ECOANALYSTS, INC.

BENTHIC COMMUNITY RESULTS

HYLEBOS WOOD DEBRIS SITE
TACOMA, WASHINGTON

Prepared for:
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ACRONYMS AND ABBREVIATIONS

CAP:	Cleanup Action Plan
CMP:	Compliance Monitoring Plan
CoC:	Chain of Custody
LPTL:	Lowest Practicable Taxon Level
NEBA:	Net Environmental Benefit Analysis
nMDS:	non-metric Multidimensional Scaling plot
PSEP:	Puget Sound Estuary Program
QA/QC:	Quality Assurance / Quality Control
SCO:	Sediment Cleanup Objectives
SD:	Standard Deviation
SIMPROF:	Similarity Profile test of significance
SMS:	Sediment Management Standards

1. INTRODUCTION

EcoAnalysts conducted a benthic community analysis as part of a remedial investigation and risk assessment being performed within the head of the Hylebos Waterway located in Tacoma, WA to examine potential wood debris impacts to biota. A Cleanup Action Plan (CAP) and Compliance Monitoring Plan (CMP) were implemented and remedial actions performed between 2001 and 2005. Two areas within the Hylebos Wood Debris Site were identified with minor wood debris impacts where no remedial action was conducted. These areas are to be characterized through a net environmental benefit analysis (NEBA) after benthic conditions in the dredged reference areas nearby have stabilized. The benthic assemblage results are included in this report, alongside the interpretation of any potential community disturbance at the Hylebos Wood Debris Site stations.

2. METHODS

2.1 Sample Collection

All field sampling and sediment collection was conducted in accordance with the Puget Sound Estuary Program protocols (PSEP 1997).

All benthic samples were collected by representatives from Anchor QEA and processed on-site by an EcoAnalysts ecologist. Three NEBA site stations and three previously dredged reference stations (HOW-B09, HOW-B10, and REF-001) were sampled for benthic community analysis on June 17th and 18th, 2020 (Table 2-1). Samples were collected at each station using a Van Veen power grab sampler. Once onboard the vessel and deemed an acceptable grab, two clean butyrate core tubes (13” long and 3.75” in diameter) were inserted into the sediment retained by the grab. These two cores represented one replicate sample with a total area of 0.016 m^2. A total of three samples were collected at each station. An overview map of all station locations is presented in Figure 2-1 and a collection Chain of Custody (CoC) is provided in Appendix A.

Table 2-1: Benthic Community Sample Collection Summary

	Station	Sample	Collection Date	Collection Time
Site Stations	HOW-B01	HOW-B01 Rep 1	6/18/20	1200
		HOW-B01 Rep 2	6/18/20	1210
		HOW-B01 Rep 3	6/18/20	1222
	HOW-B02	HOW-B02 Rep 1	6/17/20	1235
		HOW-B02 Rep 2	6/17/20	1245
		HOW-B02 Rep 3	6/17/20	1305
	HOW-B08	HOW-B08 Rep 1	6/17/20	1710
		HOW-B08 Rep 2	6/17/20	1720
		HOW-B08 Rep 3	6/17/20	1735
Reference Stations	HOW-B09	HOW-B09 Rep 1	6/18/20	1415
		HOW-B09 Rep 2	6/18/20	1430
		HOW-B09 Rep 3	6/18/20	1445
	HOW-B10	HOW-B10 Rep 1	6/17/20	1455
		HOW-B10 Rep 2	6/17/20	1510
		HOW-B10 Rep 3	6/17/20	1525
	REF-001	REF-001 Rep 1	6/18/20	1600
		REF-001 Rep 2	6/18/20	1615
		REF-001 Rep 3	6/18/20	1630

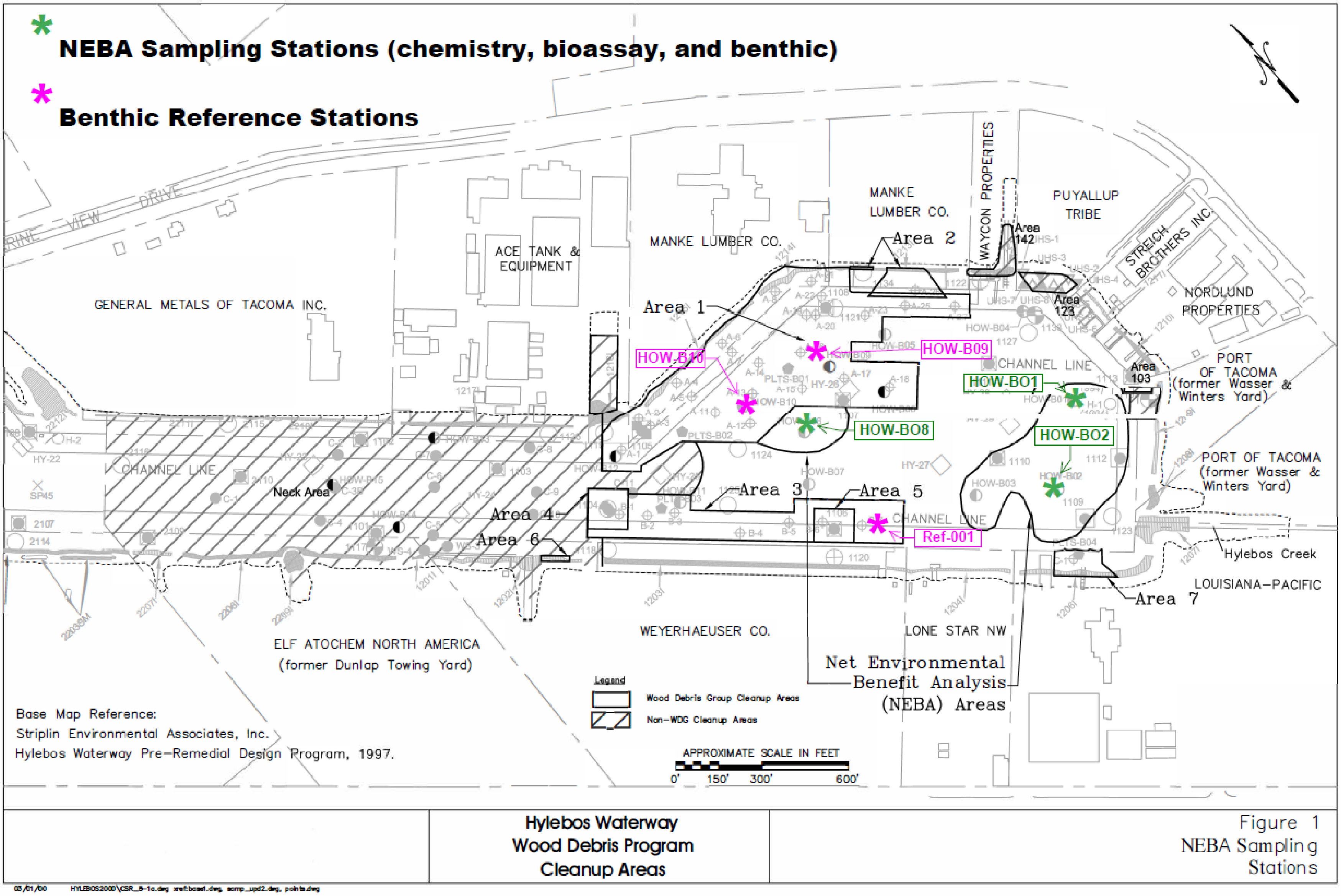

Figure 2-1: Sampling Stations (from the project SQAPP, Anchor 2020)

2.2 Sample Processing

Upon collection, all benthic infauna samples were brought to shore and sieved through a 1.0-mm mesh screen to remove sediment fines. All residual sediment, debris, shells, and benthic organisms on the screen were carefully collected into labelled wide-mouth bottles. Samples were “fixed” on-site in 10% buffered formalin and diluted by seawater to create a 5% formalin preservative. The benthic samples were stored at ambient temperature throughout transit and shipped to the EcoAnalysts benthic laboratory in Moscow, ID.

