate kick samples (0.743 m² or 8 ft²<br/>in area). Richness metrics are calculated from a rarified 500-count subsample using R.

Metrics				San	npling Sites	– October 1	999			
Metrics	DE	ME	1	<b>1</b> S	3	<b>5</b> S	<b>7</b> S	9	10	12
Total Abundance (#/composite)	529	1415	3461	9572	3158	1923	4889	3529	7161	3319
Density (#/sq-m)	711.8	1903.9	4656.7	12879.0	4249.1	2587.4	6578.1	4748.2	9635.0	4465.7
Taxa Richness (# taxa)	31.8	35.2	22.6	16.7	17.6	29.5	26.7	28.3	28.5	35.9
EPT Taxa Richness (# taxa)	16.9	19.3	12.4	7.4	8.7	15.1	16.6	15.6	16.6	19.4
Mayfly Richness (# taxa)	6.0	9.7	5.5	2.5	3.1	6.4	7.8	9.1	9.1	9.9
Stonefly Richness (# taxa)	4.0	2.5	0.2	0.3	0.0	0.7	0.8	0.0	0.4	1.3
Caddisfly Richness (# taxa)	7.0	7.1	6.7	4.7	5.7	7.9	8.1	6.4	7.1	8.1
Sensitive Taxa (# taxa)	13.0	16.1	9.4	6.1	5.7	13.3	14.2	12.1	14.1	17.1
ATI	4.15	3.09	4.45	6.29	5.90	5.36	3.71	5.37	4.94	6.36
FSBI					1	1				_
% Tolerant Taxa	6.05	3.25	26.44	80.21	65.93	43.94	9.06	35.96	28.40	74.84
% Dominant (single taxon)	23.44	30.81	19.36	59.78	37.46	27.46	20.23	27.03	31.22	57.25
Abundance by Major Taxa (%)										
Ephemeroptera	12.67	48.48	10.86	1.58	3.36	7.59	39.82	18.11	22.69	8.01
Plecoptera	21.36	9.33	3.87	0.32	5.16	5.25	9.02	2.89	3.63	0.99
Trichoptera	23.06	7.56	24.73	3.16	6.71	5.51	24.03	49.19	44.81	5.82
Coleoptera	23.44	1.13	0.09	0.01	0.06	3.69	5.54	1.76	8.85	4.04
Chironomidae	8.51	27.35	15.34	0.20	2.18	25.59	17.55	6.60	0.98	2.92
Other Diptera	4.73	2.76	1.24	0.75	0.19	1.09	1.31	2.10	1.21	0.66
Non-Insect Taxa	6.05	3.39	43.86	93.98	82.33	51.27	2.66	18.59	17.79	75.35
Abundance by Food Group (%)										
Collector-Gatherers	57.28	66.01	35.48	5.33	6.74	41.60	45.71	32.05	29.60	18.68
Filter Feeders	3.78	4.45	16.27	0.85	5.60	1.77	20.92	46.27	42.45	2.26
Scrapers/Grazers	13.04	15.34	23.09	79.50	68.37	43.16	23.15	18.50	23.22	75.99
Shredders	13.04	9.68	1.56	0.55	2.98	0.62	1.21	0.17	0.64	0.12
Predators	12.48	4.17	3.38	0.25	2.47	5.77	8.75	3.00	3.97	2.68
Parasites	0.19	0.14	0.06	0.01	0.06	0.47	0.25	0.00	0.10	0.09
Omnivores	0.19	0.21	20.17	13.51	13.77	6.60	0.00	0.00	0.01	0.18

Appendix II Table 2.Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for May<br/>2000 (Spring). Abundance metrics are estimated from four composited full-count replicate kick samples (0.743 m² or 8<br/>ft² in area). Richness metrics are calculated from a rarified 500-count subsample using R.

Metrics					Samplin	g Sites – M	ay 2000				
Metrics	CR	DE	ME	1	15	3	<b>5</b> S	<b>7</b> S	9	10	12
Total Abundance (#/composite)	2166	394	1684	5884	4420	4472	5288	8071	7609	6633	4300
Density (#/sq-m)	2914	530	2266	7917	5947	6017	7115	10859	10238	8925	5786
Taxa Richness (# taxa)	21.5	24	30.8	19.1	17.5	18.5	22.5	24.1	26.9	27.5	32.7
EPT Taxa Richness (# taxa)	10.9	17	15.4	9.5	6.8	9.9	12.5	14.8	16.4	16.1	17.4
Mayfly Richness (# taxa)	3.7	7	9.7	4.1	3.8	5.6	7.1	7.4	9.1	8.1	9.0
Stonefly Richness (# taxa)	1.0	4	1.5	0.0	0.0	0.0	0.6	0.1	0.9	0.6	1.3
Caddisfly Richness (# taxa)	6.2	6	4.3	5.4	3.0	4.2	4.8	7.3	6.3	7.4	7.1
Sensitive Taxa (# taxa)	10.0	13	12.6	7.8	6.4	7.3	10.9	12.5	15.1	14.8	16.6
ATI	4.69	3.94	3.17	4.53	4.77	5.53	4.75	4.32	4.42	4.45	4.79
FSBI		_			-				_	_	_
% Tolerant Taxa	12.74	6.35	3.21	7.29	26.81	50.67	8.21	2.95	6.33	11.01	15.30
% Dominant (single taxon)	42.29	37.31	20.01	53.72	44.50	31.51	74.68	41.95	49.84	20.97	31.81
Abundance by Major Taxa (%)											
Ephemeroptera	4.80	28.93	48.69	9.16	3.39	5.99	4.52	15.00	19.88	26.58	22.53
Plecoptera	0.88	3.81	3.03	2.75	0.59	3.24	3.39	5.66	3.48	4.55	3.26
Trichoptera	58.86	4.82	9.86	22.03	5.18	4.72	5.65	28.20	19.82	26.31	14.63
Coleoptera	14.91	14.47	2.73	0.05	0.00	0.07	0.55	3.35	1.81	11.40	5.12
Chironomidae	9.23	37.82	22.45	53.79	48.01	21.56	74.87	41.95	50.86	16.55	34.74
Other Diptera	5.77	3.05	9.20	2.48	2.10	0.20	1.13	3.13	1.42	3.51	4.09
Non-Insect Taxa	5.54	7.11	4.04	9.74	40.72	64.22	9.89	2.66	2.62	11.07	14.93
Abundance by Food Group (%)											
Collector-Gatherers	34.53	76.90	61.16	70.56	58.01	35.64	89.54	67.13	72.85	63.73	68.98
Filter Feeders	13.76	0.51	1.78	16.52	1.47	2.82	3.52	22.87	17.66	22.46	10.49
Scrapers/Grazers	48.01	16.50	23.10	5.08	25.72	44.77	1.15	2.13	5.22	6.48	13.98
Shredders	1.75	2.03	4.28	0.92	0.41	2.35	1.91	2.64	0.53	0.90	0.93
Predators	0.83	3.30	9.03	2.45	0.48	1.05	2.16	4.40	3.59	5.22	4.49
Parasites	1.06	0.76	0.53	0.17	0.16	0.34	1.42	0.82	0.13	1.21	0.98
Piercer Herbivores	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Omnivores	0.05	0.00	0.12	4.30	13.76	13.04	0.30	0.01	0.03	0.00	0.16

Appendix II Table 3.Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for May<br/>2001 (Spring). Abundance metrics are estimated from four composited 300-count replicate kick samples (0.743 m² or<br/>8 ft² in area). Richness metrics are calculated from a rarified 500-count subsample using R.

Metrics				S	ampling Site	s – May 200	1			
Metrics	CR	DE	ME	1	1S	3	<b>5</b> S	<b>7</b> S	9	10
Total Abundance (#/composite)	750	1111	2051	2735	4397	5687	5656	12435	6163	16220
Density (#/sq-m)	1010	1495	2760	3680	5916	7651	7610	16731	8292	21824
Taxa Richness (# taxa)	17.9	29.5	32.3	23.9	16.7	21.3	25.3	24.9	30.8	29.0
EPT Taxa Richness (# taxa)	9.3	15.7	18.7	14.7	6.7	10.3	13.6	14.5	16.9	16.8
Mayfly Richness (# taxa)	3.7	7.8	10.7	6.7	2.1	5.4	6.5	7.3	8.7	8.8
Stonefly Richness (# taxa)	0.7	1.0	2.3	1.0	0.4	0.6	0.4	0.0	0.6	0.3
Caddisfly Richness (# taxa)	5.0	7.0	5.8	7.0	4.2	4.3	6.7	7.2	7.6	7.7
Sensitive Taxa (# taxa)	10.3	13.9	15.1	11.5	6.7	8.6	11.6	12.7	16.4	16.5
ATI	4.12	4.17	2.66	4.33	4.97	5.81	3.49	3.61	4.19	4.02
FSBI	-	—	-			—	—		-	_
% Tolerant Taxa	3.03	6.93	0.78	5.83	41.50	50.83	6.15	1.41	11.70	3.77
% Dominant (single taxon)	39.77	32.02	42.35	39.14	28.72	44.64	25.24	20.15	17.66	17.76
Abundance by Major Taxa (%)										
Ephemeroptera	19.74	23.50	71.48	10.38	1.14	4.92	37.46	34.94	23.86	21.45
Plecoptera	0.14	4.21	1.57	5.35	1.95	3.10	8.15	7.29	2.90	2.15
Trichoptera	19.31	11.42	9.04	31.71	1.79	8.82	16.53	27.58	33.36	30.59
Coleoptera	10.23	11.05	0.43	0.00	0.08	0.00	1.44	8.70	4.24	17.83
Chironomidae	40.49	37.17	12.35	40.34	20.18	25.66	25.48	15.54	19.70	18.37
Other Diptera	6.34	5.24	4.43	6.15	2.52	0.71	2.64	2.45	5.81	4.84
Non-Insect Taxa	3.75	7.40	0.70	6.07	72.34	56.79	8.31	3.49	9.65	4.77
Abundance by Food Group (%)										
Collector-Gatherers	77.38	74.25	72.78	63.98	23.84	36.38	74.04	70.33	65.93	77.48
Filter Feeders	6.92	3.46	1.22	20.61	3.17	3.02	4.55	13.31	16.41	12.76
Scrapers/Grazers	6.92	15.54	17.57	6.39	40.36	53.53	10.22	6.10	9.26	4.07
Shredders	0.00	1.87	3.57	2.96	1.63	2.38	3.27	2.83	0.78	0.69
Predators	7.93	3.65	4.35	3.83	0.49	1.67	6.23	6.39	6.83	4.38
Parasites	0.72	1.12	0.52	0.64	0.24	1.27	1.60	0.97	0.63	0.61
Piercer Herbivores	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Omnivores	0.14	0.09	0.00	1.60	30.27	1.75	0.08	0.07	0.16	0.00

Appendix II Table 4.Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October2001 (Fall). Abundance metrics are estimated from four composited 300-count replicate kick samples (0.743 m² or 8ft² in area). Richness metrics are calculated from rarified 500-count subsamples using R.

