Adelaide Desalination Plant

2020 Infauna Survey

Final Report



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EXECUTIVE SUMMARY

This final report presents the results of the 2020 Infauna Survey of the Adelaide Desalination Plant (ADP) carried out for AdelaideAqua Pty Ltd. Two surveys were carried out; one in February 2020 and the other in September 2020, with sampling at three locations, one around the ADP outfall diffuser at Port Stanvac, and control locations to the north (North Control) and south (South Control). A total of 400 samples were collected with handheld corers by divers and analysed for sediment grain size, macrofauna and meiofauna.

In general, there were no significant differences in macrofauna or meiofauna abundance, diversity measures or community structure between Port Stanvac and the control locations for the surveys in February and September 2020, except for the macrofaunal assemblage in September 2020. Significant difference between the two control locations was only detected for macrofaunal assemblage in February 2020. Brine discharges over soft sediment habitats have the potential to change the structure and diversity of infaunal assemblages with increased dominance of nematodes and reduced diversity and abundance of polychaetes. However, the macrofaunal assemblages at Port Stanvac and the control locations were dominated by polychaetes (and crustaceans) for both surveys, and nematode abundances in the meiofaunal assemblages were the same for Port Stanvac and control locations in both surveys, indicating that the overall macrofauna and meiofauna community structure between surveys were not significantly different. At a finer spatial scale, significant differences in all measures were invariably detected between sites within each location for both surveys.

A summary of the infauna gave a total of 3,038 macrofauna individuals from 77 taxonomic groups and ten phyla were collected for Survey 1 in February 2020. The phyla Annelida (Polychaeta) and Arthropoda (Crustacea) dominated with 45% and 42% of overall abundances, respectively. A total of 11,516 individuals from 33 taxonomic groups and ten phyla of meiofauna were collected for Survey 1 in February 2020, with the phylum Nematoda accounting for 62% and Arthropoda (mostly copepods) for 31% of the overall abundance. For Survey 2 in September 2020, a total of 1,889 macrofauna individuals from 61 taxonomic groups and ten phyla were collected. The macrofaunal assemblage was again dominated by polychaete (52% of the overall abundance) and crustaceans (34%). The meiofauna sampling for Survey 2 in September 2020 yielded a total of 11,866 individuals from 30 taxonomic groups and nine phyla, with Nematoda accounting for 66% and copepods for 28% of the overall abundance.

The sediment grain size composition between Port Stanvac and the two control locations or between the two control locations were not significantly different. There was only small-scale difference between sites within a location. Consequently, the correlation between sediment grain size composition and the macroinfaunal and meiofaunal assemblages did not show consistent correlation between the two surveys. For the February 2020 survey, Port Stanvac sites were characterised by fine sand (63-250 μ m) to very coarse sand (1000-2000 μ m), while North Control sites were characterised by fine and medium sand and South Control sites by medium and coarse sand. In September 2020, the sediment composition at the three locations remained fairly similar to February 2020. Port Stanvac sites were mostly characterised by medium sand (250-500 μ m) but also variously characterised by fine to very coarse sand at some sites. North Control sites had fine, medium, and coarse sand while South Control sites had medium and coarse sand.

Comparison of the macrofaunal assemblage between 2013 and 2020 showed differences between years and between the two control locations but this was not consistent between years. Individual sites varied inconsistently for the two years with no difference detected between Port Stanvac and the control locations. Contrary to known polychaete indicators of good quality (e.g. Syllidae) or polluted areas (e.g. Capitellidae), the dominant polychaetes found in both years were not indicative of an impact from brine discharge. Meiofaunal assemblage comparisons of the 2013, 2017 and 2020 surveys detected differences across all sites over time, but there was no difference between Port Stanvac and the control locations. These differences were characterised by the dominance of major phyla with Arthropoda (mostly copepods) for 2017 and Nematoda for 2013, while 2020 sites were more variable.

The overall results suggest that the brine discharge from the desalination plant is not impacting the infaunal assemblages at Port Stanvac. However, it should be acknowledged that there is a high level of variation and inconsistency in trends among sites, which undermines the ability to draw conclusions from the comparisons between Port Stanvac and the control locations.

1. INTRODUCTION

The South Australian Government contracted AdelaideAqua Pty Ltd (the Client) to operate and maintain the Adelaide Desalination Plant, a reverse osmosis plant at Port Stanvac with an annual capacity of up to 100 gigalitres, for 20 years from 2012.

The license issued by the Environment Protection Authority South Australia for the ADP requires the licensee (AdelaideAqua) to undertake marine monitoring. A component of this monitoring schedule is the Ambient Marine Ecological Monitoring, for which a survey of infauna (macrofauna and meiofauna in the soft sediment) is required twice in a year, every third year, until 2032. This final report gives the results of the first survey carried out in February 2020 and the second survey in September 2020 and where possible, makes comparisons with previous surveys.

2. MATERIALS AND METHODS

2.1 Sampling sites

The February 2020 (Survey 1) and September 2020 (Survey 2) surveys used the same sites as the 2017 survey (Dittmann *et al.* 2017), with ten sites off Port Stanvac, in the vicinity of the ADP discharge, and five sites each at reference locations to the north (North Control) and to the south (South Control) (Figure 1, Table 1).