2.3 Benthic Sample Sorting and Taxonomy

Benthic samples arrived at the Moscow EcoAnalysts facility in good condition. All benthic samples were processed by EcoAnalysts using the PSEP protocols for identification of benthic macroinvertebrates (PSEP 1987). Upon receipt, samples were transferred to 70% ethanol for long-term preservation and storage. The sorting process entailed placing small quantities of sample in a petri dish, removing all organisms under a dissecting microscope, and placing them into vials according to major taxon categories (e.g. mollusks, crustaceans, annelids, etc.). This process was continued until 100% of the sample was sorted. Sorted material was then transferred back to the original sample container and underwent a quality assurance (QA) check to control for thoroughness and consistency in sample sorting. This sorting review was performed by staff who did not initially sort the sample.

All specimens were identified by qualified taxonomists to the lowest practicable taxonomic level (LPTL) and enumerated. In most cases this was genus or species level; those organisms identified to a higher level were due to a qualifier, such as damage or immaturity of the specimen. As a quality control (QC) check, a full taxonomic re-analysis of two samples was performed by taxonomists who did not originally identify the organisms. Any significant identification discrepancies and their resolutions were noted in the QC report. If taxonomy results between the original and QC IDs were >10% different, a reconciliation between the taxonomists occurred. All benthic data and results of the taxonomy QC are presented in Appendix B.

2.4 Statistical Analysis

All benthic data were reviewed for adherence to the PSEP framework. Statistical analyses were performed with Microsoft Excel (for mean data, ANOVAs, and t-tests on indices), GraphPad Prism 8.01 (for post-hoc analyses on ANOVA results), and PRIMER v.7 (for multivariate analyses to compare similarity between community assemblages; Clarke and Gorley 2015). When the ANOVA indicated a statistical difference, a post-hoc test using Tukey’s multiple comparison method or Fisher’s least significant difference was used to determine which stations were statistically different from the references.

Prior to any statistical analysis, benthic identifications with qualifiers (such as from damaged or juvenile specimens lacking key identifying features) were aggregated with similar or higher-level taxa to avoid artificial inflation of community richness and diversity indices. Any epifauna, such as corals or sponges, were noted if present (annotated as “large/rare” in the dataset) but not included in abundance and diversity measures.

2.4.1 Abundance and Diversity Indices

All indices were performed on individual samples and averaged to give mean values per station. In addition to taxa richness (the number of unique taxa in a sample), Mollusca richness (the number of mollusk taxa in a sample), and total abundance (the sum of organisms in a sample), three standard biodiversity measures were used to calculate benthic community diversity and evenness: the Shannon-Wiener Diversity Index, Pielou's Evenness Index, and the Swartz Dominance Index.

Shannon-Wiener Diversity Index

This index is a quantitative measure of the biodiversity within a sample based on the sample richness (number of taxa observed). The result of this diversity index increases when either abundance and/or evenness increases. The measure is depicted as H' and is calculated based on the following formula:

$$H' = -\sum_{i=1}^{R} p_i \ln p_i$$

Where *R* is the richness of the dataset in terms of total number of different taxa, p_i is the proportion of individuals belonging to the *ith* species in the dataset.

Pielou's Evenness Index

Evenness is a measure of biodiversity that quantifies how equivalently distributed the community is numerically. The evenness index (*J'*) describes how close in abundance each taxa is for a given sample. The evenness of a population can be represented by Pielou's evenness index:

$$J' = \frac{H'}{\log_e \mathrm{S}}$$

Where *S* is abundance of organisms and *H'* is Shannon-Wiener diversity. *J'* is constrained between 0 and 1, with more evenly distributed communities having higher *J'* values.

Swartz Dominance Index

The Swartz Dominance Index calculates the minimum number of taxa accounting for 75% of the total invertebrate abundance within a sample. A low dominance score indicates a sample is dominated by fewer taxa.

2.4.2 Multivariate Analyses

To gain an understanding of how similar the benthic assemblages are at the Hylebos Wood Debris stations, similarity and ordination multivariate analyses were conducted on the infaunal samples. Taxa abundances were pre-treated with a square root transformation to reduce the influence of highly abundant taxa in the similarity and resemblance matrices. This also allows for less abundant, but important components of the community, to influence the interpretation of the data.

2.4.2.1 Resemblance Matrices and Cluster Diagrams with SIMPROF Test of Significance

A Bray-Curtis Similarity Index was performed to compare similarities between sites and the reference locations. This resemblance matrix calculates the relative percent similarity between samples based primarily on the abundance of taxa present within each station.

As defined by Bray and Curtis, the index of similarity is:

$$S_{17} = 100\left(\frac{\sum_i |y_{i1} - y_{i2}|}{\sum_i y_{i1} + \sum_i y_{i2}}\right)$$

Where y_i is the count for the *i*th (of *p*) species from sample 1, $\sum_i$ (….) denotes summation over those species. The results from the Bray-Curtis similarity index are bound between 0 and 1, which is converted to a percentage for comparison purposes. Stations with a result of 1 have the same species composition while those with a result of 0 do not share any common species.

Cluster diagrams were created as a visual representation of the Bray-Curtis Similarity matrix. Individual replicate data were summed per station prior to pretreatment and Bray-Curtis analysis. Stations are arranged on the *x*-axis, with percent similarity on the *y*-axis. Stations are hierarchically linked via clusters, with those that are more similar being grouped together. A similarity profile test (SIMPROF) was performed on the clusters to determine significant difference between stations (999 permutations at a 5% significant level): horizontal line breaks in the linkages indicate a break in similarity at a specific percent between groups of samples, while dotted/dashed red lines indicate a failure to reject the null hypothesis that no significant community differences could be found between cluster stations.

2.4.2.2 Non-Metric Multidimensional Scaling (nMDS) Plots

To determine outlier samples and similarity between replicates per station, a resemblance matrix using Bray-Curtis was conducted for individual replicate samples and plotted in non-metric multidimensional scaling space (nMDS) according to their similarity rank (data points with benthic communities that are more alike are grouped closer to each other while those that are least alike are plotted farther away). Similar to cluster diagrams, a SIMPROF test of significance was performed: a dotted red line encircles stations which contain communities that are not significantly different from each other (999 permutations at a 5% significance level).

3. RESULTS

The analysis of community condition and results from the benthic community metrics are presented in the following sections. The taxonomy QC samples passed, achieving a 96.7 - 99.8% similarity between the original and QC identifications. Statistical comparisons and indices are provided in Appendix B while all benthic community data and taxonomy QC results are presented in Appendix C.