Metrics				Sai	mpling Sites	– October 20	001			
Metrics	CR	DE	ME	1	1S	3	<b>5</b> S	<b>7</b> S	9	10
Total Abundance (#/composite)	1217	1810	2596	9908	5615	5651	3426	1784	4132	6992
Density (#/sq-m)	1637	2436	3493	13330	7554	7604	4610	2401	5560	9407
Taxa Richness (# taxa)	20.1	28.5	36.1	20.9	14.4	12.8	23.4	25.8	27.7	27.1
EPT Taxa Richness (# taxa)	10.6	14.8	22.1	9.2	6.0	6.0	11.6	14.4	12.5	13.9
Mayfly Richness (# taxa)	3.0	5.9	10.4	3.1	2.2	3.2	5.4	6.4	5.3	6.4
Stonefly Richness (# taxa)	1.2	2.0	3.5	0.0	0.0	0.0	0.0	0.0	0.4	0.0
Caddisfly Richness (# taxa)	6.4	6.8	8.2	6.2	3.8	2.8	6.2	8.0	6.9	7.5
Sensitive Taxa (# taxa)	10.2	13.2	18.3	8.7	4.6	4.0	10.1	12.2	12.8	12.5
ATI	3.85	5.30	3.37	5.80	4.92	5.74	6.00	5.08	5.09	5.46
FSBI	_	_	-	-		—	—	—	—	—
% Tolerant Taxa	15.82	38.32	5.04	68.36	50.60	66.11	68.27	28.28	23.11	29.05
% Dominant (single taxon)	40.80	26.73	29.73	53.37	35.58	34.58	38.31	21.56	20.93	22.94
Abundance by Major Taxa (%)										
Ephemeroptera	44.08	8.50	42.81	1.36	4.52	1.30	7.23	8.85	5.48	7.19
Plecoptera	0.43	9.72	4.31	0.68	0.34	0.31	4.42	2.53	2.33	3.29
Trichoptera	22.39	15.51	12.67	11.51	5.80	0.76	10.52	34.68	38.49	30.66
Coleoptera	8.56	20.09	1.14	0.08	0.00	0.00	1.37	21.56	2.09	21.56
Chironomidae	3.03	2.52	25.75	0.91	0.60	0.00	2.17	1.03	30.27	7.49
Other Diptera	4.32	3.55	6.01	0.38	0.85	0.08	0.32	2.21	0.97	1.07
Non-Insect Taxa	17.20	40.09	7.23	85.09	87.88	97.56	73.98	29.07	13.69	27.06
Abundance by Food Group (%)										
Collector-Gatherers	68.71	59.25	69.62	10.90	11.60	4.89	23.37	47.16	43.88	49.69
Filter Feeders	3.80	7.01	1.38	2.65	1.28	0.38	1.12	16.98	31.72	25.99
Scrapers/Grazers	22.64	19.44	9.67	67.30	49.15	67.40	66.27	29.46	19.81	19.80
Shredders	0.52	5.51	6.42	0.30	0.17	0.15	1.29	0.87	0.81	0.76
Predators	3.89	6.54	10.89	1.21	0.26	0.23	3.61	3.71	3.06	3.59
Parasites	0.43	2.06	2.03	0.30	0.17	0.15	2.01	1.82	0.32	0.08
Piercer Herbivores	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Omnivores	0.00	0.19	0.00	17.34	37.37	26.79	2.33	0.00	0.40	0.08

Appendix II Table 5.Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October<br/>2013. Metrics are estimated from four composited kick samples (0.743 m² or 8 ft² in area), from one 500-count sample<br/>(\*), or 4 300-counts replicates (+). Richness metrics for replicates are from rarified 500-count subsamples using R in<br/>bold).

Metrics					Sam	pling Sites	– October	2013				
Metrics	CR*	DE*	ME*	1*	1S⁺	3⁺	5S*	7S⁺	9⁺	10*	12*	13*
Total Abundance (#/composite)	4916	2571	2698	12607	9717	13749	16667	10210	15449	26769	7324	11517
Density (#/sq-m)	6615	3459	3630	16962	13074	18499	22425	13737	20786	36018	9854	15496
Taxa Richness (# taxa)	25	25	31	24	16.4	24.0	28	24.3	31.0	28	28	34
EPT Taxa Richness (# taxa)	8	14	17	8	6.4	9.4	12	13.6	14.9	15	11	16
Mayfly Richness (# taxa)	2	5	8	2	1.9	4.5	4	5.9	9.1	7	4	7
Stonefly Richness (# taxa)	0	5	3	1	0	0	2	0	0	2	1	1
Caddisfly Richness (# taxa)	6	4	6	5	4.5	5.0	6	7.7	5.7	6	6	8
Sensitive Taxa (# taxa)	7	9	19	5	3.5	7.5	10	9.3	11.9	11	7	10
ATI	6.03	4.38	3.16	5.14	5.08	6.00	5.23	5.56	6.30	5.73	6.81	5.90
FSBI		—	—	-	ł	ł	—	—	—	-	—	_
% Tolerant Taxa	63.73	31.54	4.56	43.05	48.16	61.21	47.69	47.04	56.37	40.42	75.17	39.33
% Dominant (single taxon)	38.88	30.71	21.35	33.39	34.72	31.34	22.74	30.80	19.67	27.78	25.87	19.11
Abundance by Major Taxa (%)												
Ephemeroptera	1.20	21.78	35.04	4.07	4.64	3.94	3.42	8.12	10.37	10.73	2.62	4.27
Plecoptera	0.00	5.81	4.01	0.34	0.00	1.55	1.20	3.44	0.64	0.57	0.17	0.19
Trichoptera	19.24	19.29	14.42	12.71	3.95	15.11	36.75	29.48	34.05	40.80	14.69	56.77
Coleoptera	1.20	8.92	0.55	0.17	0.00	0.07	3.08	4.54	1.50	5.94	3.50	2.97
Chironomidae	6.81	5.19	29.20	1.36	0.90	1.26	2.56	0.59	3.15	0.77	3.15	4.64
Other Diptera	1.60	1.04	9.12	0.85	2.77	0.56	0.00	0.29	0.50	1.53	0.17	2.23
Non-Insect Taxa	69.94	37.97	7.66	80.51	87.73	77.51	52.82	53.55	49.36	39.46	75.35	26.35
Abundance by Food Group (%)												
Collector-Gatherers	35.47	52.90	57.85	15.25	24.67	17.50	25.47	43.45	34.76	43.10	26.40	21.15
Filter Feeders	5.41	1.45	6.93	31.02	7.14	14.41	12.48	16.31	32.90	32.95	28.32	36.92
Scrapers/Grazers	50.90	32.99	16.06	15.25	31.60	50.60	55.56	32.99	28.04	18.77	40.91	33.21
Shredders	0.00	1.04	3.65	0.34	0.69	1.05	0.51	1.17	0.21	0.19	0.00	0.00
Predators	3.41	6.22	14.23	0.51	0.76	1.97	3.76	4.17	1.79	3.45	3.15	5.57
Parasites	0.80	5.39	1.09	0.34	0.42	0.28	1.20	1.83	0.57	1.53	0.70	0.37
Piercer Herbivores	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Omnivores	3.81	0.00	0.18	37.29	34.72	14.20	1.03	0.07	1.72	0.00	0.52	2.78

Appendix II Table 6 Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for April 2014. Metrics are estimated from four composited kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area), from one 500-count sample (\*), or 4 300-counts replicates (+). Richness metrics for replicates are from rarified 500-count subsamples using R (in bold).

Metrics					Sar	npling Site	s – April 2	014				
Metrics	CR*	DE*	ME*	1*	1S⁺	3⁺	5S*	7S⁺	9⁺	10*	12*	13*
Total Abundance (#/composite)	8558	2540	1205	5318	8695	10973	8135	8228	7978	4808	9248	10919
Density (#/sq-m)	11514	3418	1622	7155	11698	14764	10946	11071	10735	6469	12443	14691
Taxa Richness (# taxa)	14	26	33	21	18.4	20.6	28	24.8	29.4	36	29	33
EPT Taxa Richness (# taxa)	6	17	17	7	6.2	8.9	15	13.9	15.3	18	15	18
Mayfly Richness (# taxa)	2	9	9	3	2.5	4.7	6	7.3	8.5	8	6	6
Stonefly Richness (# taxa)	1	2	4	1	0	0	3	0	0.3	3	3	3
Caddisfly Richness (# taxa)	3	6	4	3	3.7	4.2	6	6.6	6.5	7	6	9
Sensitive Taxa (# taxa)	4	11	19	4	5.4	6.6	10	9.9	11.6	15	10	11
ATI	7.17	5.25	3.54	5.51	5.99	5.90	4.94	5.05	4.91	5.45	5.10	5.47
FSBI	—	-	—	-	l	ł	—	—	—	—	—	—
% Tolerant Taxa	79.06	38.90	10.27	36.77	48.50	56.36	23.43	29.98	22.52	36.61	26.99	35.23
% Dominant (single taxon)	78.49	38.11	24.42	19.89	35.26	29.58	27.27	25.21	16.76	24.79	17.38	23.09
Abundance by Major Taxa (%)												
Ephemeroptera	3.70	24.72	47.61	5.07	2.07	5.59	15.91	15.44	18.45	13.14	6.28	11.94
Plecoptera	0.14	2.99	1.42	1.31	0.43	1.25	1.92	3.79	1.54	1.83	1.29	0.98
Trichoptera	1.71	5.35	8.85	11.07	7.91	12.21	16.96	26.65	29.75	17.64	25.88	29.75
Coleoptera	0.43	9.76	0.18	0.00	0.00	0.00	4.37	5.98	2.77	13.64	2.22	1.57
Chironomidae	12.82	12.76	23.89	24.20	23.50	10.38	32.34	13.02	21.45	7.99	27.54	9.59
Other Diptera	0.00	2.05	5.31	0.56	1.14	0.15	0.52	0.45	0.31	1.00	1.85	2.35
Non-Insect Taxa	81.20	42.36	12.57	57.79	64.96	70.42	27.97	34.67	25.67	44.76	34.94	43.84
Abundance by Food Group (%)												
Collector-Gatherers	95.30	71.02	66.19	48.03	62.61	51.95	81.99	74.34	69.56	66.89	65.25	46.97
Filter Feeders	0.57	4.25	2.12	10.51	7.76	8.17	4.55	9.61	15.60	10.65	9.61	15.46
Scrapers/Grazers	1.57	15.28	20.35	26.64	12.96	26.49	6.64	8.02	6.76	15.47	12.94	22.50
Shredders	0.14	2.05	1.42	1.31	0.21	1.03	1.75	2.57	0.61	1.00	0.37	1.17
Predators	2.28	3.46	8.32	0.38	1.21	1.55	2.45	4.01	6.38	2.33	11.46	12.92
Parasites	0.00	3.94	1.59	3.38	4.06	0.22	1.22	1.36	0.77	3.49	0.18	0.78
Piercer Herbivores	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Omnivores	0.00	0.00	0.00	9.76	11.18	10.60	1.40	0.08	0.31	0.17	0.00	0.20

Appendix II Table 7.Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October<br/>2014. Metrics are estimated from four composited kick samples (0.743 m² or 8 ft² in area), from one 500-count sample<br/>(\*), or 4 300-counts replicates (+). Richness metrics for replicates are from rarified 500-count subsamples using R (in<br/>bold).