2.2 Field sampling

The field sampling was carried out over three days for both surveys. Survey 1 was from 5 to 7 February 2020, while Survey 2 was on 31 August, 5 and 9 September 2020. On arrival at each site, located using pre-loaded coordinates (Table 1), a drop line was deployed to mark site position. Divers used hand-held corers (67 mm internal diameter) to collect 10 sediment samples to 100 mm depth at each site, haphazardly located within 5 m of the shotline. The hand-held corer provided consistent sample size, without loss of sediment, thereby allowing quantitative assessment of infaunal assemblages. During Survey 1, the extruded sample was cut into quarters, with three quarters of the sample used for macrofaunal assessment and the remaining quarter used for meiofaunal assessment (retained on a 53 µm sieve), with larger sediment fractions retained on a 500 µm sieve added to the macrofaunal sample. For Survey 2, the whole sample from the hand-held corers were used for macrofaunal assessment and smaller corers (30 mm internal diameter) were used to collect ten samples for meiofauna assessment. This change was made as extruded samples from some sites were sloppy and cutting the samples was difficult. This change did not affect the results because all counts were standardised to unit area, making the data comparable. All sediment samples for infauna assessment were labelled and preserved in 70% ethanol. For both surveys, ten samples were also collected using the larger corer (67 mm internal diameter) for sediment grain size analysis. Overlying water for these samples was gently decanted before the sample was extruded onto a tray and the top 40 mm of each core was sliced off and individually wrapped in Al-foil, labelled, and sealed in Ziploc bags.



Figure 1 Location of the ten sites at Port Stanvac around the ADP outfall diffuser and vicinity, and the five sites each at North Control off Glenelg (NC) and South Control off Noarlunga (SC).

Site ID	Longitude	Latitude	Easting	Northing
Port Stanvac				
PS01	138.47113	-35.09740	269484.94	6113229.50
PS02	138.46892	-35.09608	269279.13	6113370.43
PS03	138.46668	-35.09488	269072.12	6113498.38
PS04	138.46527	-35.09365	268939.47	6113631.91
PS05	138.46595	-35.09200	268997.12	6113816.54
PS06	138.46733	-35.09012	269117.94	6114028.67
PS07	138.46832	-35.08858	269203.27	6114201.05
PS08	138.47078	-35.08945	269430.63	6114110.62
PS09	138.47243	-35.09023	269583.29	6114027.54
PS10	138.47432	-35.09175	269759.28	6113863.65
North Control				
NC01	138.41915	-34.98712	264428.76	6125342.26
NC02	138.42323	-34.98998	264809.76	6125033.87
NC03	138.42245	-34.99432	264750.66	6124551.31
NC04	138.41627	-34.99437	264186.33	6124531.17
NC05	138.41603	-34.99005	264152.63	6125009.49
South Control				
SC01	138.43910	-35.14977	266713.82	6107345.51
SC02	138.44328	-35.15167	267100.41	6107144.53
SC03	138.44177	-35.15578	266973.97	6106684.29
SC04	138.43708	-35.15598	266547.85	6106651.12
SC05	138.43567	-35.15193	266407.19	6107097.08

Table 1Coordinates in decimal degrees (WGS84) as provided by AdelaideAqua and converted
Easting and Northing (GDA94, Zone 54) of the sites for sediment sampling at Port
Stanvac, North Control and South Control.

2.3 Laboratory processing

For the macrofauna samples, the ethanol solution in the sample jar was decanted before further processing. The samples were then gently washed and screened using 500 μ m sieves. Animals in the retained sediment were picked out with the aid of a stereomicroscope and identified. More common animals were identified to intermediate taxonomic levels, mostly to the family level. This is generally sufficient for characterisation of natural and anthropogenic influences on spatial and temporal variability of assemblages in sediments (Olsgard and Somerfield 2000, Somerfield and Clarke 1995). Less common animals were identified to phylum, sub-phylum, class or order. The animals were enumerated and preserved in 70% ethanol for storage. For Survey 1, the meiofauna samples were initially processed similarly to the macrofauna, washed through stacked 500 μ m and 53 μ m sieves. The material retained on the 500 μ m sieve was further processed using a modified LudoxTM flotation method for

meiofauna (Somerfield and Warwick 2013). The meiofauna were then identified, enumerated, and preserved in 70% ethanol for storage. For Survey 2, the meiofauna samples from the smaller corer were washed only through 53 μ m sieve with subsequent processing similar to Survey 1.

The sediment grain size samples were processed by SARDI Aquatic Sciences Environment and Analytical Laboratories. The samples were oven-dried at 90°C. Each of the dried samples was gently homogenised and a 50 g subsample was weighed into a dish. The subsample was dry sieved through 2 mm and 1 mm sieves with the fraction retained on each sieve weighed to obtain the coarse fractions. The fine fraction (<1 mm) was kept for further analysis using laser diffraction on a Mastersizer 3000 Particle Size Analyser. The samples were stirred in a sonicator with a dispersing agent (50 g/L sodium hexametaphosphate in MilliQ water) for 15 minutes before analysis in the Mastersizer 3000.