3.1 Abundance and Diversity Indices

The total abundance of organisms, taxa richness, and community composition indices were calculated for each sample and averaged to present mean values per station (Table 3-1). Overall, sites had similar abundance and richness to the reference stations, which averaged 63 - 98 individuals per 0.016 m^2 and 9 - 10 unique taxa. The lowest abundance was found at station HOW-B08 (averaging 50 individuals per 0.016 m^2) while the highest abundance was at station HOW-B02 (averaging 153 individuals per 0.016 m^2). Similar to the reference stations, taxa richness at the sites was low and ranged from an average of 7 to 10 taxa per 0.016 m^2. Mollusca richness ranged from 2 to 3 taxa at all stations.

Table 3-1: Average Abundance, Richness, and Mollusca Richness Results

	Station	Abundance (# of indiv / 0.016 m^2)		Richness (# of taxa / 0.016 m^2)		Mollusca Richness (# of taxa / 0.016 m^2)	
		Mean[1]	SD	Mean[1]	SD	Mean[1]	SD
Site	HOW-B01	66	11.0	7	2.3	2	0.00
	HOW-B02	153	35.2	10	1.0	3	1.2
	HOW-B08	50	29.2	7	1.2	2	0.58
Reference	HOW-B09	63	35.4	10	2.6	2	0.58
	HOW-B10	98	19.4	10	5.0	3	0.58
	REF-001	82	7.6	9	0.6	3	0.58

[1] n = 3 reps per station

Diversity scores were also similar between the reference and site locations (Table 3-2). Average scores for site stations ranged between 0.90 to 1.29 whereas the average score for the reference stations were 1.21 - 1.41. Communities were dominated by few species that were recovered in high numbers, resulting in moderate evenness scores (averaging between 0.42 to 0.68) and low dominance scores (averaging 2 at each site). The reference stations scored similarly with average evenness scores of 0.56 to 0.63 as well as low average dominance scores of 2 to 3.

Table 3-2: Average Diversity, Evenness, and Dominance Results

	Station	Shannon-Wiener Diversity		Pielou's Evenness		Swartz Dominance	
		Mean[1]	SD	Mean[1]	SD	Mean[1]	SD
Site	HOW-B01	0.90	0.28	0.90	0.28	2	0.58
	HOW-B02	0.97	0.25	0.97	0.25	2	0.58
	HOW-B08	1.29	0.28	1.29	0.28	2	0.58
Reference	HOW-B09	1.39	0.16	1.39	0.16	3	0.58
	HOW-B10	1.41	0.47	1.41	0.47	3	1.0
	REF-001	1.21	0.14	1.21	0.14	2	0.00

[1] n = 3 reps per station

The sediment management standards (SMS) for cleanup sites compares the abundance of three major taxa groups (Polychaeta, Mollusca, and Crustacea) between sites and reference locations (Ecology 2019). All three NEBA sites and reference stations had a high abundance of mollusks but few to no crustaceans (Table 3-3).

Table 3-3: Average Abundance of Major Taxa Groups at Stations

	Station	Polychaeta Avg Abundance[1] (# of indiv / 0.016 m^2)	Mollusca Avg Abundance[1] (# of indiv / 0.016 m^2)	Crustacea Avg Abundance[1] (# of indiv / 0.016 m^2)
Site	HOW-B01	3.1	25.3	1.0
	HOW-B02	6.1	40.5	0.0
	HOW-B08	5.7	13.0	0.0
Reference	HOW-B09	3.3	15.4	1.0
	HOW-B10	6.5	14.6	1.0
	REF-001	3.6	19.3	1.5

1 n = 3 reps per station

Overall, the community compositions at each of the site stations were similar to each other as well as each of the reference stations (Figure 3-1). Approximately 78% of the abundance recovered at REF-001 was comprised of mollusks and 21% was polychaetous annelids while HOW-B10 had a noticeably higher percentage of "other" taxa (nemerteans and phoronids) collected in one of the sample replicates. Station HOW-B08 contained more annelids than all other stations (comprising 67% of the abundance at that station). The dominant species found at the site and reference locations was *Axinopsida serricata* (a small clam) and *Scoletoma luti* (a polychaete). The clam, *Nutricola lordi*, was predominantly found at REF-001 while sedentary polychaetes in the Cirratulidae family were dominant members of the community at stations HOW-B02, HOW-B08, HOW-B09, and HOW-B10 but were sparse at HOW-B01 and REF-001.

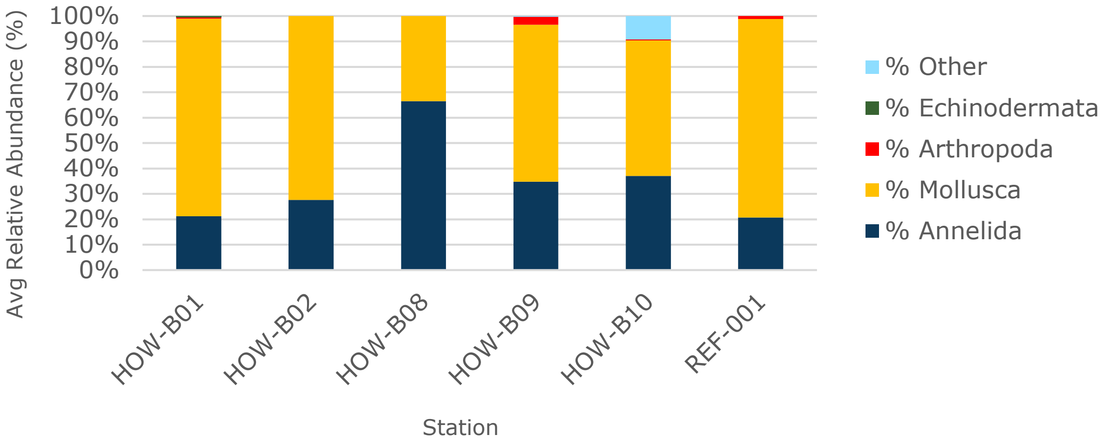

Figure 3-1: Relative Percent Abundance of Phyla at Each Station

ANOVA results (Table 3-4) indicate that the NEBA sites were not significantly different from any of the reference locations for richness (p=0.462), Mollusca richness (p=0.110), diversity (p=0.204), and dominance (0.112). There were significant differences in the abundance and evenness results. Total abundance at station HOW-B02 was found to be significantly different from the reference locations HOW-B09 and REF-001 (Table 3-5). However, it had significantly greater abundance than both reference stations, not lower. HOW-B02 was also found to have significantly lower evenness than both HOW-B09 and HOW-B10, but not REF-001 (Table 3-6). Station HOW-B01 had significantly lower evenness than HOW-B10, but only marginally so (p=0.04).