Metrics					Samj	oling Sites	– October	2014				
Metrics	CR*	DE*	ME*	1*	1S⁺	3⁺	5S*	7S⁺	9+	10*	12*	13*
Total Abundance (#/composite)	12927	2120	3315	10965	14229	12895	12381	5738	8694	23508	12241	11724
Density (#/sq-m)	17393	2852	4460	14754	19145	17350	16658	7721	11698	31630	16470	15775
Taxa Richness (# taxa)	21	29	27	22	17.6	20.0	25	25.1	27.1	29	24	32
EPT Taxa Richness (# taxa)	6	14	16	8	5.6	6.7	13	12.4	11.5	14	12	16
Mayfly Richness (# taxa)	1	5	6	2	1.8	2.0	4	4.8	6.8	7	4	5
Stonefly Richness (# taxa)	0	5	4	1	0	0	4	0	0	3	2	2
Caddisfly Richness (# taxa)	5	4	6	5	3.9	4.7	5	7.6	4.6	4	6	9
Sensitive Taxa (# taxa)	4	13	17	6	6.2	5.2	9	9.8	10.8	11	7	10
ATI	5.99	5.69	3.35	5.92	5.60	6.31	5.29	5.14	5.78	5.17	5.72	5.39
FSBI	—		—	—	ł	ł	—	—		—	—	—
% Tolerant Taxa	43.40	41.51	1.92	52.53	48.97	63.36	26.13	22.80	38.70	32.58	49.43	35.29
% Dominant (single taxon)	41.58	40.94	30.37	24.12	23.07	24.55	20.11	28.50	22.68	18.18	25.48	19.07
Abundance by Major Taxa (%)												
Ephemeroptera	10.73	10.75	42.76	2.14	2.98	2.18	14.85	15.43	14.48	18.56	2.47	9.98
Plecoptera	0.00	3.96	5.93	0.39	0.00	1.50	2.63	3.88	0.51	1.70	0.95	0.53
Trichoptera	4.95	17.55	9.25	20.43	7.33	10.29	21.99	36.70	34.97	26.33	35.36	41.53
Coleoptera	0.66	7.36	1.05	0.00	0.08	0.00	1.88	9.50	1.32	12.31	4.75	1.96
Chironomidae	31.02	8.11	33.33	2.92	2.44	4.05	17.86	3.04	10.61	4.36	4.94	3.03
Other Diptera	4.46	2.64	3.66	2.14	7.10	2.63	7.52	2.13	0.80	2.08	0.19	0.71
Non-Insect Taxa	47.69	49.62	4.01	71.98	80.06	79.35	33.27	29.26	35.19	34.47	50.57	38.32
Abundance by Food Group (%)												
Collector-Gatherers	82.51	61.89	67.89	29.38	21.77	18.84	54.89	38.15	35.11	50.19	25.10	20.68
Filter Feeders	10.56	14.53	4.19	29.38	14.90	14.04	26.88	32.90	32.92	20.83	19.39	26.38
Scrapers/Grazers	1.82	8.87	11.87	21.60	34.45	52.33	7.33	17.25	26.04	22.16	52.09	43.32
Shredders	0.00	0.94	8.20	0.39	0.00	1.20	0.38	0.53	0.22	0.19	0.00	0.00
Predators	3.30	6.79	6.11	1.75	0.46	1.20	7.33	8.51	3.73	5.11	3.23	6.95
Parasites	0.50	6.98	1.75	1.17	0.46	0.45	0.75	2.66	0.44	1.52	0.00	0.36
Piercer Herbivores	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Omnivores	1.32	0.00	0.00	16.34	27.96	11.94	2.44	0.00	1.54	0.00	0.19	2.32

Appendix II Table 8.Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for April<br/>2015. Metrics are estimated from four composited kick samples (0.743 m² or 8 ft² in area), from one 500-count sample<br/>(\*), or 4 300-counts replicates (+). Richness metrics for replicates are from rarified 500-count subsamples using R (in<br/>bold).

Metrics					Sar	npling Site	s – April 2	015				
Wetrics	CR*	DE*	ME*	1*	1S+	3⁺	5S*	7S⁺	9⁺	10*	12*	13*
Total Abundance (#/composite)	10097	2632	4937	9801	11286	7296	5246	5493	5884	10260	6633	7195
Density (#/sq-m)	13585	3541	6643	13187	15185	9817	7058	7390	7918	13805	8924	9681
Taxa Richness (# taxa)	24	27	31	24	15.1	22.6	31	27.7	32.7	32	33	31
EPT Taxa Richness (# taxa)	10	16	16	10	4.7	9.5	14	15.0	15.1	19	19	19
Mayfly Richness (# taxa)	4	8	7	4	1.5	4.0	6	6.9	9.6	9	8	8
Stonefly Richness (# taxa)	0	3	3	2	0	0.4	2	0.0	0.4	3	4	3
Caddisfly Richness (# taxa)	6	5	6	4	3.1	5.2	6	8.1	5.1	7	7	8
Sensitive Taxa (# taxa)	6	12	16	8	5.0	7.2	10	11.8	13.8	14	12	13
ATI	7.15	4.67	3.81	5.58	5.60	5.75	4.88	4.98	4.80	4.86	5.30	4.75
FSBI	—	—	—	—	ľ	I	—	—	—	—	—	—
% Tolerant Taxa	81.14	23.60	2.74	36.38	33.16	32.65	26.10	25.85	14.36	21.88	28.07	13.11
% Dominant (single taxon)	78.83	23.24	37.57	23.32	26.90	32.25	24.90	22.75	19.28	20.92	26.32	40.26
Abundance by Major Taxa (%)												
Ephemeroptera	3.91	23.96	29.35	5.22	4.90	8.00	22.91	26.07	30.34	17.85	12.63	20.41
Plecoptera	0.00	2.16	1.57	1.12	0.15	3.41	2.59	3.90	0.92	1.34	1.40	2.06
Trichoptera	4.27	4.68	8.22	7.09	2.34	6.10	21.12	20.69	25.50	24.76	37.89	57.68
Coleoptera	0.53	13.87	0.59	0.00	0.00	0.00	2.39	6.48	3.23	20.92	8.07	2.43
Chironomidae	7.30	22.34	46.77	6.34	11.68	6.18	11.75	7.36	15.44	2.69	4.39	2.25
Other Diptera	0.53	4.32	8.81	23.32	25.17	32.25	4.78	1.33	5.76	4.80	2.28	3.93
Non-Insect Taxa	83.27	28.65	4.50	56.90	55.76	44.06	34.46	34.17	17.13	27.64	32.98	11.05
Abundance by Food Group (%)												
Collector-Gatherers	91.81	68.11	69.08	33.96	43.41	34.94	59.36	60.46	50.92	54.13	37.19	27.90
Filter Feeders	1.42	1.44	7.24	30.04	27.58	38.27	17.13	16.49	31.03	19.58	32.98	48.13
Scrapers/Grazers	3.74	21.08	11.94	17.72	5.80	15.21	12.35	10.24	9.52	17.47	20.35	17.98
Shredders	0.00	1.80	3.52	0.56	0.23	2.77	1.59	2.28	0.38	0.58	0.35	1.50
Predators	2.31	3.42	6.85	0.93	0.68	1.27	5.58	7.22	7.07	4.22	7.37	3.00
Parasites	0.36	3.96	1.17	1.49	5.73	1.35	2.39	3.09	0.92	4.03	1.75	1.50
Piercer Herbivores	0.36	0.00	0.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Omnivores	0.00	0.18	0.00	15.30	16.58	6.18	1.59	0.22	0.15	0.00	0.00	0.00

## APPENDIX III – SINGLE 500-COUNT SUMMARY METRICS BY PERIOD & SITES



Appendix III Table 1. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October 1999 (Fall). Metrics are estimated from a single rarified 500-count subsample using R from four composited full-count replicate kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area).

Metrics				Sar	npling Sites	– October 1	999			
Metrics	DE	ME	1	15	3	<b>5</b> S	<b>7</b> S	9	10	12
Total Abundance (#/subsample)	500	500	500	500	500	500	500	500	500	500
Density (#/sq-m)	-	-	—	—	—			—	-	—
Taxa Richness (# taxa)	35	37	21	17	19	30	26	28	30	31
EPT Taxa Richness (# taxa)	18	23	11	7	9	15	17	16	19	17
Mayfly Richness (# taxa)	7	10	4	2	2	5	6	8	10	8
Stonefly Richness (# taxa)	5	5	2	1	3	4	4	2	3	1
Caddisfly Richness (# taxa)	6	8	5	4	4	6	7	6	6	8
Sensitive Taxa (# taxa)	14	24	11	8	9	12	10	11	15	10
ATI	4.13	3.11	4.39	6.35	5.92	5.50	3.69	5.41	5.02	6.34
FSBI	70	180	70	25	60	80	80	95	105	80
% Tolerant Taxa	6.4	3	25	81.8	67.6	45.4	9.4	34.8	27.4	74
% Dominant (single taxon)	23.2	31.8	20.4	60.2	35.4	27.6	21.6	28.8	32	56.4
Abundance by Major Taxa (%)										
Ephemeroptera	12.6	49.0	11.4	1.8	3.0	6.8	44.6	17.6	21.6	8.4
Plecoptera	21.8	8.6	2.8	0.6	5.6	2.6	8.4	3.2	3.2	0.2
Trichoptera	22.6	7.0	23.0	2.8	6.6	7.2	23.0	51.6	45.6	7.0
Coleoptera	23.2	1.2	0.0	0.0	0.0	3.2	4.4	2.2	10.0	4.2
Chironomidae	8.8	28.0	16.6	0.4	2.2	27.8	15.2	5.6	1.4	3.0
Other Diptera	4.4	2.8	1.2	0.6	0.4	1.2	1.0	2.4	1.0	0.4
Non-Insect Taxa	6.4	3.4	45.0	93.8	82.2	51.2	3.4	17.2	17.2	74.6
Abundance by Food Group (%)										
Collector-Gatherers	56.8	68.0	37.0	5.8	5.6	43.2	45.2	31.8	32.8	19.8
Filter Feeders	3.6	4.0	15.0	0.8	6.0	1.6	20.0	48.8	43.0	3.2
Scrapers/Grazers	13.6	14.0	22.2	80.2	68.2	45.8	24.8	15.6	20.0	75.0
Shredders	13.4	8.8	1.2	0.2	3.4	1.0	1.2	0.0	0.4	0.0
Predators	12.2	4.8	2.2	0.8	2.4	3.0	8.4	3.8	3.8	1.6
Parasites	0.2	0.2	0.2	0.2	0.0	0.4	0.4	0.0	0.0	0.0
Piercer Herbivores	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Omnivores	0.2	0.2	22.2	12.0	14.4	5.0	0.0	0.0	0.0	0.4

Appendix III Table 2. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for May 2000 (Spring). Metrics are estimated from a single rarified 500-count subsample using R from four composited full-count replicate kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area).