2.4 Data Analysis

The grain size distributions for fractions greater than 1 mm were determined as % weight by sieving through graded sieves, while the distribution of finer fractions (<1 mm) was given as % volume by laser diffraction. The data were normalised before further analysis. The software package GRADISTAT was used to determine grain size parameters, which were calculated using the Folk and Ward method as it is relatively insensitive to large variations in the tails of the sediment distribution (Blott and Pye 2001). The parameters included the mean, sorting (the spread of the sizes around the mean, equivalent to standard deviation), the symmetry or the preferential spread (skewness) to one side of the mean, and the degree of concentration of the grains (kurtosis) relative to the mean (Table 2). The sediment grain size was initially analysed into 12 size fractions, from clay (< 2 µm) to gravel (> 2000 µm) for each sample, but these were combined into six categories for plotting and interpretation (Table 2). Permutation-based analysis of variance (PERMANOVA) was used to evaluate variations in sediment grain size composition, with Treatment as a fixed factor (Control and Port Stanvac), Location (North Control, South Control and Port Stanvac) nested in Treatment and Sites nested in Location.

Parameter	Value range	Description and definition	Collapsed categories		
Mean (µm) /	< 2	Clay	Clay		
Size fraction	ze fraction 2-4 Very fine silt		٦		
	4 – 8	Fine silt	Silt		
	8 – 16	Medium silt			
	16 – 32	Coarse silt			
	63 to 125	Very fine sand	Fine sand		
	125 to 250	Fine sand			
	250 to 500	Medium sand	Medium sand		
	500 to 1000	Coarse sand			
	1000 to 2000	Very coarse sand	_ Coarse sand		
	>2000	Gravel	Gravel		
Parameter	Value range	Description and	d definition		
Sorting	< 1.27	Very well sorted (s	Very well sorted (small spread)		
(standard	1.27 to 1.41	Well sorted			
deviation)	1.41 to 1.62	Moderately well sorted			
	1.62 to 2.00	Moderately	sorted		
	2.00 to 4.00	Poorly sorted			
	4.00 to 16.00	Very poorly	sorted		
	>16.00	Extremely poorly sorted (large spread)			
Skewness	-0.3 to -1.0	Very fine sl	kewed		
	-0.1 to -0.3	Fine skewed			
	-0.1 to +0.1	Symmetrical			
	+0.1 to +0.3	Coarse sk	ewed		
	+0.3 to +1.0	Very coarse skewed			
Kurtosis	<0.67	Very platykurtic (very flattened distribution)			
	0.67 to 0.90	Platykurtic (flattene	ed distribution)		
	0.90 to 1.11	Mesokurtic (normal distribution)			
	1.11 to 1.50	Leptokurtic (peaked distribution)			
	1.50 to 3.00	Very leptokurtic (very peaked distribution)			
	>3.00	Extremely leg	otokurtic		

Table 2Definitions and criteria for the calculated grain size distribution parameters (modified
from (Blott and Pye 2001).

The raw infaunal data were filtered to remove ambiguous identifications, unidentified juveniles and colonial taxa, accounting for ~0.07% and ~0.05% of total infauna in Survey 1 and Survey 2. The macrofaunal data were expressed as numbers per core while the meiofaunal data were converted to numbers per cm² before further analysis.

To characterise the sites, a suite of metrics and diversity indices were calculated. These included abundances (*A*) expressed as number of individuals per core (area of corer 0.0035 m²), the number of taxonomic groups (*S*), the Shannon-Wiener diversity index, *H*', and Pielou's evenness *J*', a measure of how evenly the individuals are distributed among the different taxonomic groups. Permutation-based analysis of variance (PEMANOVA) was then used to evaluate these univariate measures with Treatment as a fixed factor (Control and Port Stanvac), Location (North Control, Port Stanvac and South Control) nested in Treatment and Sites nested in Location.

PERMANOVA tests were also used to evaluate variations in multivariate community structure using the same statistical model as given above, followed by non-metric Multidimensional Scaling ordination (nMDS) to visualise any patterns. To determine which taxa contributed the most to the similarities within each of the three locations (North Control, Port Stanvac and South Control) and to the dissimilarities between the three locations, the SIMPER (Similarity Percentages) procedure was applied.

Multivariate analyses of infaunal data were based on Bray-Curtis similarities to eliminate the effects of joint absences of taxa (Clarke *et al.* 2006) after square root or fourth root transformation to decrease the influence of dominant species, allowing intermediate abundance taxa to play a part (Clarke *et al.* 2014). Univariate data were not transformed, and analyses were based on Euclidean distances. P-values were calculated from 9999 permutations of the residuals under a reduced model to calculate probability values in PERMANOVA.

To examine correlations between infaunal assemblages and sediment grain size distributions, the data was further analysed with the Distance-based linear model (DISTLM) routine. The macrofaunal and meiofaunal assemblage structure were separately compared to sediment grain size distribution using a stepwise procedure, adjusted R² criteria with all fractions integrated in a multiple regression model, and 9999 permutations. To show the relationships, distance-based redundancy plots (dbRDA) were used to visualise the model output from DISTLM, followed by the RELATE routine to determine any correlations between the resemblance matrices of infauna and sediment.

Change in infaunal assemblages and sediment grain size distribution between Surveys 1 and 2 was examined using PERMANOVA analyses. Survey and Treatment were fixed factors with Location nested in Treatment and Sites nested in Location. The first two axes from Principle Coordinate Ordination (PCO) were then used to visualise any changes between surveys.