Table 3-4: Richness, Diversity, and Dominance ANOVA Results of Sites vs Reference Stations

	P Value	Significant?
Richness	0.462	No
Mollusca Richness	0.110	No
Diversity	0.204	No
Swartz Dominance	0.112	No
n=3 reps per station		

Table 3-5: Abundance ANOVA Results and Post-Hoc Analysis of Sites vs Reference Stations

	P Value		**Significant?**		
Abundance	0.004		Yes		
Site	**Reference**	**Mean Diff**	**95% CI of Diff**	**Ind P Value**	**Significant?**
HOW-B01	**HOW-B09**	2.667	-67.2 to 72.53	>0.9999	No
	HOW-B10	-32.67	-102.5 to 37.2	0.6303	No
	REF-001	-16.67	-86.53 to 53.2	0.9618	No
HOW-B02	**HOW-B09**	90.00	20.14 to 159.9	0.0098	**Yes**
	HOW-B10	54.67	-15.2 to 124.5	0.1634	No
	REF-001	70.67	0.8049 to 140.5	0.0469	**Yes**
HOW-B08	**HOW-B09**	-12.67	-82.53 to 57.2	0.9883	No
	HOW-B10	-48.00	-117.9 to 21.86	0.2625	No
	REF-001	-32.00	-101.9 to 37.86	0.6487	No
Post-hoc analysis conducted with a Tukey’s multiple comparison, n=3 reps per station					

Table 3-6: Evenness ANOVA Results and Post-Hoc Analysis of Sites vs Reference Stations

	P Value		**Significant?**		
Evenness	0.033		Yes		
Site	**Reference**	**Mean Diff**	**95% CI of Diff**	**Ind P Value**	**Significant?**
HOW-B01	**HOW-B09**	-0.1702	-0.34 to 0.0008	0.0510	No
	HOW-B10	-0.1787	-0.35 to -0.01	0.0419	**Yes**
	REF-001	-0.1064	-0.28 to 0.06	0.2002	No
HOW-B02	**HOW-B09**	-0.2018	-0.37 to -0.03	0.0245	**Yes**
	HOW-B10	-0.2103	-0.38 to -0.04	0.0200	**Yes**
	REF-001	-0.1381	-0.31 to 0.03	0.1040	No
HOW-B08	**HOW-B09**	0.05922	-0.11 to 0.23	0.4651	No
	HOW-B10	0.05069	-0.12 to 0.22	0.5305	No
	REF-001	0.123	-0.05 to 0.29	0.1431	No
Post-hoc analysis conducted with Uncorrected Fisher’s LSD, n=3 reps per station					

3.2 Community Similarities and Dissimilarities

Stations were also investigated for community similarities between samples at each station as well as similarities/dissimilarities between each station and the reference locations with a Bray-Curtis Similarity Index and cluster diagram (Figure 3-2). A SIMPROF test of significance on the stations indicates that none of them were significantly different from each other as well as the reference stations.

Individual station replicates were also compared to determine if any outlier samples were significantly different from those collected at the reference locations (Figure 3-3). A Bray-Curtis matrix was applied, and samples mapped on a nMDS plot alongside a SIMPROF analysis. Results indicate that none of the replicates were found to have communities that were significantly different from the reference samples (as displayed with a dashed red line encompassing all samples).

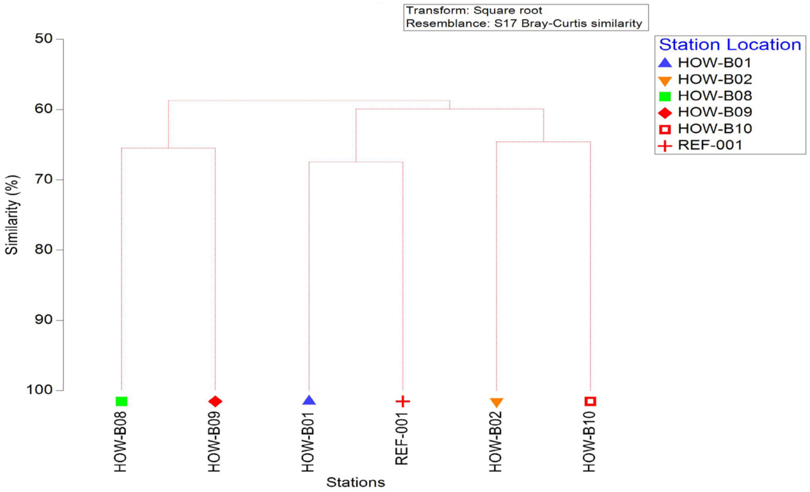

Figure 3-2: Community Similarity Cluster Groupings of Stations

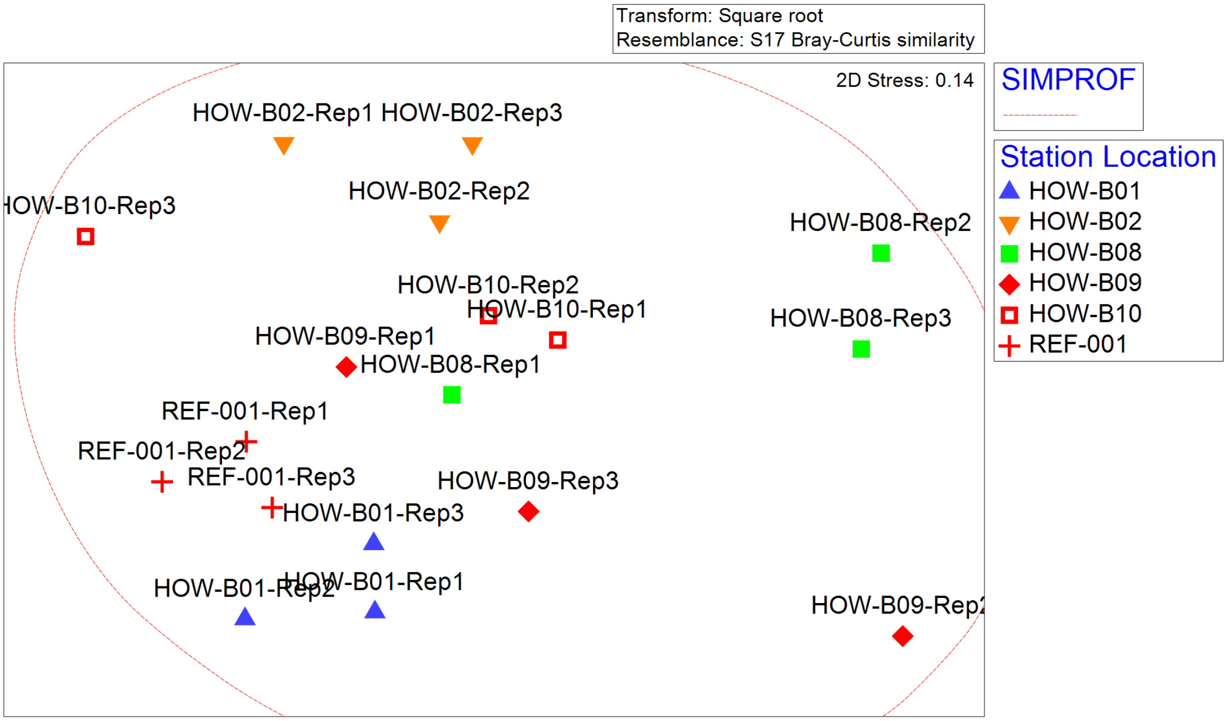

Figure 3-3: nMDS Plot of Station Replicate Samples

4. DISCUSSION

The clam *Axinopsida serricata* and polychaete *Scoletoma luti* were recovered at nearly every site and reference station in abundant numbers. *A. serricata* is known to be an indicator species tolerant of high organics and low dissolved oxygen (SCCWRP 2013). Similarly, *S. luti* is a stress-tolerant polychaete and commonly found in silt and fine sand sediments. Arthropod crustaceans were noticeably low in abundance across all stations and absent at sites HOW-B02 and HOW-B08. Nearly all stations were composed primarily of bivalve mollusks, with station HOW-B08 having a higher abundance of polychaetes from the family Cirratulidae. While HOW-B02 had significantly lower evenness than two of the reference stations, it had a higher total abundance.