Metrics					Samplir	ng Sites – M	ay 2000				
Metrics	CR	DE	ME	1	15	3	<b>5</b> S	<b>7</b> S	9	10	12
Total Abundance (#/subsample)	500	394	500	500	500	500	500	500	500	500	500
Density (#/sq-m)	_	—	_	—	—	_	—	_	_	—	_
Taxa Richness (# taxa)	23	24	32	19	20	22	23	25	24	24	35
EPT Taxa Richness (# taxa)	13	17	19	10	10	11	14	16	15	15	21
Mayfly Richness (# taxa)	6	7	10	4	4	6	7	6	7	7	9
Stonefly Richness (# taxa)	1	4	3	2	2	2	2	3	3	3	3
Caddisfly Richness (# taxa)	6	6	6	4	4	3	5	7	5	5	9
Sensitive Taxa (# taxa)	9	13	20	9	10	11	12	12	12	13	12
ATI	4.66	3.94	3.11	4.48	4.73	5.41	4.81	4.30	4.39	4.36	4.90
FSBI	55	100	130	65	65	85	110	105	110	110	110
% Tolerant Taxa	13.2	6.3	3.4	7.4	24.8	46.6	9.2	3.8	6.4	11.4	14.4
% Dominant (single taxon)	43.4	37.3	20.4	53.8	48.2	27.6	74.4	40.6	50.8	21.8	32
Abundance by Major Taxa (%)											
Ephemeroptera	5.6	28.9	48.2	10.8	3.0	6.2	4.2	15.6	19.4	27.2	23.2
Plecoptera	0.8	3.8	2.8	2.6	0.8	3.6	2.4	6.2	3.8	5.4	2.4
Trichoptera	59.2	4.8	11.6	22.2	4.4	5.2	5.8	27.8	18.8	28.0	17.0
Coleoptera	12.6	14.5	2.2	0.0	0.0	0.2	0.4	3.6	1.2	9.4	4.4
Chironomidae	9.0	37.8	22.8	53.8	50.8	24.4	74.4	40.6	52.4	16.6	34.6
Other Diptera	7.4	3.0	8.2	1.0	1.6	0.2	1.6	3.2	1.6	2.6	4.4
Non-Insect Taxa	5.4	7.1	4.2	9.6	39.4	60.2	11.2	2.6	2.8	10.8	13.4
Abundance by Food Group (%)											
Collector-Gatherers	33.6	76.9	61.8	72.2	58.6	39.0	89.4	67.0	73.6	62.8	68.2
Filter Feeders	14.0	0.5	1.2	15.0	1.0	3.6	3.6	22.8	16.6	23.6	12.2
Scrapers/Grazers	49.0	16.5	22.0	4.6	24.4	40.2	1.6	2.4	5.4	6.0	14.2
Shredders	1.4	2.0	5.4	1.2	0.6	2.8	1.6	2.2	1.0	1.0	0.8
Predators	1.2	3.3	9.0	2.2	0.8	1.0	2.2	5.0	3.4	5.4	4.4
Parasites	0.8	0.8	0.6	0.2	0.0	0.2	1.4	0.6	0.0	1.2	0.2
Piercer Herbivores	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Omnivores	0.0	0.0	0.0	4.6	14.6	13.2	0.2	0.0	0.0	0.0	0.0

Appendix III Table 3. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for May 2001 (Spring). Metrics are estimated from a single rarified 500-count subsample using R from four composited 300-count replicate kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area).

Matrice	Sampling Sites – May 2001										
Wietrics	CR	DE	ME	1	1S	3	<b>5</b> S	<b>7</b> S	9	10	
Total Abundance (#/subsample)	500	500	500	500	500	500	500	500	500	500	
Density (#/sq-m)	—	—	—	—	-	—	—	—	—	—	
Taxa Richness (# taxa)	20	28	30	25	19	27	27	26	33	32	
EPT Taxa Richness (# taxa)	10	17	23	13	7	12	15	16	18	20	
Mayfly Richness (# taxa)	4	6	12	5	1	6	7	6	8	9	
Stonefly Richness (# taxa)	0	4	3	3	2	3	3	3	3	3	
Caddisfly Richness (# taxa)	6	7	8	5	4	3	5	7	7	8	
Sensitive Taxa (# taxa)	6	13	21	12	5	12	11	12	11	15	
ATI	4.06	4.12	2.66	4.33	4.97	5.77	3.46	3.63	4.25	4.11	
FSBI	30	95	145	70	30	85	110	95	85	125	
% Tolerant Taxa	2.6	6.8	0.6	6.4	41.4	50	4.4	2.2	12.2	4.4	
% Dominant (single taxon)	38.6	31.6	40.8	41.8	29.2	43.6	26.6	19.6	16.8	20.6	
Abundance by Major Taxa (%)											
Ephemeroptera	20.4	25.0	70.0	10.2	0.8	6.8	36.2	38.2	21.2	18.0	
Plecoptera	0.0	4.0	1.2	4.4	1.4	2.6	9.4	6.8	2.6	3.0	
Trichoptera	18.6	12.6	10.6	31.6	1.4	8.0	16.6	25.8	35.0	27.6	
Coleoptera	10.8	10.8	0.0	0.0	0.2	0.0	2.6	6.8	3.8	18.0	
Chironomidae	39.2	35.8	12.4	43.4	21.0	25.8	26.6	16.6	19.2	21.8	
Other Diptera	7.2	4.4	5.4	4.8	2.6	0.6	2.2	2.2	6.2	5.8	
Non-Insect Taxa	3.8	7.4	0.4	5.6	72.6	56.2	6.4	3.6	11.4	5.8	
Abundance by Food Group (%)											
Collector-Gatherers	78.4	72.4	69.4	65.8	23.2	38.4	73.0	69.2	66.0	77.2	
Filter Feeders	6.0	4.6	1.0	19.2	3.2	2.6	4.4	14.8	17.0	11.8	
Scrapers/Grazers	6.6	17.4	20.6	8.2	41.2	51.8	10.2	6.8	9.2	5.0	
Shredders	0.0	1.8	3.4	2.2	1.2	2.4	3.6	2.0	0.6	1.2	
Predators	7.8	3.0	5.2	3.8	0.2	1.2	7.2	6.8	5.8	4.2	
Parasites	1.0	0.8	0.4	0.2	0.2	2.0	1.6	0.4	1.0	0.6	
Piercer Herbivores	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Omnivores	0.2	0.0	0.0	0.6	30.8	1.6	0.0	0.0	0.4	0.0	

Appendix III Table 4. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October 2001 (Fall). Metrics are estimated from a single rarified 500-count subsample using R from four composited 300-count replicate kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area).

Motrice	Sampling Sites – October 2001											
Wethes	CR	DE	ME	1	1S	3	<b>5</b> S	<b>7</b> S	9	10		
Total Abundance (#/subsample)	500	500	500	500	500	500	500	500	500	500		
Density (#/sq-m)	—	—	_	_	_	—	_	—	—	—		
Taxa Richness (# taxa)	20	29	34	20	17	11	22	26	27	28		
EPT Taxa Richness (# taxa)	10	17	20	9	6	4	8	14	14	13		
Mayfly Richness (# taxa)	3	7	9	2	3	1	3	5	4	6		
Stonefly Richness (# taxa)	1	5	4	2	0	2	3	3	3	2		
Caddisfly Richness (# taxa)	6	5	7	5	3	1	2	6	7	5		
Sensitive Taxa (# taxa)	7	13	21	8	5	2	9	11	8	11		
ATI	3.87	5.37	3.42	5.84	4.69	5.62	6.02	5.03	5.30	5.57		
FSBI	35	80	170	45	35	30	55	90	80	95		
% Tolerant Taxa	15.2	38.2	5	69.6	46.8	64.2	69	28.2	27.4	31.6		
% Dominant (single taxon)	39.6	26.4	26.4	54.2	38.6	32.8	40.6	20.4	20.2	24.6		
Abundance by Major Taxa (%)												
Ephemeroptera	43.2	6.6	39.2	1.6	5.2	0.8	6.0	9.4	4.4	5.6		
Plecoptera	0.2	8.8	3.6	0.8	0.0	0.4	4.0	1.8	1.8	2.4		
Trichoptera	23.8	16.4	14.6	10.4	6.6	0.4	10.6	35.4	39.2	32.8		
Coleoptera	9.6	22.4	0.6	0.2	0.0	0.0	2.2	20.4	3.0	19.4		
Chironomidae	3.2	1.4	28.6	0.4	0.4	0.0	1.6	1.2	31.0	7.4		
Other Diptera	3.6	3.2	6.4	0.6	0.6	0.0	1.0	2.6	1.0	1.0		
Non-Insect Taxa	16.4	41.2	7.0	86.0	87.2	98.4	74.6	29.2	15.2	29.6		
Abundance by Food Group (%)												
Collector-Gatherers	70.0	59.2	67.4	10.0	12.0	2.6	22.6	47.6	44.2	50.4		
Filter Feeders	3.8	7.2	1.4	2.6	0.8	0.4	0.8	15.8	33.4	27.4		
Scrapers/Grazers	22.2	18.8	12.2	68.2	46.4	67.0	67.6	29.6	19.8	18.6		
Shredders	0.2	4.2	6.2	0.4	0.0	0.2	1.0	0.6	1.0	0.6		
Predators	3.4	7.4	10.6	1.2	0.2	0.2	3.8	3.8	1.4	2.6		
Parasites	0.4	3.0	2.2	0.8	0.2	0.0	2.4	2.6	0.0	0.2		
Piercer Herbivores	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		
Omnivores	0.0	0.2	0.0	16.8	40.4	29.6	1.8	0.0	0.2	0.2		

Appendix III Table 5. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October 2013. Metrics are estimated from a single rarified 500-count subsample using R taken from four composited kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area), either as one 500-count sample (\*), or 4 300-counts replicates (+).

Motrice	Sampling Sites – October 2013											
Wietrics	CR*	DE*	ME*	1*	1S⁺	3⁺	5S*	7S⁺	<b>9</b> +	10*	12*	13*
Total Abundance (#/subsample)	500	500	500	500	500	500	500	500	500	500	500	500
Density (#/sq-m)	—	—	—	-	—	—	-	—	—	—	—	—
Taxa Richness (# taxa)	24	23	27	20	20	27	27	26	32	24	26	29
EPT Taxa Richness (# taxa)	8	12	15	7	7	10	12	13	15	12	11	14
Mayfly Richness (# taxa)	2	4	7	2	1	3	4	4	8	6	4	6
Stonefly Richness (# taxa)	0	5	2	1	0	2	2	3	1	1	1	1
Caddisfly Richness (# taxa)	6	3	6	4	6	5	6	6	6	5	6	7
Sensitive Taxa (# taxa)	7	8	16	5	6	8	10	10	11	9	6	9
ATI	5.91	4.60	3.21	5.23	5.14	5.94	5.25	5.60	6.18	5.83	6.71	5.89
FSBI	20	80	160	35	20	55	70	80	90	85	35	70
% Tolerant Taxa	61.2	35	4.8	44.2	49	60.2	47.6	48.8	54.8	42.6	73.4	40
% Dominant (single taxon)	38.6	33.2	21.2	30.4	33.6	32.8	22.4	33	19.6	27.6	29	18.6
Abundance by Major Taxa (%)												
Ephemeroptera	1.4	22.4	35.0	5.4	4.0	3.8	3.2	9.4	12.8	9.8	3.0	5.0
Plecoptera	0.0	5.8	4.0	0.6	0.0	2.0	1.2	2.6	0.2	0.4	0.2	0.2
Trichoptera	19.4	16.0	14.4	11.8	5.2	15.0	37.8	26.2	30.8	40.4	14.4	56.6
Coleoptera	0.8	10.0	0.6	0.0	0.0	0.2	2.6	4.0	1.4	4.4	2.8	2.6
Chironomidae	8.4	5.0	28.8	2.6	1.0	1.6	1.6	0.8	3.4	0.8	3.8	4.0
Other Diptera	2.8	1.2	8.6	1.0	3.8	0.8	0.0	0.2	0.4	1.6	0.0	2.0
Non-Insect Taxa	67.2	39.6	8.6	78.6	86.0	76.6	53.2	56.8	50.6	42.0	75.4	26.8
Abundance by Food Group (%)												
Collector-Gatherers	35.4	57.6	59.6	17.0	26.0	16.2	23.6	47.0	38.0	43.8	26.8	20.6
Filter Feeders	5.6	1.6	5.4	30.4	7.8	13.4	13.4	14.2	29.6	33.0	23.0	34.8
Scrapers/Grazers	48.8	30.2	14.4	17.0	31.0	52.8	55.8	33.0	27.4	18.8	44.8	36.6
Shredders	0.0	1.4	4.2	0.6	0.4	1.0	0.4	0.6	0.0	0.0	0.0	0.0
Predators	5.0	5.8	15.0	0.2	0.6	3.8	3.8	3.2	2.6	3.6	3.8	5.6
Parasites	0.6	3.4	1.4	0.6	0.6	0.2	1.6	2.0	0.4	0.8	1.0	0.6
Piercer Herbivores	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Omnivores	4.4	0.0	0.0	34.2	33.6	12.6	1.4	0.0	2.0	0.0	0.6	1.8

Appendix III Table 6 Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for April 2014. Metrics are estimated from a single rarified 500-count subsample using R taken from four composited kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area), either as one 500-count sample (\*), or 4 300-counts replicates (+).