For between-year comparisons, datasets used were from 2013 survey (Loo *et al.* 2014), 2017 survey (Dittmann *et al.* 2017) and the current 2020 survey. Data provided by AdelaideAqua for 2013 were abundance per core, while data for 2017 were abundance per unit area (per m² for macrofauna and per cm² for meiofauna). As different sampling gears were used for each survey (HAPS corer in 2013, box corer in 2017 and handheld corer in 2020), all data were standardised to abundance per unit area for each survey to enable comparisons between years. With sites for the 2013 survey being different from the 2017 and 2020 surveys, sites for the latter surveys included only those within ~500m of the 2013 survey sites (Figure 2). All sites were

included for the 2013 survey, while sites for 2017 and 2020 surveys included Sites NC02, NC03 and NC05 for North Control, Sites PS06 to PS10 for Port Stanvac and all sites for South Control. Due to the differences in taxonomic resolution between surveys, the data were analysed at the phylum level. The 2013 survey was carried out in June 2012 and February 2013, while the 2017 and 2020 surveys were carried out in February and September of 2017 and 2020. Spatial and temporal variation of sites across all locations were reported in both the 2013 (Loo *et al.* 2014) and 2017 (Dittmann *et al.* 2017) surveys, and Dittmann (2017) suggested that any comparisons over time should be carried out for particular season. As such, only data from the February surveys for all monitoring years were used for comparisons.



Figure 2 Location of the ten sites at Port Stanvac (PS) around the ADP outfall diffuser and vicinity, and the five sites each at North Control (NC) and South Control (SC) for the 2017 and 2020 surveys (green) and the sites for the 2013 survey (orange).

3. RESULTS

3.1 Survey 1 (February 2020)

3.1.1 Sediment grain size

The analysis of sediment grain fractions showed variability among all sites, including among sites within the same location. Across all the sites, the highest proportion of gravel was at Site PS05 (24.8%). For coarse, medium, and fine sand, the highest proportions were recorded at Site PS07 (69.5%), Site SC05 (47.5%) and Site PS08 (41.9%) respectively. Site PS03 had the highest proportion of silt (11.5%) and SC03 had clay (0.12%, Figure 3).

Principle Component Analysis (PCA) of the sediment fractions confirmed the variability among all sites. In the PCA plot with superimposed vectors, PC1 accounted for 68% of the variability, differentiating sites with fine sand from sites with coarse sand/gravel (left to right), while PC2 accounted for a further 23%, differentiating sites with fine sand from medium sand (Figure 4). The results of PERMANOVA indicated no significant difference between Port Stanvac and the control locations (p = 0.6504) or between the two control locations (p = 0.0579), but there was significant small-scale variation between sites within a location (p = 0.0001, Table 3).

GRADISTAT analysis showed that sediment grain size distribution for all sites at Port Stanvac were variable. The ten sites at Port Stanvac were characterised by fine sand (63-250 µm) to very coarse sand (1000-2000 µm). For the control locations, North Control was characterised by fine and medium sand, while South Control by medium and coarse sand. Most sites have leptokurtic to very leptokurtic distribution and poor to very poor sorting, except for Sites PS05 and PS09 which had platykurtic distribution (see Table 2 for definition of terms). Skewness ranged from fine skewed to coarse skewed and only Sites PS04, PS06 and PS10 had symmetrical distribution (Table 4). Sediment grain size distribution for sites at North Control were mesokurtic, coarse skewed with poorly sorted distribution, except for Site NC04 which had mesokurtic, symmetrical and moderately sorted distribution of fine sand (Table 4). Three sites at South Control were leptokurtic and poorly sorted distribution (SC02, SC03 and SC05). Sites SC01 and SC04 were mesokurtic but differed in sorting and skewness. Site SC01 had symmetrical distribution with moderately sorted medium sand while Site SC04 had coarse skewed distribution with poorly sorted medium sand (Table 4).







Figure 4 PCO plot of sediment grain size for the sites at Port Stanvac (PS), North Control (NC) and South Control (SC) from Survey 1 with superimposed vectors of sediment fractions. Vector length reflects the correlation between each fraction in PC1 and PC2, with the circle representing the vector length for a correlation of 1.

Table 3	PERMANOVA results showing highly variable sites as characterised by sediment composition for Survey 1. Significant differences ($p < 0.05$) are in bold.

Source	df	MS	Pseudo F	<i>p</i> (perm)
Treatment	1	18675	0.7968	0.6504
Location(Treatment)	1	18012	3.0491	0.0579
Sites(Location(Treatment))	17	101040	41.5460	0.0001
Residual	179	25606		
Total	198	163380		

Table 4 Sediment grain size distribution and GRADISTAT-calculated parameters for sites at Port Stanvac (PS), North Control (NC) and South Control (SC) from Survey 1. x-axis show particle size class (0-2000 µm) and y-axis show normalised % proportions of sediment fractions.









3.1.2 Macrofauna

A total of 3,038 macrofauna individuals from 77 taxonomic groups and ten phyla were collected for Survey 1 in February 2020. The phylum Annelida (Polychaeta) dominated with 1,364 individuals (45% of overall abundance). The next most abundant phylum was Arthropoda (Crustacea) with 1283 individuals (42%). The remaining eight phyla accounted for the remaining 13% of the overall abundance. The family Syllidae dominated the polychaetes (15%) and five other abundant families included Dorvilleidae (13%), Spionidae (12%), Capitellidae (10%), Lumbrineridae (9%) and Saccocirridae (9%). Tanaidacea (58%) dominated the crustaceans, followed by amphipods (34%) with gammaridean amphipods being the most abundant (20%). Echinoderms comprised ophiuroids (46%), echinoids (34%) and holothurians (20%). Bivalves were the most abundant molluscs (83%). A list of macrofauna and total abundance at each location is provided in Appendix 1.