The sediment management standards (SMS) for cleanup sites compares the abundance of three major taxa groups (Polychaeta, Mollusca, and Crustacea) between sites and reference locations (Ecology 2019). For SMS calculations and scoring purposes, abundance of the major taxa groups of the three reference stations were averaged to present a single pooled reference to compare against. A site will “fail” sediment cleanup objectives (SCO) if the site-to-reference abundance ratio is less than 0.50 for any one of the three major taxa groups. All three NEBA sites had a high abundance of mollusks but few, if any, crustaceans. As such, following SMS guidance, stations HOW-B02 and HOW-B08 would fail to meet the SCO when compared against the pooled reference (Table 4-1; p=0.01 for HOW-B02 and HOW-B08). However, it is important to stress that the abundance of crustaceans was low at all stations, including the reference stations which averaged only 1 individual per sample. Therefore, it is not advisable to rely upon the SMS comparison alone for each station as a true reflection of community condition and disturbance level.

Table 4-1: SMS Results for NEBA Sites

	Site Compared to Pooled Reference (A_T / A_R)			Fail SCO/SQS? (A_T / A_R < 0.50)[2]
Site	Polychaeta Avg Abundance[1]	Mollusca Avg Abundance[1]	Crustacea Avg Abundance[1]	
HOW-B01	0.68	1.54	0.86*	No
HOW-B02	1.37	2.46	**0.00***	Yes*
HOW-B08	1.28	0.79	**0.00***	Yes*

* Due to the low abundance or absence of crustaceans at all stations (including the reference), the SCO score is unreliable
[1] n = 3 reps per station
[2] Failure occurs if abundance in site vs reference is < 0.50 for any one of three major taxa groups (as per Ecology 2019)
Bold = abundance is significantly lower than the pooled reference (t test, p=0.01)
A_T = Abundance in Treatment (Site)
A_R = Abundance in Reference (all 3 reference stations pooled together for SMS calculations and scoring purposes)

Additional comparisons between the NEBA sites and the reference stations demonstrated that, despite the SMS scores, the benthic infauna community at the Hylebos Wood Debris Site stations was not found to be significantly different from any of the dredged reference locations. All stations, including the references, had low taxa richness and were characterized overall by a dominant species that comprised approximately half of the abundance collected, resulting in unevenly distributed community assemblages.

5. CONCLUSION

Benthic community assemblages at all three of the Hylebos Wood Debris Site NEBA stations were not found to be adversely affected when compared to the prior-dredged reference locations.

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APPENDIX A

CHAIN-OF-CUSTODY FORM

CHAIN OF CUSTODY

ECOANALYSTS
LIFE IN WATER

EcoAnalysts, Inc.
4770 NE View Dr., Port Gamble, WA. 98364
Tel: (360) 297-6040

Destination: EcoAnalysts	Sample Originator (Organization): EcoAnalysts	Report Results To: Michelle Knowlen	Phone: 360 -297-6040 ex 6056
Destination Contact: Megan Payne	PERSON WHO COLLECTED SAMPLE: Michelle Knowlen	Contact Name:	Fax: --
Date: 6/18/20 Turn-Around-Time: Standard	Address: 4770 NE View Dr, Port Gamble WA 98364	Lab Address: 4770 NE View Dr, Port Gamble WA 98364	Email: mknowlen@ecoanalysts.com
Project Name: Anchor Hylebos Wood Debris (PG1374)	Phone: 360 -297-6040 ex 6056	Analyses:	Invoicing To:
	Fax: --		Comments or Special Instructions:
Contract/PO:	E-mail: mknowlen@ecoanalysts.com		

No.	Sample ID	Matrix	Volume & Type of Container	Date & Time	Benthic Enumeration						Preservation	Sample Temp Upon Receipt	LAB ID
1	HOW-B02-Rep1-200617	Fauna	1L Plastic	6/17/20 1235	X						10% Formalin		
2	HOW-B02-Rep2-200617			1245									
3	HOW-B02-Rep3-200617			1305									
4	HOW-B10-Rep1-200617			1455									
5	HOW-B10-Rep2-200617			1510									
6	HOW-B10-Rep3-200617			1525									
7	HOW-B08-Rep1-200617			1710									
8	HOW-B08-Rep2-200617			1720									
9	HOW-B08 Rep3-200617			1735									
10	HOW-B01-Rep1-200618			6/18/20 1200									
11	HOW-B01-Rep2-200618			1210									
12	HOW-B01-Rep3-200618			1222									
13	HOW-B09-Rep1-200618			1415									
14	HOW-B09-Rep2-200618			1430									
15	HOW-B09-Rep3-200618			1445									
16	REF-001-Rep1-200618			1600									
17	REF-001-Rep2-200618			1615									
18	REF-001-Rep3-200618	↓	↓	↓ 1630	↓						↓		
19													
20													

Relinquished by:	Received by:	Relinquished by:	Received by:
Print Name: Michelle Knowlen	Print Name: Max Rios	Print Name:	Print Name:
Signature:	Signature:	Signature:	Signature:
Affiliation: EcoAnalysts	Affiliation: EcoAnalysts, Inc.	Affiliation:	Affiliation:
Date/Time: 6/19/20 1230	Date/Time: 6/22/20 1500	Date/Time:	Date/Time:

Matrix Codes

FW = Fresh Water

SB = Salt & Brackish Water

SS = Soil & Sediment

APPENDIX B

INDICES AND STATISTICAL COMPARISONS

DIVERSE

Univariate Diversity indices

Data worksheet
Name: 2020 PG-Anchor Hylebos Wood Debris Benthic Data
Data type: Abundance
Sample selection: All
Variable selection: All

```
Sample         S   N     d     J'  H'(loge) 1-Lambda'
HOW-B01-Rep1   6  62 1.211 0.3468    0.6214    0.2676
HOW-B01-Rep2  10  78 2.066   0.51     1.174    0.5195
HOW-B01-Rep3   6  57 1.237 0.4986    0.8934    0.4367
HOW-B02-Rep1   9 113 1.692 0.3183    0.6994    0.2884
HOW-B02-Rep2  11 167 1.954 0.4946     1.186    0.5536
HOW-B02-Rep3  10 179 1.735 0.4476     1.031    0.5086
HOW-B08-Rep1   6  84 1.128 0.5936     1.064    0.5694
HOW-B08-Rep2   6  33  1.43 0.6771     1.213    0.6042
HOW-B08-Rep3   8  34 1.985 0.7728     1.607    0.7683
HOW-B09-Rep1  11  95 2.196 0.5234     1.255    0.5498
HOW-B09-Rep2   7  25 1.864 0.8046     1.566    0.7667
HOW-B09-Rep3  12  69 2.598 0.5379     1.337    0.5597
HOW-B10-Rep1   5 103 0.863 0.5813    0.9356     0.518
HOW-B10-Rep2  10  77 2.072 0.6156     1.418    0.6938
HOW-B10-Rep3  15 115 2.951 0.6946     1.881    0.7628
REF-001-Rep1   9  77 1.842  0.579     1.272    0.5482
REF-001-Rep2   9  91 1.773 0.5924     1.302    0.5834
REF-001-Rep3   8  79 1.602 0.5032     1.046    0.4667
```