Motrico	Sampling Sites – April 2014											
Metrics	CR*	DE*	ME*	1*	1S⁺	3⁺	5S*	7S⁺	<b>9</b> +	10*	12*	13*
Total Abundance (#/subsample)	500	500	500	500	500	500	500	500	500	500	500	500
Density (#/sq-m)	-	—	—	—	-	-	-	-	-	—	—	—
Taxa Richness (# taxa)	12	20	31	21	23	24	25	24	32	31	27	27
EPT Taxa Richness (# taxa)	5	13	16	7	10	9	12	12	14	16	14	16
Mayfly Richness (# taxa)	2	8	9	3	3	4	5	6	6	6	6	5
Stonefly Richness (# taxa)	1	2	3	1	2	2	2	2	3	3	3	2
Caddisfly Richness (# taxa)	2	3	4	3	5	3	5	4	5	7	5	9
Sensitive Taxa (# taxa)	3	9	18	4	6	7	8	8	10	13	9	9
ATI	7.08	5.29	3.38	5.43	6.01	5.85	4.98	5.12	4.93	5.64	5.19	5.46
FSBI	15	105	140	20	35	50	55	75	90	80	65	60
% Tolerant Taxa	76.4	41.2	8.8	35.6	50.8	56	22	32.6	23	39.8	27.8	35.2
% Dominant (single taxon)	75.8	41	25.6	19.2	38.6	30.4	26.4	27.6	17.4	27.4	18.6	21.4
Abundance by Major Taxa (%)												
Ephemeroptera	4.2	26.6	50.8	5.4	2.6	5.8	17.2	13.8	18.2	11.0	5.4	13.2
Plecoptera	0.4	1.8	1.4	1.2	0.4	1.4	1.2	2.8	2.0	2.8	1.0	1.2
Trichoptera	1.8	4.8	8.4	13.4	5.8	9.8	16.6	29.2	27.6	13.8	25.4	30.2
Coleoptera	0.2	9.0	0.0	0.0	0.0	0.0	4.8	6.2	3.8	15.2	1.6	2.2
Chironomidae	15.8	11.6	23.2	23.8	23.6	11.2	31.8	11.6	22.0	8.0	29.6	10.0
Other Diptera	0.0	1.2	5.6	1.2	2.0	0.8	1.0	0.6	0.6	1.2	2.2	2.0
Non-Insect Taxa	77.6	45.0	10.4	55.0	65.6	71.0	27.4	35.8	25.8	48.0	34.8	41.2
Abundance by Food Group (%)												
Collector-Gatherers	96.0	74.4	65.2	51.0	66.4	53.4	82.2	77.4	68.8	68.2	63.4	48.2
Filter Feeders	0.4	4.0	1.2	11.0	7.0	6.4	5.4	9.2	15.4	9.6	11.0	15.6
Scrapers/Grazers	1.6	14.6	23.2	23.8	11.4	25.2	6.0	6.6	6.8	14.6	14.6	22.8
Shredders	0.4	1.0	1.6	1.2	0.4	0.8	1.2	1.8	1.4	1.2	0.2	1.6
Predators	1.4	2.6	7.6	0.4	0.8	2.6	3.0	4.0	6.6	3.2	10.2	10.8
Parasites	0.0	3.4	1.2	2.6	2.8	0.2	1.0	1.0	0.8	3.0	0.0	0.6
Piercer Herbivores	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Omnivores	0.0	0.0	0.0	10.0	11.2	11.4	1.2	0.0	0.2	0.2	0.0	0.4

Appendix III Table 7. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October 2014. Metrics are estimated from a single rarified 500-count subsample using R taken from four composited kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area), either as one 500-count sample (\*), or 4 300-counts replicates (+).

Motrice	Sampling Sites – October 2014											
Wietrics	CR*	DE*	ME*	1*	1S+	3⁺	5S*	7S⁺	9⁺	10*	12*	13*
Total Abundance (#/subsample)	500	500	500	500	500	500	500	500	500	500	500	500
Density (#/sq-m)	—	—	—	—	—	—	-	—	—	—	—	—
Taxa Richness (# taxa)	18	26	26	22	21	23	20	27	28	25	22	29
EPT Taxa Richness (# taxa)	6	13	16	8	5	8	9	15	15	14	10	15
Mayfly Richness (# taxa)	1	5	6	2	1	2	3	6	8	7	3	5
Stonefly Richness (# taxa)	0	5	4	1	0	2	2	3	1	3	2	1
Caddisfly Richness (# taxa)	5	3	6	5	4	4	4	6	6	4	5	9
Sensitive Taxa (# taxa)	3	11	17	6	4	7	6	10	8	10	6	9
ATI	6.01	5.77	3.23	5.96	5.56	6.30	5.49	4.96	5.79	5.13	5.88	5.28
FSBI	25	85	100	25	5	40	30	75	75	85	60	50
% Tolerant Taxa	43.6	42.8	2	54.4	48.4	63.4	30.6	20.8	36.6	35	52.8	33.2
% Dominant (single taxon)	42.6	42.4	31	26.4	23.2	23.6	22.2	28.6	26.6	19.2	27.8	21.2
Abundance by Major Taxa (%)												
Ephemeroptera	9.0	11.0	43.4	2.6	3.6	1.8	11.8	16.2	16.2	19.8	2.6	7.0
Plecoptera	0.0	4.0	7.2	0.8	0.0	1.6	2.8	4.2	0.2	2.4	0.8	0.2
Trichoptera	5.2	14.6	10.4	17.2	7.0	8.0	22.2	39.4	39.8	29.0	32.8	43.8
Coleoptera	0.6	8.0	0.6	0.0	0.4	0.0	1.4	8.2	1.0	7.8	3.6	2.0
Chironomidae	32.8	10.2	31.4	3.0	1.8	4.6	16.6	3.0	10.0	3.2	5.6	4.4
Other Diptera	4.2	2.6	3.4	1.8	7.2	3.6	7.4	2.0	0.4	2.4	0.2	1.2
Non-Insect Taxa	47.8	49.6	3.6	74.6	80.0	80.4	37.8	27.0	31.2	35.4	53.8	38.0
Abundance by Food Group (%)												
Collector-Gatherers	83.6	66.2	67.4	32.2	21.0	22.0	52.0	35.6	36.8	46.4	27.0	20.4
Filter Feeders	9.6	13.4	2.8	26.2	14.0	11.8	27.2	32.4	39.0	21.4	17.2	28.0
Scrapers/Grazers	1.8	7.2	11.8	23.2	34.6	50.8	9.2	20.0	19.8	24.8	53.2	40.6
Shredders	0.0	1.2	10.2	0.8	0.0	1.2	0.0	0.4	0.2	0.8	0.0	0.0
Predators	3.4	6.0	6.4	1.4	1.0	1.4	8.4	8.6	3.0	5.0	2.0	7.0
Parasites	0.6	6.0	1.4	0.8	0.2	0.8	0.4	3.0	0.4	1.6	0.0	0.2
Piercer Herbivores	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Omnivores	1.0	0.0	0.0	15.4	29.2	12.0	2.8	0.0	0.8	0.0	0.6	3.8

Appendix III Table 8. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for April 2015. Metrics are estimated from a single rarified 500-count subsample using R taken from four composited kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area), either as one 500-count sample (\*), or 4 300-counts replicates (+).

Motrice	Sampling Sites – April 2015												
Wietrics	CR*	DE*	ME*	1*	1S+	3⁺	5S*	7S⁺	9+	10*	12*	13*	
Total Abundance (#/subsample)	500	500	500	500	500	500	500	500	500	500	500	500	
Density (#/sq-m)													
Taxa Richness (# taxa)	20	23	29	21	15	24	27	32	34	27	32	24	
EPT Taxa Richness (# taxa)	8	13	16	8	5	9	13	17	17	15	18	14	
Mayfly Richness (# taxa)	3	6	7	3	2	3	6	7	9	8	8	6	
Stonefly Richness (# taxa)	0	2	3	2	1	2	2	3	2	3	3	2	
Caddisfly Richness (# taxa)	5	5	6	3	2	4	5	7	6	4	7	6	
Sensitive Taxa (# taxa)	6	9	16	7	2	9	10	12	11	11	12	9	
ATI	7.20	4.62	3.86	5.59	5.57	5.84	5.10	4.91	4.78	4.88	5.16	4.70	
FSBI	45	80	135	45	15	55	80	100	90	90	115	85	
% Tolerant Taxa	82.8	22	3.2	35.6	34.8	36.2	27	25.6	13.8	20.6	26.8	13.4	
% Dominant (single taxon)	80.4	21.6	38.4	24.6	27.2	30.4	26	23	19.6	23.2	25.2	37.2	
Abundance by Major Taxa (%)													
Ephemeroptera	3.4	22.8	28.0	6.2	6.6	6.8	20.6	26.4	28.2	17.8	14.0	21.0	
Plecoptera	0.0	2.8	1.6	0.6	0.4	3.8	2.6	5.4	0.8	1.2	1.8	1.8	
Trichoptera	4.4	4.4	10.0	6.2	2.2	5.8	19.6	20.6	25.4	22.4	37.8	54.6	
Coleoptera	0.6	15.2	0.8	0.0	0.0	0.0	3.2	6.4	5.2	23.2	9.0	3.0	
Chironomidae	5.0	22.6	47.0	7.4	10.0	5.2	12.0	6.8	17.2	4.0	3.2	2.4	
Other Diptera	0.6	5.0	7.2	24.6	23.0	30.4	6.0	1.0	4.6	5.8	2.4	4.2	
Non-Insect Taxa	85.6	27.2	5.2	55.0	57.8	48.0	36.0	33.4	17.2	25.6	31.4	13.0	
Abundance by Food Group (%)													
Collector-Gatherers	91.0	67.2	70.2	36.8	43.8	37.4	60.6	60.0	50.4	54.8	38.0	29.8	
Filter Feeders	1.0	1.2	6.6	30.2	25.0	36.0	19.4	15.6	30.2	19.6	31.6	45.2	
Scrapers/Grazers	4.2	21.2	10.0	17.0	7.6	14.0	9.4	11.0	9.8	17.2	19.6	18.4	
Shredders	0.0	2.4	3.6	0.4	0.4	3.4	1.2	4.4	0.2	0.6	0.0	1.8	
Predators	2.8	4.4	7.6	0.6	0.2	1.4	5.4	6.2	8.2	4.2	9.4	2.8	
Parasites	0.4	3.2	1.8	1.6	5.4	1.0	2.2	2.2	1.0	3.6	1.4	2.0	
Piercer Herbivores	0.6	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Omnivores	0.0	0.4	0.0	13.4	17.6	6.8	1.8	0.6	0.2	0.0	0.0	0.0	

## APPENDIX IV – 500-COUNT SIMULATION SUMMARY METRICS BY PERIOD & SITE



Appendix IV Table 1. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October 1999 (Fall). Metrics are estimated from 1000 simulated 500-count subsamples using R from four composited full-count replicate kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area).