Polychaetes and crustaceans dominated at each of the locations. They accounted for 91% of total abundance at Port Stanvac sites, 84% at North Control sites and 76% at South Control sites. Contributions from all other phyla were variable across the locations. A summary of the percent abundance of major phyla for each location is given in Table 5.

Key Phylum	North Control	Port Stanvac	South Control
Number of sites	5	10	5
Number of samples	50	100	50
Annelida	21.3	52.8	46.9
Arthropoda	62.9	37.8	29.5
Echinodermata	4.8	2.1	3.7
Mollusca	3.2	1.5	1.6
Nematoda	3.5	3.0	11.9
Nemertea	3.8	2.5	5.7
Sipuncula	0.3	0.2	0.2
Others	0.1	0.1	0.5

Table 5Number of sites and samples collected with the percent abundance of major phyla of
macrofauna at North Control, Port Stanvac and South Control for Survey 1.

Analyses of the number of individuals (*A*), number of taxonomic groups (*S*), Shannon-Wiener diversity (*H*') and Pielou's evenness (*J*') for macrofauna separately, indicated that there was significant small-scale variation between sites within each location. However, there were no significant differences between the control locations and Port Stanvac or between the two control locations for any of these measures (Table 6). Table 6PERMANOVA results for abundance (A), number of taxonomic groups (S), Shannon-
Wiener diversity (H') and Pielou's evenness (J) of macrofauna between Treatment
(Control and Port Stanvac) with Locations (Port Stanvac, North Control and South
Control) nested within Treatment and Sites nested within Locations for Survey 1.
Significant differences (p < 0.05) are in bold.

Number of individuals (A)						
Source	df	MS	Pseudo-F	<i>p</i> (perm)		
Treatment	1	3200.00	3.9494	0.3544		
Location(Treatment)	1	600.25	0.8432	0.3647		
Site(Location(Treatment))	17	711.88	3.2882	0.0002		
Residual	180	216.49				
Number of taxonomic groups (S)						
Source	df	MS	Pseudo F	<i>p</i> (perm)		
Treatment	1	162.00	1.6513	0.5049		
Location(Treatment)	1	72.25	2.1297	0.1632		
Site(Location(Treatment))	17	33.93	4.4645	0.0001		
Residual	180	7.60				
Shannon-Wiener Diversity	Shannon-Wiener Diversity (H')					
Source	df	MS	Pseudo F	<i>p</i> (perm)		
Treatment	1	0.7331	0.8797	0.6353		
Location(Treatment)	1	0.7647	1.3854	0.2542		
Site(Location(Treatment))	17	0.5520	2.8352	0.0002		
Residual	180	0.1947				
Pielou's evenness (J')						
Source	df	MS	Pseudo F	<i>p</i> (perm)		
Treatment	1	0.1261	0.9682	0.5770		
Location(Treatment)	1	0.1044	2.0457	0.1668		
Site(Location(Treatment))	17	0.0510	4.8978	0.0001		
Residual	180	0.0104				

Mean macrofaunal abundances were variable across sites at all locations ranging from 5.5 individuals per core at Site SC04 to 42.5 individuals per core at PS05 (Figure 5a). Mean abundances at Port Stanvac sites ranged from 8.6 ± 1.5 (mean \pm SE) to 42.5 ± 18.7 individuals, while at North Control sites, mean abundances were 8.0 ± 1.4 to 23.8 ± 2.5 , and South Control sites had mean abundances from 5.5 ± 1.5 to 15.2 ± 3.4 (Figure 5a). The lowest mean number of taxonomic groups was recorded at Site SC04 and the highest was at Site PS07 (Figure 5b). For all Port Stanvac sites, the mean number of taxonomic groups were between 5.6 ± 0.4 and 12.1 ± 1.1 , while North Control sites were between 5.4 ± 0.7 and 8.2 ± 0.5 and South Control sites were between 4.2 ± 0.8 and 7.2 ± 0.6 (Figure 5b). All locations had highly diverse assemblages with the Shannon-Wiener diversity index greater than one at all sites (Figure 6a). The lowest diversity was recorded at Sites SC04 and SC05, and the highest at Site PS07. There was generally an even distribution of taxa across all sites

with Pielou's evenness greater than 0.8, except for Sites PS01 (0.68) and NC01 (0.72, Figure 6b). Mean values for evenness for Port Stanvac ranged from 0.68 ± 0.03 to 0.95 ± 0.02 , while the North Control sites were from 0.72 ± 0.05 to 0.95 ± 0.02 and those for South Control were in the range of 0.89 ± 0.03 to 0.97 ± 0.02 .



Figure 5 Mean (a) abundance A (individuals per core) and (b) number of taxonomic groups S, with SE bars (n=10) of macrofauna for each of the 20 sites sampled at North Control (NC), Port Stanvac (PS) and South Control (SC) for Survey 1.







PERMANOVA analysis of all replicate samples showed significant difference in macrofaunal assemblage structure between the North and South Control locations and variations between sites within a location, but no significant difference between Port Stanvac and the control locations (Table 7). The nMDS ordination using mean abundance per site yielded a two-dimensional plot with a high stress value of 0.19

(meaning the plot is useful but not in the details) showing some separation of the three locations (Figure 7).

Table 7PERMANOVA results of comparisons of macrofaunal assemblage structure between
Treatment (Control and Port Stanvac) with Location (Port Stanvac, North Control and
South Control) nested within Treatment and Site nested within Location for Survey 1.
Significant differences (p < 0.05) are in bold.