	Swartz Dominance	Mollusca Richness
HOW-B01-Rep1	1	2
HOW-B01-Rep2	2	2
HOW-B01-Rep3	2	2
HOW-B02-Rep1	1	4
HOW-B02-Rep2	2	2
HOW-B02-Rep3	2	2
HOW-B08-Rep1	2	2
HOW-B08-Rep2	2	2
HOW-B08-Rep3	3	1
HOW-B09-Rep1	2	2
HOW-B09-Rep2	3	3
HOW-B09-Rep3	3	2
HOW-B10-Rep1	2	2
HOW-B10-Rep2	3	3
HOW-B10-Rep3	4	3
REF-001-Rep1	2	3
REF-001-Rep2	2	4
REF-001-Rep3	2	3

Anova: Single Factor (**ABUNDANCE**)

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
HOW-B01	3	197	65.66667	120.3333
HOW-B02	3	459	153	1236
HOW-B08	3	151	50.33333	850.3333
HOW-B09	3	189	63	1252
HOW-B10	3	295	98.33333	377.3333
REF-001	3	247	82.33333	57.33333

ANOVA

rce of Varia	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between G	20601.78	5	4120.356	6.349863	**0.00418**	3.105875
Within Gro	7786.667	12	648.8889			
Total	28388.44	17				

Anova: Single Factor (**RICHNESS**)

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
HOW-B01	3	22	7.333333	5.333333
HOW-B02	3	30	10	1
HOW-B08	3	20	6.666667	1.333333
HOW-B09	3	30	10	7
HOW-B10	3	30	10	25
REF-001	3	26	8.666667	0.333333

ANOVA

rce of Varia	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between G	33.11111	5	6.622222	0.993333	**0.461612**	3.105875
Within Gro	80	12	6.666667			
Total	113.1111	17				

Anova: Single Factor (**DIVERSITY**)

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
HOW-B01	3	2.689155	0.896385	0.076457
HOW-B02	3	2.915964	0.971988	0.061775
HOW-B08	3	3.883938	1.294646	0.078799
HOW-B09	3	4.157408	1.385803	0.025932
HOW-B10	3	4.234044	1.411348	0.223438
REF-001	3	3.620293	1.206764	0.019507

ANOVA

rce of Varia	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between G	0.69655	5	0.13931	1.7202	**0.204478**	3.105875
Within Gro	0.971818	12	0.080985			
Total	1.668368	17				

Anova: Single Factor (**EVENNESS**)

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
HOW-B01	3	1.35544	0.451813	0.008304
HOW-B02	3	1.260479	0.42016	0.008334
HOW-B08	3	2.043582	0.681194	0.008042
HOW-B09	3	1.865919	0.621973	0.02507
HOW-B10	3	1.891506	0.630502	0.003372
REF-001	3	1.674641	0.558214	0.002314

ANOVA

rce of Varia	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between G	0.164279	5	0.032856	3.556071	**0.033315**	3.105875
Within Gro	0.110872	12	0.009239			
Total	0.275151	17				

Anova: Single Factor (**SWARTZ DOMINANCE**)

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
HOW-B01	3	5	1.666667	0.333333
HOW-B02	3	5	1.666667	0.333333
HOW-B08	3	7	2.333333	0.333333
HOW-B09	3	8	2.666667	0.333333
HOW-B10	3	9	3	1
REF-001	3	6	2	0

ANOVA

rce of Varia	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between G	4.444444	5	0.888889	2.285714	0.111759	3.105875
Within Gro	4.666667	12	0.388889			
Total	9.111111	17				

Anova: Single Factor (**MOLLUSCA RICHNESS**)

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
HOW-B01	3	6	2	0
HOW-B02	3	8	2.666667	1.333333
HOW-B08	3	5	1.666667	0.333333
HOW-B09	3	7	2.333333	0.333333
HOW-B10	3	8	2.666667	0.333333
REF-001	3	10	3.333333	0.333333

ANOVA

rce of Varia	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between G	5.111111	5	1.022222	2.3	0.110123	3.105875
Within Gro	5.333333	12	0.444444			
Total	10.44444	17				

ANOVA Post-Hoc Analyses: Abundance

Table format: **Column**	**Group A**	**Group B**	**Group C**	**Group D**	**Group E**	**Group F**
	HOW-B01	HOW-B02	HOW-B08	HOW-B09	HOW-B10	REF-001
	Y	**Y**	**Y**	**Y**	**Y**	**Y**
1	62	113	84	95	103	77
2	78	167	33	25	77	91
3	57	179	34	69	115	79

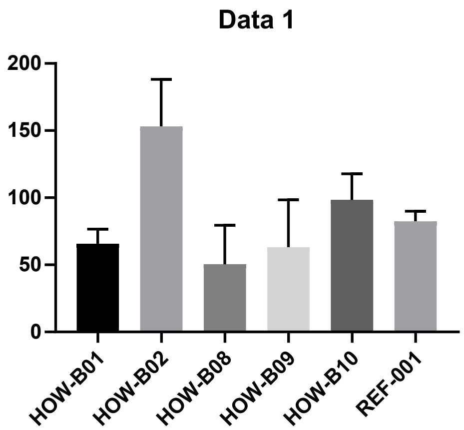
ANOVA Post-Hoc Analyses: Abundance

1way ANOVA ANOVA						
1	Table Analyzed	Data 1				
2	Data sets analyzed	A : HOW-B01	B : HOW-B02	C : HOW-B08	D : HOW-B09	E : HOW-B10
3						
4	ANOVA summary					
5	F	6.35				
6	P value	0.0042				
7	P value summary	**				
8	Significant diff. among means (P < 0.05)?	Yes				
9	R square	0.7257				
10						
11	Brown-Forsythe test					
12	F (DFn, DFd)	0.4475 (5, 12)				
13	P value	0.8073				
14	P value summary	ns				
15	Are SDs significantly different (P < 0.05)?	No				
16						
17	Bartlett's test					
18	Bartlett's statistic (corrected)					
19	P value					
20	P value summary					
21	Are SDs significantly different (P < 0.05)?					
22						
23	ANOVA table	SS	DF	MS	F (DFn, DFd)	P value
24	Treatment (between columns)	20602	5	4120	F (5, 12) = 6.35	P=0.0042
25	Residual (within columns)	7787	12	648.9		
26	Total	28388	17			
27						
28	Data summary					
29	Number of treatments (columns)	6				
30	Number of values (total)	18				