Matrice	Sampling Sites – October 1999											
Wetrics	DE	ME	1	<b>1</b> S	3	<b>5</b> S	<b>7</b> S	9	10	12		
Subsample Count	502.8	507.6	518.0	550.9	516.1	510.5	525.4	518.7	537.4	517.4		
Total Abundance (#/composite)	531.6	1424.1	3501.8	9905.9	3212.7	1946.2	4969.3	3573.8	7354.9	3353.0		
Density (#/sq-m)	715.3	1916.0	4711.6	13328.3	4322.7	2618.6	6686.2	4808.5	9896.0	4511.5		
Taxa Richness (# taxa)	34.49	35.49	22.31	15.33	19.16	29.03	26.80	26.89	27.28	29.55		
EPT Taxa Richness (# taxa)	17.85	21.20	11.86	6.05	8.34	14.51	16.59	16.21	17.12	16.04		
Mayfly Richness (# taxa)	6.90	9.16	4.22	1.72	2.23	5.48	7.01	7.83	8.35	7.12		
Stonefly Richness (# taxa)	5.00	4.37	2.15	1.26	2.44	3.51	3.68	2.41	3.12	1.72		
Caddisfly Richness (# taxa)	5.95	7.68	5.49	3.08	3.67	5.53	5.90	5.98	5.66	7.20		
Sensitive Taxa (# taxa)	13.89	22.55	10.50	6.07	7.98	12.25	12.11	10.74	12.75	9.26		
ATI	4.15	3.09	4.45	6.28	5.90	5.37	3.71	5.37	4.94	6.36		
FSBI	69.94	161.10	75.01	26.78	53.55	78.19	95.11	98.47	101.09	72.79		
% Tolerant Taxa	6.05	3.25	26.40	80.14	66.03	43.99	9.04	35.98	28.30	74.81		
% Dominant (single taxon)	23.45	30.87	19.84	59.78	37.56	27.83	20.36	27.04	31.22	57.28		
Abundance by Major Taxa (%)												
Ephemeroptera	12.64	48.54	10.86	1.58	3.30	7.56	39.78	18.08	22.76	8.01		
Plecoptera	21.36	9.31	3.85	0.33	5.13	5.24	9.03	2.88	3.68	1.00		
Trichoptera	23.08	7.56	24.75	3.16	6.65	5.52	24.07	49.20	44.76	5.85		
Coleoptera	23.45	1.13	0.09	0.01	0.06	3.71	5.56	1.76	8.83	4.04		
Chironomidae	8.50	27.32	15.35	0.20	2.18	25.55	17.56	6.66	1.00	2.93		
Other Diptera	4.72	2.75	1.23	0.75	0.19	1.10	1.27	2.08	1.21	0.65		
Non-Insect Taxa	6.05	3.40	43.87	93.97	82.49	51.32	2.67	18.58	17.74	75.32		
Abundance by Food Group (%)												
Collector-Gatherers	57.29	66.01	35.46	5.33	6.68	41.58	45.74	32.03	29.56	18.73		
Filter Feeders	3.78	4.44	16.28	0.85	5.56	1.77	20.92	46.30	42.41	2.30		
Scrapers/Grazers	13.03	15.37	23.06	79.42	68.48	43.17	23.11	18.51	23.27	75.91		
Shredders	13.05	9.65	1.57	0.56	2.96	0.62	1.19	0.17	0.65	0.11		
Predators	12.48	4.18	3.36	0.25	2.44	5.77	8.79	2.99	3.98	2.68		
Parasites	0.19	0.15	0.05	0.01	0.06	0.47	0.24	0.00	0.10	0.09		
Omnivores	0.19	0.21	20.21	13.58	13.81	6.62	0.00	0.00	0.02	0.18		

Appendix IV Table 2. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for May 2000 (Spring). Metrics are estimated from 1000 simulated 500-count subsamples using R from four composited full-count replicate kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area).

Motrice	Sampling Sites – May 2000										
Metrics	CR	DE	ME	1	15	3	5S	<b>7</b> S	9	10	12
Subsample Count	511.8	394	509.0	530.5	524.3	524.5	528.6	541.2	538.4	536.4	523.0
Total Abundance (#/composite)	2193.1	394	1700.1	6000.4	4541.6	4582.6	5405.0	8387.9	7848.7	6814.1	4402.8
Density (#/sq-m)	2950.8	530.1	2287.5	8073.5	6110.7	6165.8	7272.3	11285.9	10560.3	9168.3	5923.9
Taxa Richness (# taxa)	22.71	24	31.10	20.55	19.34	19.52	22.19	23.42	26.44	27.08	34.00
EPT Taxa Richness (# taxa)	12.19	17	18.39	10.41	8.51	10.02	12.30	15.14	16.60	16.59	19.96
Mayfly Richness (# taxa)	4.66	7	9.57	3.99	3.71	5.21	6.28	6.55	8.73	7.30	9.89
Stonefly Richness (# taxa)	1.23	4	3.02	2.09	1.61	1.99	3.00	3.07	2.94	2.99	3.21
Caddisfly Richness (# taxa)	6.31	6	5.81	4.33	3.19	2.81	3.03	5.52	4.93	6.29	6.87
Sensitive Taxa (# taxa)	8.43	13	20.29	9.42	8.83	8.64	11.31	11.33	11.94	12.76	13.71
ATI	4.69	3.94	3.17	4.53	4.77	5.54	4.75	4.32	4.42	4.45	4.79
FSBI	45.04	100	124.37	64.48	53.23	73.55	91.80	108.13	102.87	113.49	116.77
% Tolerant Taxa	12.70	6.35	3.21	7.30	26.76	50.70	8.20	2.93	6.32	11.02	15.36
% Dominant (single taxon)	42.22	37.31	20.32	53.68	44.47	31.59	74.72	41.93	49.94	21.00	31.74
Abundance by Major Taxa (%)											
Ephemeroptera	4.85	28.93	48.70	9.19	3.41	6.00	4.53	14.94	19.87	26.52	22.62
Plecoptera	0.89	3.81	3.02	2.74	0.60	3.22	3.37	5.73	3.48	4.59	3.22
Trichoptera	58.83	4.82	9.88	22.06	5.17	4.71	5.59	28.20	19.76	26.31	14.63
Coleoptera	14.91	14.47	2.72	0.05	0.00	0.07	0.56	3.32	1.80	11.41	5.10
Chironomidae	9.16	37.82	22.41	53.75	47.98	21.61	74.91	41.93	50.96	16.56	34.68
Other Diptera	5.81	3.05	9.24	2.47	2.12	0.20	1.14	3.15	1.40	3.52	4.08
Non-Insect Taxa	5.56	7.11	4.04	9.75	40.72	64.19	9.90	2.68	2.63	11.07	14.97
Abundance by Food Group (%)											
Collector-Gatherers	34.53	76.90	61.19	70.57	57.99	35.69	89.61	67.04	72.88	63.69	68.97
Filter Feeders	13.77	0.51	1.77	16.53	1.48	2.82	3.47	22.86	17.62	22.46	10.53
Scrapers/Grazers	47.95	16.50	23.12	5.09	25.68	44.81	1.14	2.14	5.22	6.48	13.98
Shredders	1.79	2.03	4.26	0.90	0.42	2.34	1.90	2.68	0.53	0.92	0.93
Predators	0.84	3.30	9.02	2.45	0.47	1.04	2.15	4.44	3.60	5.25	4.44
Parasites	1.09	0.76	0.52	0.17	0.16	0.35	1.42	0.83	0.14	1.20	0.98
Omnivores	0.05	0.00	0.12	4.29	13.80	12.96	0.31	0.01	0.02	0.00	0.17

Appendix IV Table 3. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for May 2001 (Spring). Metrics are estimated from 1000 simulated 500-count subsamples using R from four composited 300-count replicate kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area).

Motrice	Sampling Sites – May 2001										
Methes	CR	DE	ME	1	1S	3	<b>5</b> S	<b>7</b> S	9	10	
Subsample Count	504.0	505.8	510.5	515.0	523.0	529.5	530.2	567.5	533.4	584.4	
Total Abundance (#/composite)	754.2	1120.0	2070.9	2769.7	4496.3	5826.7	5752.4	13002.1	6353.8	16961.1	
Density (#/sq-m)	1014.8	1506.9	2786.4	3726.6	6049.7	7839.7	7739.8	17494.1	8548.9	22820.9	
Taxa Richness (# taxa)	19.43	30.25	30.02	23.91	18.28	24.53	25.87	25.36	31.51	29.97	
EPT Taxa Richness (# taxa)	10.00	17.97	21.23	13.03	7.05	11.36	13.86	15.83	19.03	18.42	
Mayfly Richness (# taxa)	3.65	7.11	10.65	4.99	1.92	4.73	5.50	6.32	8.83	8.23	
Stonefly Richness (# taxa)	0.68	3.90	3.25	2.35	1.91	2.88	3.31	3.00	2.97	2.95	
Caddisfly Richness (# taxa)	5.67	6.96	7.33	5.70	3.22	3.75	5.05	6.51	7.22	7.25	
Sensitive Taxa (# taxa)	6.65	14.22	20.34	11.91	5.86	11.60	11.47	11.55	12.73	14.04	
ATI	4.12	4.17	2.66	4.33	4.98	5.81	3.49	3.61	4.19	4.02	
FSBI	29.83	102.26	146.12	75.39	35.90	77.77	92.04	103.11	114.54	118.87	
% Tolerant Taxa	2.97	6.91	0.74	5.80	41.67	50.97	6.13	1.40	11.67	3.77	
% Dominant (single taxon)	40.09	32.35	42.67	39.38	29.25	44.78	25.30	20.16	17.79	18.91	
Abundance by Major Taxa (%)											
Ephemeroptera	19.76	23.60	71.92	10.27	1.12	4.94	37.48	34.96	23.74	21.40	
Plecoptera	0.14	4.08	1.43	5.34	1.91	3.11	8.11	7.26	2.91	2.16	
Trichoptera	19.13	11.19	8.88	31.76	1.70	8.79	16.59	27.56	33.53	30.62	
Coleoptera	10.26	11.15	0.39	0.00	0.07	0.00	1.41	8.71	4.26	17.84	
Chironomidae	40.76	37.32	12.47	40.54	20.28	25.61	25.52	15.60	19.70	18.38	
Other Diptera	6.33	5.31	4.32	6.10	2.50	0.70	2.62	2.43	5.82	4.86	
Non-Insect Taxa	3.62	7.35	0.58	5.98	72.44	56.84	8.26	3.48	9.57	4.75	
Abundance by Food Group (%)											
Collector-Gatherers	77.65	74.54	73.17	64.17	23.88	36.33	74.12	70.40	65.91	77.54	
Filter Feeders	6.83	3.38	1.18	20.58	3.11	2.98	4.56	13.31	16.52	12.74	
Scrapers/Grazers	6.89	15.56	17.57	6.28	40.52	53.66	10.20	6.08	9.22	4.03	
Shredders	0.00	1.82	3.46	2.95	1.60	2.39	3.26	2.82	0.80	0.69	
Predators	7.84	3.54	4.15	3.84	0.44	1.67	6.19	6.35	6.80	4.40	
Parasites	0.66	1.07	0.48	0.63	0.23	1.24	1.60	0.96	0.61	0.60	
Omnivores	0.13	0.09	0.00	1.56	30.23	1.73	0.07	0.07	0.13	0.00	

Appendix IV Table 4. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October 2001 (Fall). Metrics are estimated from 1000 simulated 500-count subsamples using R from four composited 300-count replicate kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area).