Source	df	MS	Pseudo F	<i>p</i> (perm)
Treatment	1	24817	1.0079	0.5245
Location(Treatment)	1	18819	2.5882	0.0155
Site(Location(Treatment))	17	7271	2.9979	0.0001
Residual	180	2425		



Figure 7 Two-dimensional nMDS ordination plot of square-root transformed mean abundance data of benthic macrofaunal assemblages from Port Stanvac, North Control and South Control for Survey 1.

Within location aimilarity

SIMPER analysis for within-location similarities showed that they were above 50% for all locations (Table 8). Within each location, 14 taxonomic groups variously contributed to ~60% of the similarity, of which only three were found across all three locations (Table 8). The crustacean order Tanaidacea and Gammaridea were the top two contributors to similarity within Port Stanvac and North Control sites, while South Control had the polychaete family Spionidae and the phylum Nematoda (Table 8).

Table 8Macrofaunal taxonomic groups listed in order of contribution to a cumulative
percentage of ~60% of overall within-location similarities at North Control, Port
Stanvac and South Control for Survey 1 (taxa in italic are unique to that location).

within-location similarity		
62.4	55.4	53.7
North Control	Port Stanvac	South Control
Gammaridea	Tanaidacea	Spionidae
Tanaidacea	Gammaridea	Nematoda
Spionidae	Spionidae	Syllidae
Phoxocephalidae	Capitellidae	Nemertea
Nemertea	Lumbrineridae	Phoxocephalidae
Ophiuroidea	Nemertea	Capitellidae
Urohaustoriidae	Syllidae	Poecilochaetidae
Anthuroidea	Nephtyidae	Tanaidacea
Nematoda		

The between-location SIMPER analysis showed that dissimilarity between Port Stanvac and North Control was 44%, between Port Stanvac and South Control was 46% and between the two control locations was 44% (Table 9). There were 15 discriminating taxonomic groups contributing cumulatively to ~50% of the dissimilarity between Port Stanvac and North Control and 14 taxonomic groups between Port Stanvac and South Control (Table 9). Fourteen taxonomic groups contributed to the dissimilarity between North and South Control. The crustacean order Tanaidacea and polychaete family Dorvilleidae were the top two contributors to the dissimilarity between the two control locations, while dissimilarity between the two control locations had the crustacean orders Tanaidacea and Gammaridea (Table 9).

Table 9Macrofaunal taxonomic groups listed in order of contribution to a cumulative
percentage of ~50% of the dissimilarity between each pair of locations (North Control,
Port Stanvac and South Control) for Survey 1.

Between-location dissimilarity					
47.7	50.1	44.0			
Port Stanvac	Port Stanvac	North Control			
North Control	South Control	South Control			
Tanaidacea	Tanaidacea	Tanaidacea			
Dorvilleidae	Dorvilleidae	Gammaridea			
Urohaustoriidae	Gammaridea	Urohaustoriidae			
Syllidae	Syllidae	Anthuroidea			
Nephtyidae	Lumbrineridae	Calanoida			
Saccocirridae	Saccocirridae	Ophiuroidea			
Capitellidae	Nephtyidae	Nematoda			
Ophiuroidea	Nematoda	Oedicerotidae			
Gammaridea	Capitellidae	Syllidae			
Anthuroidea	Oedicerotidae	Phoxocephalidae			
Lumbrineridae	Phoxocephalidae	Capitellidae			
Paraonidae	Glyceridae	Phyllodocidae			
Calanoida	Ampharetidae	Magelonidae			
Nematoda	Hesionidae	Glyceridae			
Phoxocephalidae					
3.1.3 Meiofauna

A total of 11,516 individuals from 33 taxonomic groups and ten phyla of meiofauna were collected for Survey 1 in February 2020. The phylum Nematoda accounted for 62% of the overall abundance. Arthropoda (Crustacea) was the next most abundant at 31% and Annelida (Polychaeta) at 5% of overall abundance. Other than Nemertea (1%), the remaining phyla contributed less than 1% to the overall abundance. abundance. A list and total abundance of meiofauna at each location are provided in Appendix 2.

Syllidae was the dominant polychaete family with 56% of the total polychaete abundance. Polychaete juvenile contributed 39% and the remaining 11 families contributed 5%. Copepods (80%) dominated the crustaceans, and the other abundant crustaceans were Ostracoda (9%) and crustacean nauplii (8%). A summary of percent abundance of meiofauna at each of the three locations, North Control, Port Stanvac and South Control is given in Table 10.

Key Taxa	North Control	Port Stanvac	South Control
Number of sites	5	10	5
Number of samples	50	100	50
Annelida	1.80	5.42	5.45
Arthropoda	16.87	35.36	32.51
Mollusca		0.02	0.03
Nematoda	79.36	57.49	59.43
Nemertea	1.17	1.00	1.52
Sipuncula	0.78	0.69	0.98
Others	0.02	0.02	0.08

Table 10	Number of sites and samples collected with the percent abundance of major phyla of
	meiofauna at North Control, Port Stanvac and South Control for Survey 1.

Analyses of each of the univariate measures indicated only small-scale significant differences between sites within each location for all measures. There was no significant difference between Port Stanvac sites and the control sites (Table 11).