ANOVA Post-Hoc Analyses: Abundance

1way ANOVA Multiple comparisons									
1	Number of families	1							
2	Number of comparisons per family	15							
3	Alpha	0.05							
4									
5	Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value			
6									
7	HOW-B01 vs. HOW-B02	-87.33	-157.2 to -17.47	Yes	*	0.0121	A-B		
8	HOW-B01 vs. HOW-B08	15.33	-54.53 to 85.2	No	ns	0.9730	A-C		
9	HOW-B01 vs. HOW-B09	2.667	-67.2 to 72.53	No	ns	>0.9999	A-D		
10	HOW-B01 vs. HOW-B10	-32.67	-102.5 to 37.2	No	ns	0.6303	A-E		
11	HOW-B01 vs. REF-001	-16.67	-86.53 to 53.2	No	ns	0.9618	A-F		
12	HOW-B02 vs. HOW-B08	102.7	32.8 to 172.5	Yes	**	0.0036	B-C		
13	HOW-B02 vs. HOW-B09	90	20.14 to 159.9	Yes	**	0.0098	B-D		
14	HOW-B02 vs. HOW-B10	54.67	-15.2 to 124.5	No	ns	0.1634	B-E		
15	HOW-B02 vs. REF-001	70.67	0.8049 to 140.5	Yes	*	0.0469	B-F		
16	HOW-B08 vs. HOW-B09	-12.67	-82.53 to 57.2	No	ns	0.9883	C-D		
17	HOW-B08 vs. HOW-B10	-48	-117.9 to 21.86	No	ns	0.2625	C-E		
18	HOW-B08 vs. REF-001	-32	-101.9 to 37.86	No	ns	0.6487	C-F		
19	HOW-B09 vs. HOW-B10	-35.33	-105.2 to 34.53	No	ns	0.5568	D-E		
20	HOW-B09 vs. REF-001	-19.33	-89.2 to 50.53	No	ns	0.9311	D-F		
21	HOW-B10 vs. REF-001	16	-53.86 to 85.86	No	ns	0.9678	E-F		
22									
23									
24	Test details	Mean 1	Mean 2	Mean Diff.	SE of diff.	n1	n2	q	DF
25									
26	HOW-B01 vs. HOW-B02	65.67	153	-87.33	20.8	3	3	5.938	12
27	HOW-B01 vs. HOW-B08	65.67	50.33	15.33	20.8	3	3	1.043	12
28	HOW-B01 vs. HOW-B09	65.67	63	2.667	20.8	3	3	0.1813	12
29	HOW-B01 vs. HOW-B10	65.67	98.33	-32.67	20.8	3	3	2.221	12
30	HOW-B01 vs. REF-001	65.67	82.33	-16.67	20.8	3	3	1.133	12
31	HOW-B02 vs. HOW-B08	153	50.33	102.7	20.8	3	3	6.981	12
32	HOW-B02 vs. HOW-B09	153	63	90	20.8	3	3	6.12	12
33	HOW-B02 vs. HOW-B10	153	98.33	54.67	20.8	3	3	3.717	12
34	HOW-B02 vs. REF-001	153	82.33	70.67	20.8	3	3	4.805	12
35	HOW-B08 vs. HOW-B09	50.33	63	-12.67	20.8	3	3	0.8613	12
36	HOW-B08 vs. HOW-B10	50.33	98.33	-48	20.8	3	3	3.264	12
37	HOW-B08 vs. REF-001	50.33	82.33	-32	20.8	3	3	2.176	12
38	HOW-B09 vs. HOW-B10	63	98.33	-35.33	20.8	3	3	2.402	12
39	HOW-B09 vs. REF-001	63	82.33	-19.33	20.8	3	3	1.315	12
40	HOW-B10 vs. REF-001	98.33	82.33	16	20.8	3	3	1.088	12

ANOVA Post-Hoc Analyses: Abundance



ANOVA Post-Hoc Analyses: Evenness

Table format: **Column**	**Group A**	**Group B**	**Group C**	**Group D**	**Group E**	**Group F**
	HOW-B01	HOW-B02	HOW-B08	HOW-B09	HOW-B10	REF-001
	Y	**Y**	**Y**	**Y**	**Y**	**Y**
1	0.346797	0.318297	0.593619	0.523425	0.581301	0.579033
2	0.510023	0.494593	0.677131	0.804612	0.615649	0.592404
3	0.498620	0.447589	0.772833	0.537882	0.694555	0.503204

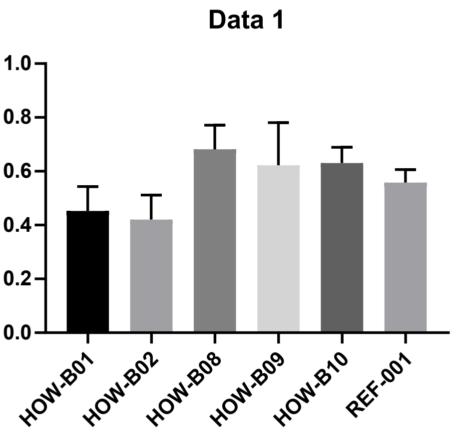
ANOVA Post-Hoc Analyses: Evenness

1way ANOVA ANOVA						
1	Table Analyzed	Data 1				
2	Data sets analyzed	A : HOW-B01	B : HOW-B02	C : HOW-B08	D : HOW-B09	E : HOW-B10
3						
4	ANOVA summary					
5	F	3.556				
6	P value	0.0333				
7	P value summary	*				
8	Significant diff. among means (P < 0.05)?	Yes				
9	R square	0.597				
10						
11	Brown-Forsythe test					
12	F (DFn, DFd)	0.2231 (5, 12)				
13	P value	0.9455				
14	P value summary	ns				
15	Are SDs significantly different (P < 0.05)?	No				
16						
17	Bartlett's test					
18	Bartlett's statistic (corrected)					
19	P value					
20	P value summary					
21	Are SDs significantly different (P < 0.05)?					
22						
23	ANOVA table	SS	DF	MS	F (DFn, DFd)	P value
24	Treatment (between columns)	0.1643	5	0.03286	F (5, 12) = 3.556	P=0.0333
25	Residual (within columns)	0.1109	12	0.009239		
26	Total	0.2752	17			
27						
28	Data summary					
29	Number of treatments (columns)	6				
30	Number of values (total)	18				