Motrice	Sampling Sites – October 2001										
Wethes	CR	DE	ME	1	1S	3	<b>5</b> S	<b>7</b> S	9	10	
Subsample Count	506.3	509.5	513.4	552.7	529.8	530.8	518.0	509.2	522.0	538.8	
Total Abundance (#/composite)	1222.0	1827.8	2626.1	10420.3	5743.1	5805.2	3484.3	1801.0	4233.6	7203.8	
Density (#/sq-m)	1644.2	2459.2	3533.4	14020.4	7727.2	7810.8	4688.1	2423.2	5696.3	9692.7	
Taxa Richness (# taxa)	20.81	27.54	34.45	18.44	15.27	13.62	23.38	26.24	28.16	28.17	
EPT Taxa Richness (# taxa)	11.24	16.43	20.82	8.37	5.92	5.39	9.63	13.67	14.55	14.53	
Mayfly Richness (# taxa)	3.00	6.12	9.33	2.20	2.07	2.61	3.88	4.96	4.47	6.20	
Stonefly Richness (# taxa)	1.88	4.96	4.89	1.62	1.18	1.05	2.72	2.96	2.29	2.81	
Caddisfly Richness (# taxa)	6.35	5.35	6.60	4.55	2.67	1.73	3.02	5.74	7.79	5.53	
Sensitive Taxa (# taxa)	7.89	13.14	21.65	6.94	4.66	4.23	8.76	10.05	8.39	11.21	
ATI	3.84	5.31	3.37	5.81	4.92	5.75	6.01	5.08	5.09	5.46	
FSBI	36.19	77.11	160.41	40.49	35.81	30.02	63.31	91.48	74.14	95.94	
% Tolerant Taxa	15.76	38.55	4.98	68.44	50.60	66.21	68.46	28.29	23.16	29.04	
% Dominant (single taxon)	41.12	26.94	30.01	53.48	35.77	34.62	38.47	21.70	21.16	23.48	
Abundance by Major Taxa (%)											
Ephemeroptera	44.34	8.39	42.94	1.37	4.53	1.26	7.14	8.70	5.46	7.12	
Plecoptera	0.41	9.78	4.21	0.68	0.33	0.27	4.43	2.50	2.32	3.31	
Trichoptera	22.27	15.45	12.61	11.48	5.74	0.73	10.50	34.77	38.55	30.60	
Coleoptera	8.60	20.28	1.12	0.07	0.00	0.00	1.37	21.70	2.08	21.59	
Chironomidae	2.96	2.43	25.93	0.89	0.55	0.00	2.18	0.96	30.28	7.60	
Other Diptera	4.28	3.37	5.95	0.38	0.83	0.07	0.27	2.17	0.91	1.06	
Non-Insect Taxa	17.15	40.30	7.16	85.12	88.02	97.66	74.12	29.15	13.65	27.06	
Abundance by Food Group (%)											
Collector-Gatherers	68.85	59.48	69.85	10.90	11.55	4.85	23.31	47.30	43.82	49.73	
Filter Feeders	3.73	6.95	1.32	2.65	1.24	0.35	1.09	16.99	31.80	25.98	
Scrapers/Grazers	22.66	19.45	9.61	67.38	49.17	67.54	66.40	29.45	19.90	19.78	
Shredders	0.49	5.50	6.43	0.28	0.16	0.14	1.31	0.84	0.81	0.77	
Predators	3.86	6.44	10.78	1.21	0.24	0.21	3.56	3.62	2.98	3.59	
Parasites	0.41	2.07	2.00	0.30	0.15	0.14	2.00	1.80	0.31	0.08	
Omnivores	0.00	0.11	0.00	17.29	37.48	26.77	2.33	0.00	0.38	0.07	

Appendix IV Table 5. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October 2013 from four composited kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area), as one 500-count sample (\*) or 4 300-counts replicates (+). Metrics for replicates are estimated from 1000 simulated 500-count subsamples using R (in bold).

Motrice	Sampling Sites – October 2013											
Wethes	CR*	DE*	ME*	1*	1S⁺	3⁺	5S*	7S⁺	9+	10*	12*	13*
Subsample Count	499	482	548	590	552.7	576.25	585	553.6	583.5	522	572	539
Total Abundance (#/composite)	4916.3	2570.7	2698.2	12606.8	10136.7	14471.4	16666.7	10562.4	16333.5	26769.2	7323.9	11517.1
Density (#/sq-m)	6614.8	3458.8	3630.4	16962.4	13638.8	19471.1	22424.8	14211.6	21976.6	36017.7	9854.3	15496.1
Taxa Richness (# taxa)	25	25	31	24	19.50	25.45	28	25.60	31.41	28	28	34
EPT Taxa Richness (# taxa)	8	14	17	8	5.37	9.76	12	12.28	14.65	15	11	16
Mayfly Richness (# taxa)	2	5	8	2	1.00	2.95	4	4.54	7.48	7	4	7
Stonefly Richness (# taxa)	0	5	3	1	0.00	1.94	2	2.55	1.66	2	1	1
Caddisfly Richness (# taxa)	6	4	6	5	4.37	4.87	6	5.19	5.51	6	6	8
Sensitive Taxa (# taxa)	7	9	19	5	4.52	7.79	10	8.73	9.65	11	7	10
ATI	6.03	4.38	3.16	5.14	5.07	6.00	5.23	5.56	6.30	5.73	6.81	5.90
FSBI	20.00	80.00	160.00	35.00	15.68	52.48	70.00	81.01	92.60	110.00	35.00	70.00
% Tolerant Taxa	63.73	31.54	4.56	43.05	48.22	61.29	47.69	47.04	56.26	40.42	75.17	39.33
% Dominant (single taxon)	38.88	30.71	21.35	33.39	34.82	31.42	22.74	30.75	20.13	27.78	25.87	19.11
Abundance by Major Taxa (%)												
Ephemeroptera	1.20	21.78	35.04	4.07	4.65	3.92	3.42	8.07	10.37	10.73	2.62	4.27
Plecoptera	0.00	5.81	4.01	0.34	0.00	1.55	1.20	3.42	0.64	0.57	0.17	0.19
Trichoptera	19.24	19.29	14.42	12.71	3.86	15.12	36.75	29.50	34.14	40.80	14.69	56.77
Coleoptera	1.20	8.92	0.55	0.17	0.00	0.07	3.08	4.53	1.51	5.94	3.50	2.97
Chironomidae	6.81	5.19	29.20	1.36	0.90	1.24	2.56	0.58	3.14	0.77	3.15	4.64
Other Diptera	1.60	1.04	9.12	0.85	2.75	0.56	0.00	0.28	0.50	1.53	0.17	2.23
Non-Insect Taxa	69.94	37.97	7.66	80.51	87.84	77.55	52.82	53.62	49.28	39.46	75.35	26.35
Abundance by Food Group (%)												
Collector-Gatherers	35.47	52.90	57.85	15.25	24.68	17.48	25.47	43.37	34.80	43.10	26.40	21.15
Filter Feeders	5.41	1.45	6.93	31.02	7.07	14.44	12.48	16.32	32.94	32.95	28.32	36.92
Scrapers/Grazers	50.90	32.99	16.06	15.25	31.60	50.66	55.56	33.08	27.97	18.77	40.91	33.21
Shredders	0.00	1.04	3.65	0.34	0.68	1.05	0.51	1.16	0.22	0.19	0.00	0.00
Predators	3.41	6.22	14.23	0.51	0.74	1.93	3.76	4.18	1.78	3.45	3.15	5.57
Parasites	0.80	5.39	1.09	0.34	0.41	0.28	1.20	1.82	0.56	1.53	0.70	0.37
Omnivores	3.81	0.00	0.18	37.29	34.82	14.16	1.03	0.07	1.73	0.00	0.52	2.78

Appendix IV Table 6 Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for April 2014 from four composited kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area), as one 500-count sample (\*) or 4 300-counts replicates (+). Metrics for replicates are estimated from 1000 simulated 500-count subsamples using R (in bold).

Matrice	Sampling Sites – April 2014											
Wetrics	CR*	DE*	ME*	1*	1S+	3⁺	5S*	7S⁺	9⁺	10*	12*	13*
Subsample Count	702	635	565	533	546.3	555.2	572	541.9	543.2	601	541	511
Total Abundance (#/composite)	8557.8	2540.0	1205.3	5317.8	9012.6	11477.7	8135.4	8521.9	8214.7	4808.0	9247.9	10918.8
Density (#/sq-m)	11514.5	3417.5	1621.8	7155.0	12126.3	15443.2	10946.1	11466.1	11052.8	6469.1	12442.9	14691.1
Taxa Richness (# taxa)	14	26	33	21	22.46	23.70	28	25.34	29.95	36	29	33
EPT Taxa Richness (# taxa)	6	17	17	7	8.22	9.80	15	13.55	14.81	18	15	18
Mayfly Richness (# taxa)	2	9	9	3	2.52	4.62	6	6.19	7.28	8	6	6
Stonefly Richness (# taxa)	1	2	4	1	1.32	1.70	3	2.00	2.68	3	3	3
Caddisfly Richness (# taxa)	3	6	4	3	4.38	3.48	6	5.36	4.86	7	6	9
Sensitive Taxa (# taxa)	4	11	19	4	5.21	7.88	10	8.87	9.65	15	10	11
ATI	7.17	5.25	3.54	5.51	5.99	5.90	4.94	5.05	4.91	5.45	5.10	5.47
FSBI	20.00	115.00	140.00	20.00	27.05	57.10	80.00	86.21	84.52	100	65	90
% Tolerant Taxa	79.06	38.90	10.27	36.77	48.56	56.38	23.43	30.01	22.55	36.61	26.99	35.23
% Dominant (single taxon)	78.49	38.11	24.42	19.89	35.32	29.67	27.27	25.27	16.97	24.79	17.38	23.09
Abundance by Major Taxa (%)												
Ephemeroptera	3.70	24.72	47.61	5.07	2.08	5.59	15.91	15.36	18.37	13.14	6.28	11.94
Plecoptera	0.14	2.99	1.42	1.31	0.42	1.26	1.92	3.80	1.52	1.83	1.29	0.98
Trichoptera	1.71	5.35	8.85	11.07	7.88	12.20	16.96	26.67	29.91	17.64	25.88	29.75
Coleoptera	0.43	9.76	0.18	0.00	0.00	0.00	4.37	5.99	2.79	13.64	2.22	1.57
Chironomidae	12.82	12.76	23.89	24.20	23.54	10.45	32.34	13.03	21.38	7.99	27.54	9.59
Other Diptera	0.00	2.05	5.31	0.56	1.17	0.14	0.52	0.44	0.31	1.00	1.85	2.35
Non-Insect Taxa	81.20	42.36	12.57	57.79	64.91	70.35	27.97	34.72	25.65	44.76	34.94	43.84
Abundance by Food Group (%)												
Collector-Gatherers	95.30	71.02	66.19	48.03	62.70	52.12	81.99	74.41	69.55	66.89	65.25	46.97
Filter Feeders	0.57	4.25	2.12	10.51	7.78	8.13	4.55	9.61	15.68	10.65	9.61	15.46
Scrapers/Grazers	1.57	15.28	20.35	26.64	12.94	26.42	6.64	7.96	6.72	15.47	12.94	22.50
Shredders	0.14	2.05	1.42	1.31	0.21	1.04	1.75	2.60	0.62	1.00	0.37	1.17
Predators	2.28	3.46	8.32	0.38	1.18	1.51	2.45	3.98	6.37	2.33	11.46	12.92
Parasites	0.00	3.94	1.59	3.38	4.04	0.22	1.22	1.37	0.75	3.49	0.18	0.78
Omnivores	0.00	0.00	0.00	9.76	11.15	10.55	1.40	0.07	0.30	0.17	0.00	0.20

Appendix IV Table 7. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for October 2014. from four composited kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area), as one 500-count sample (\*) or 4 300-counts replicates (+). Metrics for replicates are estimated from 1000 simulated 500-count subsamples using R (in bold).