Mean meiofaunal abundances (*A*) at each site were variable for all three locations (Figure 8a). Site PS10 at Port Stanvac had the highest mean abundance with 106.3 ± 10.9 individuals while Site SC03 had the lowest with 25.3 ± 5.6 . Sites at North Control had mean abundances ranging from 30.2 ± 5.7 to 56.1 ± 5.1 , while sites at South Control had means ranging from 25.3 ± 5.6 to 71.8 ± 10.7 . The mean number of taxonomic groups for sites at Port Stanvac ranged from 6.1 ± 0.4 to 10.1 ± 6.2 (Figure 8b). North Control sites had number of taxonomic groups ranging between 6.0 ± 0.3 and 8.0 ± 0.6 while sites at South Control had a higher range between 7.5 ± 098 and

9.1 ± 0.3. The Shannon-Wiener diversity index were variable across all sites with low diversity at most sites (H' < 1) indicating that the meiofaunal assemblages were not diverse (Figure 9a). Port Stanvac sites had both the lowest and highest mean diversity across all sites ranging from 0.44 ± 0.07 to 1.35 ± 0.04. North Control sites had low diversity ranging from 0.69 ± 0.05 to 0.89 ± 0.10, while South Control sites had more variable diversity ranging from 0.60 ± 0.04 to 1.26 ± 0.05 (Figure 9a). The meiofaunal assemblages were not evenly distributed as values for Pielou's evenness (J') were mostly < 0.5 at all sites (Figure 9b). Port Stanvac sites had values ranging from 0.23 ± 0.03 to 0.61 ± 0.01. North Control sites had values from 0.35 ± 0.03 to 0.48 ± 0.05 and South Control sites had values from 0.29 ± 0.02 to 0.64 ± 0.02.

PERMANOVA results for the meiofaunal assemblages showed significant variations for sites within a location but no differences between control locations or between control locations and Port Stanvac (Table 12). The nMDS ordination plot of the sites showed no distinct separation of the three locations, with sites scattered across the plot (Figure 10).

Table 11PERMANOVA results for comparisons of mean abundance (A), number of taxonomic
groups (S), Shannon-Wiener diversity (H') and Pielou's evenness (J) of meiofauna
between Treatment (Control and Port Stanvac) with Locations (Port Stanvac, North
Control and South Control) nested within Treatment and Sites nested within Locations for
Survey 1. Significant differences (p < 0.05) are in bold.

Abundance (A)				
Source	Df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	20950	35.336	0.1215
Location(Treatment)	1	426	0.131	0.7232
Site(Location(Treatment))	17	3245	5.704	0.0001
Residual	180	569		
Number of taxonomic group	os (S)			
Source	Df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	0.845	0.111	0.9634
Location(Treatment)	1	51.840	3.370	0.0878
Site(Location(Treatment))	17	15.382	5.820	0.0001
Residual	180	2.643		
Shannon-Wiener Diversity (Ή')			
Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	0.005	0.139	0.9450
Location(Treatment)	1	2.328	2.416	0.1342
Site(Location(Treatment))	17	0.963	21.980	0.0001
Residual	180	0.044		
Pielou's evenness (J')				
Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	0.024	0.232	0.8832
Location(Treatment)	1	0.320	1.825	0.1915
Site(Location(Treatment))	17	0.175	19.520	0.0001
Residual	180	0.009		













Table 12PERMANOVA results of comparisons of meiofaunal assemblage structure between
Treatment (Control and Port Stanvac) with Locations (Port Stanvac, North Control and
South Control) nested within Treatment and Sites nested within Locations for Survey 1.
Significant differences (p < 0.05) are in bold.

Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	5708	1.445	0.4175
Location(Treatment)	1	3492	0.939	0.4043
Site(Location(Treatment))	17	3720	10.745	0.0001
Residual	180	346		



Figure 10 Two-dimensional nMDS ordination plot of square-root transformed mean abundance data of benthic meiofaunal assemblages from Port Stanvac, North Control and South Control for Survey 1.

SIMPER analyses showed high within-location similarity for all locations, with similarity for North Control at 83%, Port Stanvac at 71% and South Control at 72% (Table 13). All three locations were dominated by Nematoda and Copepoda, which accounted for >60% of similarity within each location. For Port Stanvac, Ostracoda, Syllidae, Polychaeta juvenile, Nemertea and Sipuncula contributed further up to ~90% of within-location similarity. North Control had Ostracoda, Nemertea, Syllidae and Polychaeta juvenile contributing further to within-location similarity up to ~90%, while South Control had Syllidae, Ostracoda, Nemertea, Polychaeta juvenile, Crustacean nauplii and Sipuncula (Table 13). Dissimilarities between locations were all low (<30%), with

similar discriminating taxa for all locations. The top four discriminating taxa, Copepoda, Nematoda, Crustacean nauplii and Syllidae, contributed up to 50% of dissimilarity between any two locations (Table 14).

Table 13Meiofaunal taxonomic groups listed in order of contribution to a cumulative percentage
of ~80% of overall within-location similarities at North Control, Port Stanvac and South
Control for Survey 1 (taxa in italic are unique to that location).

83.2	70.9	71.8
North Control	Port Stanvac	South Control
Nematoda	Nematoda	Nematoda
Copepoda	Copepoda	Copepoda
Ostracoda	Ostracoda	Syllidae
Nemertea	Syllidae	Ostracoda
Syllidae	Polychaeta juvenile	Nemertea
		Polychaeta juvenile

Table 14Meiofaunal taxonomic groups listed in order of contribution to a cumulative percentage
of ~80% of the dissimilarity between each pair of locations (North Control, Port
Stanvac and South Control) for Survey 1.