ANOVA Post-Hoc Analyses: Evenness

1way ANOVA Multiple comparisons									
1	Number of families	1							
2	Number of comparisons per family	15							
3	Alpha	0.05							
4									
5	Uncorrected Fisher's LSD	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Individual P Value			
6									
7	HOW-B01 vs. HOW-B02	0.03165	-0.1393 to 0.2027	No	ns	0.6938	A-B		
8	HOW-B01 vs. HOW-B08	-0.2294	-0.4004 to -0.05838	Yes	*	0.0128	A-C		
9	HOW-B01 vs. HOW-B09	-0.1702	-0.3412 to 0.0008402	No	ns	0.0510	A-D		
10	HOW-B01 vs. HOW-B10	-0.1787	-0.3497 to -0.007688	Yes	*	0.0419	A-E		
11	HOW-B01 vs. REF-001	-0.1064	-0.2774 to 0.0646	No	ns	0.2002	A-F		
12	HOW-B02 vs. HOW-B08	-0.261	-0.432 to -0.09003	Yes	**	0.0060	B-C		
13	HOW-B02 vs. HOW-B09	-0.2018	-0.3728 to -0.03081	Yes	*	0.0245	B-D		
14	HOW-B02 vs. HOW-B10	-0.2103	-0.3813 to -0.03934	Yes	*	0.0200	B-E		
15	HOW-B02 vs. REF-001	-0.1381	-0.3091 to 0.03295	No	ns	0.1040	B-F		
16	HOW-B08 vs. HOW-B09	0.05922	-0.1118 to 0.2302	No	ns	0.4651	C-D		
17	HOW-B08 vs. HOW-B10	0.05069	-0.1203 to 0.2217	No	ns	0.5305	C-E		
18	HOW-B08 vs. REF-001	0.123	-0.04802 to 0.294	No	ns	0.1431	C-F		
19	HOW-B09 vs. HOW-B10	-0.008529	-0.1795 to 0.1625	No	ns	0.9153	D-E		
20	HOW-B09 vs. REF-001	0.06376	-0.1072 to 0.2348	No	ns	0.4324	D-F		
21	HOW-B10 vs. REF-001	0.07229	-0.09871 to 0.2433	No	ns	0.3752	E-F		
22									
23									
24	Test details	Mean 1	Mean 2	Mean Diff.	SE of diff.	n1	n2	t	DF
25									
26	HOW-B01 vs. HOW-B02	0.4518	0.4202	0.03165	0.07848	3	3	0.4033	12
27	HOW-B01 vs. HOW-B08	0.4518	0.6812	-0.2294	0.07848	3	3	2.923	12
28	HOW-B01 vs. HOW-B09	0.4518	0.622	-0.1702	0.07848	3	3	2.168	12
29	HOW-B01 vs. HOW-B10	0.4518	0.6305	-0.1787	0.07848	3	3	2.277	12
30	HOW-B01 vs. REF-001	0.4518	0.5582	-0.1064	0.07848	3	3	1.356	12
31	HOW-B02 vs. HOW-B08	0.4202	0.6812	-0.261	0.07848	3	3	3.326	12
32	HOW-B02 vs. HOW-B09	0.4202	0.622	-0.2018	0.07848	3	3	2.571	12
33	HOW-B02 vs. HOW-B10	0.4202	0.6305	-0.2103	0.07848	3	3	2.68	12
34	HOW-B02 vs. REF-001	0.4202	0.5582	-0.1381	0.07848	3	3	1.759	12
35	HOW-B08 vs. HOW-B09	0.6812	0.622	0.05922	0.07848	3	3	0.7546	12
36	HOW-B08 vs. HOW-B10	0.6812	0.6305	0.05069	0.07848	3	3	0.6459	12
37	HOW-B08 vs. REF-001	0.6812	0.5582	0.123	0.07848	3	3	1.567	12
38	HOW-B09 vs. HOW-B10	0.622	0.6305	-0.008529	0.07848	3	3	0.1087	12
39	HOW-B09 vs. REF-001	0.622	0.5582	0.06376	0.07848	3	3	0.8124	12
40	HOW-B10 vs. REF-001	0.6305	0.5582	0.07229	0.07848	3	3	0.9211	12

ANOVA Post-Hoc Analyses: Evenness



APPENDIX C

TAXA LIST AND ABUNDANCE DATA, TAXONOMY QC REPORT

Taxon	HOW-B01-Rep1	HOW-B01-Rep2	HOW-B01-Rep3	HOW-B02-Rep1	HOW-B02-Rep2	HOW-B02-Rep3	HOW-B08-Rep1	HOW-B08-Rep2	HOW-B08-Rep3	HOW-B09-Rep1	HOW-B09-Rep2	HOW-B09-Rep3	HOW-B10-Rep1	HOW-B10-Rep2	HOW-B10-Rep3	REF-001-Rep1	REF-001-Rep2	REF-001-Rep3	Phyla
Aphelochaeta glandaria Complex		2																	Annelida
Bipalponephtys cornuta					1	1													Annelida
Cirratulidae			1	9	33	43	19	20	13	7	7	7	24	21	11	3		1	Annelida
Euchone limnicola	2	1			5	3		2	2				1	1					Annelida
Euclymeninae		1		1	1			1		1									Annelida
Glycera nana				1		1								1	1		1		Annelida
Heteromastus filiformis					1		1			1		1		1	3		3		Annelida
Levinsenia gracilis									1			2							Annelida
Nephtys ferruginea									1			1							Annelida
Paraprionospio alata		1																	Annelida
Pholoe minuta					1									1					Annelida
Pista wui	1	9	2	2	4	1	1			4		1		1	5	4	6	3	Annelida
Praxillella gracilis	1									1		1							Annelida
Prionospio sp.												1							Annelida
Scalibregma californicum									1										Annelida
Scoletoma luti	4	8	9		13	5	11	6	6	14	3	7	10	14	8	7	9	8	Annelida
Scoletoma tetraura Complex				2		5										2			Annelida
Sternaspis affinis										1					1			1	Annelida
Terebellides californica		1			1	1				2		1				1		2	Annelida
Trochochaeta franciscana									1										Annelida
Americhelidium sp.											1				1				Arthropoda
Brachyura											1								Arthropoda
Euphilomedes producta												1				2	1		Arthropoda
Foxiphalus similis			1																Arthropoda
Amphiodia sp.		1																	Echinodermata
Alia gausapata													1						Mollusca
Axinopsida serricata	53	53	42	95	106	118	51	3	9	62	10	45	67	35	51	51	57	57	Mollusca
Bivalvia											1								Mollusca
Ennucula tenuis		1	2	1			1							1			1	1	Mollusca
Evalea tenuisculpta															1				Mollusca
Macoma calcarea				1															Mollusca
Macoma sp.						1													Mollusca
Mendicula ferruginosa				1	1					1				1		1	2		Mollusca
Nutricola lordi	1														1	6	11	6	Mollusca
Parvilucina tenuisculpta								1			2	1							Mollusca
Enopla															1				Nemertea
Lineidae															1				Nemertea
Paranemertes californica										1					3				Nemertea
Tubulanus polymorphus															10				Nemertea
Phoronis sp.															17				Phoronida
Total Abundance	**62**	**78**	**57**	**113**	**167**	**179**	**84**	**33**	**34**	**95**	**25**	**69**	**103**	**77**	**115**	**77**	**91**	**79**	

8148.1-18 Comparison Date: 07/20/2020 02:09:01

Component: Crustacea

Collection Date	**Sample ID**
06/18/2020	REF-001-Rep3-200618

		Original Taxonomist - D. Drumm		QC Taxonomist - M. Hill		
TIN	TAXON	NOTE	AB	AB	NOTE	DIFF.
					Difference =	
					Percent Similarity =	N/A

8148.1-18 Comparison Date: 07/20/2020 02:13:24

Component: General Taxa

Collection Date	**Sample ID**
06/18/2020	REF-001-Rep3-200618

		Original Taxonomist - S. Hengen		QC Taxonomist - M. Hill		
TIN	TAXON	NOTE	AB	AB	NOTE	DIFF.
6460	Axinopsida serricata		57	56		1
6456	Ennucula tenuis		1	1		0
6524	Nutricola lordi		6	6		0
			64	63	Difference =	1
					Percent Similarity =	99.83

8148.1-18 Comparison Date: 07/20/2020 02:16:43

Component: Annelids

Collection Date	**Sample ID**
06/18/2020	REF-001-Rep3-200618

		Original Taxonomist - C. Barrett		QC Taxonomist - M. Hill		
TIN	TAXON	NOTE	AB	AB	NOTE	DIFF.
6151	Cirratulidae		1	1		0
7605	Pista wui		3	3		0
7598	Scoletoma luti		8	7		1
9767	Sternaspis affinis		1	1		0
8011	Terebellides californica		2	2		0
			15	14	Difference =	1
					Percent Similarity =	96.67