Metrics	Sampling Sites – October 2014											
	CR*	DE*	ME*	1*	1S⁺	3⁺	5S*	7S⁺	9+	10*	12*	13*
Subsample Count	606	530	573	514	577.6	567.6	532	529.9	545.6	528	526	561
Total Abundance (#/composite)	12926.6	2120.0	3315.0	10965.3	14817.3	13412.0	12380.7	5918.5	9023.2	23508.5	12241.1	11724.1
Density (#/sq-m)	17392.6	2852.4	4460.3	14753.7	19936.5	18045.7	16658.1	7963.3	12140.6	31630.4	16470.3	15774.7
Taxa Richness (# taxa)	21	29	27	22	19.84	22.36	25	26.70	29.44	29	24	32
EPT Taxa Richness (# taxa)	6	14	16	8	4.86	7.86	13	13.88	14.56	14	12	16
Mayfly Richness (# taxa)	1	5	6	2	1.34	1.99	4	5.49	7.33	7	4	5
Stonefly Richness (# taxa)	0	5	4	1	0.00	1.83	4	2.67	1.42	3	2	2
Caddisfly Richness (# taxa)	5	4	6	5	3.52	4.05	5	5.72	5.81	4	6	9
Sensitive Taxa (# taxa)	4	13	17	6	3.90	6.03	9	9.11	8.06	11	7	10
ATI	5.99	5.69	3.35	5.92	5.60	6.31	5.29	5.14	5.78	5.17	5.72	5.39
FSBI	30	90	100	25	8.42	31.20	55.00	76.34	78.16	95.00	60.00	65.00
% Tolerant Taxa	43.40	41.51	1.92	52.53	48.98	63.46	26.13	22.81	38.81	32.58	49.43	35.29
% Dominant (single taxon)	41.58	40.94	30.37	24.12	23.22	24.89	20.11	28.50	22.71	18.18	25.48	19.07
Abundance by Major Taxa (%)												
Ephemeroptera	10.73	10.75	42.76	2.14	3.00	2.12	14.85	15.40	14.43	18.56	2.47	9.98
Plecoptera	0.00	3.96	5.93	0.39	0.00	1.52	2.63	3.86	0.50	1.70	0.95	0.53
Trichoptera	4.95	17.55	9.25	20.43	7.33	10.34	21.99	36.68	35.07	26.33	35.36	41.53
Coleoptera	0.66	7.36	1.05	0.00	0.07	0.00	1.88	9.60	1.31	12.31	4.75	1.96
Chironomidae	31.02	8.11	33.33	2.92	2.41	4.04	17.86	3.01	10.58	4.36	4.94	3.03
Other Diptera	4.46	2.64	3.66	2.14	7.10	2.62	7.52	2.09	0.77	2.08	0.19	0.71
Non-Insect Taxa	47.69	49.62	4.01	71.98	80.08	79.37	33.27	29.29	35.21	34.47	50.57	38.32
Abundance by Food Group (%)												
Collector-Gatherers	82.51	61.89	67.89	29.38	21.82	18.82	54.89	38.21	35.08	50.19	25.10	20.68
Filter Feeders	10.56	14.53	4.19	29.38	14.92	14.07	26.88	32.86	33.02	20.83	19.39	26.38
Scrapers/Grazers	1.82	8.87	11.87	21.60	34.38	52.39	7.33	17.16	26.02	22.16	52.09	43.32
Shredders	0.00	0.94	8.20	0.39	0.00	1.22	0.38	0.52	0.21	0.19	0.00	0.00
Predators	3.30	6.79	6.11	1.75	0.45	1.20	7.33	8.58	3.68	5.11	3.23	6.95
Parasites	0.50	6.98	1.75	1.17	0.45	0.46	0.75	2.66	0.44	1.52	0.00	0.36
Omnivores	1.32	0.00	0.00	16.34	27.98	11.84	2.44	0.00	1.55	0.00	0.19	2.32

Appendix IV Table 8. Summary of metrics calculated for benthic invertebrate samples obtained from the lower Deschutes River for April 2015 from four composited kick samples (0.743 m<sup>2</sup> or 8 ft<sup>2</sup> in area), as one 500-count sample (\*) or 4 300-counts replicates (+). Metrics for replicates are estimated from 1000 simulated 500-count subsamples using R (in bold).

Metrics	Sampling Sites – April 2015											
	CR*	DE*	ME*	1*	1S+	3⁺	5S*	7S⁺	<b>9</b> ⁺	10*	12*	13*
Subsample Count	562	555	511	536	560.2	539.0	502	529.2	531	521	570	534
Total Abundance (#/composite)	10097.0	2631.6	4937.2	9800.7	11836.6	7543.9	5245.6	5627.9	6057.8	10259.9	6632.5	7194.8
Density (#/sq-m)	13585.4	3540.8	6642.9	13186.7	15926.0	10150.3	7057.8	7572.2	8150.7	13804.6	8924.0	9680.6
Taxa Richness (# taxa)	24	27	31	24	16.56	24.45	31	30.02	34.83	32	33	31
EPT Taxa Richness (# taxa)	10	16	16	10	4.64	9.68	14	15.88	19.09	19	19	19
Mayfly Richness (# taxa)	4	8	7	4	1.62	3.86	6	6.90	10.11	9	8	8
Stonefly Richness (# taxa)	0	3	3	2	0.60	2.28	2	2.89	2.18	3	4	3
Caddisfly Richness (# taxa)	6	5	6	4	2.41	3.54	6	6.09	6.80	7	7	8
Sensitive Taxa (# taxa)	6	12	16	8	3.02	8.84	10	10.91	12.83	14	12	13
ATI	7.15	4.67	3.81	5.58	5.60	5.75	4.88	4.98	4.80	4.86	5.30	4.75
FSBI	50.00	95.00	135.00	60.00	10.78	59.35	80.00	96.04	101.74	95.00	125.00	115.00
% Tolerant Taxa	81.14	23.60	2.74	36.38	33.13	32.61	26.10	25.86	14.31	21.88	28.07	13.11
% Dominant (single taxon)	78.83	23.24	37.57	23.32	27.39	32.33	24.90	22.81	19.40	20.92	26.32	40.26
Abundance by Major Taxa (%)												
Ephemeroptera	3.91	23.96	29.35	5.22	4.93	8.03	22.91	26.08	30.35	17.85	12.63	20.41
Plecoptera	0.00	2.16	1.57	1.12	0.16	3.39	2.59	3.91	0.89	1.34	1.40	2.06
Trichoptera	4.27	4.68	8.22	7.09	2.35	6.06	21.12	20.66	25.55	24.76	37.89	57.68
Coleoptera	0.53	13.87	0.59	0.00	0.00	0.00	2.39	6.47	3.18	20.92	8.07	2.43
Chironomidae	7.30	22.34	46.77	6.34	11.63	6.17	11.75	7.41	15.53	2.69	4.39	2.25
Other Diptera	0.53	4.32	8.81	23.32	25.18	32.33	4.78	1.29	5.74	4.80	2.28	3.93
Non-Insect Taxa	83.27	28.65	4.50	56.90	55.75	44.03	34.46	34.17	17.07	27.64	32.98	11.05
Abundance by Food Group (%)												
Collector-Gatherers	91.81	68.11	69.08	33.96	43.37	34.96	59.36	60.62	50.99	54.13	37.19	27.90
Filter Feeders	1.42	1.44	7.24	30.04	27.63	38.28	17.13	16.42	31.08	19.58	32.98	48.13
Scrapers/Grazers	3.74	21.08	11.94	17.72	5.78	15.20	12.35	10.17	9.48	17.47	20.35	17.98
Shredders	0.00	1.80	3.52	0.56	0.23	2.76	1.59	2.28	0.38	0.58	0.35	1.50
Predators	2.31	3.42	6.85	0.93	0.66	1.27	5.58	7.19	7.00	4.22	7.37	3.00
Parasites	0.36	3.96	1.17	1.49	5.78	1.37	2.39	3.12	0.91	4.03	1.75	1.50
Omnivores	0.00	0.18	0.00	15.30	16.55	6.16	1.59	0.21	0.15	0.00	0.00	0.00

## APPENDIX V – ADDITIONAL MACROINVERTEBRATE RESULT FIGURES





Appendix V Figure 1. Comparison of 4 different EPT taxa richness estimates at sites in the lower Deschutes River downstream from the reregulation dam and three reference sites for the pre-SWW period of 1999-2001.



Appendix V Figure 2. Comparison of 4 different EPT taxa richness estimates at sites in the lower Deschutes River downstream from the reregulation dam and three reference sites for the post-SWW period of 2013-2015.



Appendix V Figure 3. Comparison of 4 different sensitive taxa richness estimates at sites in the lower Deschutes River downstream from the re-regulation dam and three reference sites for the pre-SWW period of 1999-2001.



Appendix V Figure 4. Comparison of 4 different sensitive taxa richness estimates at sites in the lower Deschutes River downstream from the re-regulation dam and three reference sites for the post-SWW period of 2013-2015.



Appendix V Figure 5. Average Fall and Spring density estimates (no./m<sup>2</sup>) in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies. Bars within the blue box are the results used in Linear Model Effects (LME) univariate statistical tests (see Table 3).



Appendix V Figure 6. Average Fall and Spring total taxa richness estimates in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies. Bars within the blue box are the results used in Linear Model Effects (LME) univariate statistical tests (see Table 4), based on the simulation estimation data set.


Appendix V Figure 7. Average Fall and Spring EPT taxa richness estimates in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies. Bars within the blue box are the results used in Linear Model Effects (LME) univariate statistical tests (see Table 4), based on the simulation estimation data set.



Appendix V Figure 8. Average Fall and Spring number of taxa classified as "sensitive" (ATI score ≤ 3) in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies. Bars within the blue box are the results used in Linear Model Effects (LME) univariate statistical tests (see Table 4), based on the simulation estimation data set.



Appendix V Figure 9. Average Spring and Fall Assemblage Tolerance Index (ATI) scores in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies. Higher scores indicate greater stream impairment. Bars within the blue box were the results used in Linear Model Effects (LME) univariate statistical tests (see Table 3).



Appendix V Figure 10. Average Fall and Spring relative abundances of "tolerant" taxa (ATI score ≥ 7) in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies. Bars within the blue box are the results used in Linear Model Effects (LME) univariate statistical tests (see Table 3).



Appendix V Figure 11. Average Spring and Fall Fine Sediment Biotic Index (FSBI) scores in the lower Deschutes River downstream from the re-regulation dam and three reference sites for both baseline (Pre-SWW) and current (Post-SWW) studies. Bars within the blue box were the results used in Linear Model Effects (LME) univariate statistical tests (see Table 4).