	Between-location dissimilarity	
26.6	28.5	25.7
Port Stanvac North Control	Port Stanvac South Control	North Control South Control
Copepoda	Copepoda	Nematoda
Nematoda	Nematoda	Copepoda
Crustacean nauplii	Crustacean nauplii	Crustacean nauplii
Syllidae	Syllidae	Syllidae
Ostracoda	Ostracoda	Polychaeta juvenile
Polychaeta juvenile	Polychaeta juvenile	Ostracoda
Halacaroidea	Halacaroidea	Nemertea
Nemertea	Nemertea	Halacaroidea
Sipuncula	Sipuncula	Sipuncula
	Tanaidacea	Tanaidacea
		Capitellidae

3.1 Survey 2 (September 2020)

3.2.1 Sediment Grain Size

Analysis of sediment grain fractions from Survey 2 showed variability among all sites and among sites within the same location (Figure 11). The highest proportion of gravel across all sites was at Site SC03 (22.5%). Highest proportion of fine, medium and coarse sand were recorded at Site NC04 (65.9%), Site SC05 (49.1%) and Site PS10 (69.1%) respectively. Clay fractions were sampled only at six sites with highest proportion recorded at Site SC03 (0.06%) and silt fraction was highest at Site PS03 (11.7%).

The variability of the sediment grain fractions among all sites were confirmed by PCA. PC1 accounted for 61% of the variability while PC2 accounted for a further 30%. In the PCA plot with superimposed vectors, PC1 differentiated sites with fine sand from sites with very coarse sand/gravel (left to right) and PC2 differentiated sites with fine sand from medium sand (Figure 12).

PERMANOVA indicated no significant difference between Port Stanvac and the control locations (p = 0.4170) or between the two control locations (p = 0.2617) and confirmed significant small-scale variation between sites within a location (p = 0.0001, Table 15).

Sediment grain size distribution for all sites were variable as shown by GRADISTAT analysis (see Table 2 for definition of terms). Medium sand (250-500 μ m) characterised most of the sites at Port Stanvac except for fine sand (125-250 μ m) at Site PS06, coarse sand at Sites PS07 and PS10 and very coarse sand (1000-2000 μ m) at Site PS05 (Table 16). North Control sites were characterised by fine, medium, and coarse sand while South Control sites by medium and coarse sand (Table 16). Sties at Port Stanvac sites were mostly poorly sorted with mesokurtic distribution and symmetrical skewness (Table 16). North Control sites had mesokurtic distribution except for Site NC02 with platykurtic distribution with either symmetrical or coarse skewness. South Control sites were variable, having two sites each with mesokurtic and leptokurtic distribution and one site with platykurtic distribution, while skewness were either symmetrical or coarse and only Site SC03 had fine skewness (Table 16).



Figure 11 Sediment grain size composition showing the six sediment fractions for the ten sites at Port Stanvac (PS), five sites each at North Control (NC) and South Control (SC) from Survey 2.



Figure 12 PCO plot of sediment grain size for the sites at Port Stanvac (PS), North Control (NC) and South Control (SC) from Survey 2 with superimposed vectors of sediment fractions. Vector length reflects the correlation between each fraction in PC1 and PC2, with the circle representing the vector length for a correlation of 1.

Table 15	PERMANOVA results showing highly variable sites as characterised by sediment composition for Survey 2. Significant differences ($p < 0.05$) are in bold.

Source	df	MS	Pseudo F	<i>p</i> (perm)
Treatment	1	16666	1.5365	0.4170
Location(Treatment)	1	8578	1.3742	0.2617
Sites(Location(Treatment))	17	106310	48.2460	0.0001
Residual	180	23331		
Total	199	154300		

Table 16 Sediment grain size distribution and GRADISTAT-calculated parameters for sites at Port Stanvac (PS), North Control (NC) and South Control (SC) for Survey 2. x-axis show particle size class (0-2000 µm) and y-axis show normalised % proportions of sediment fractions.









3.2.2 Macrofauna

From the 200 samples collected for Survey 2 in September 2020, three of the replicates yielded no animals (one each from Sites PS09, NC04 and SC05). The remaining 197 yielded a total of 1,889 macrofauna individuals from 61 taxonomic groups and ten phyla. The phylum Annelida (Polychaeta) dominated with 986 individuals comprising 52% of the overall abundance. The next most abundant phylum was Arthropoda (Crustacea) with 644 individuals (34%), followed by Echinodermata with 91 individuals (5%). The remaining seven phyla accounted for the remaining 9% of the overall abundance. The family Syllidae dominated the polychaetes (15%) and three other abundant families included Lumbrineridae (13%), Capitellidae (12%), and Spionidae (9%). As in Survey 1, Tanaidacea dominated the crustaceans (59%). Gammaridea amphipods (22%) was the next most abundant crustacean. Echinoderms comprised ophiuroids (39%), holothurians (37%) and echinoids (23%). A single asteroid was collected in this survey. Bivalves were the most abundant molluscs (72%). A list of macrofauna and total abundance at each location is provided in Appendix 3.

Polychaetes and crustaceans dominated at each of the locations. At Port Stanvac sites, they accounted for 85% of the total abundance. For the control sites, they accounted for 8% at North Control sites and 71% at South Control sites. Contributions from all other phyla were variable across the locations. A summary of the percent abundance of major phyla for each location is given in Table 17.

Key Phylum	North Control	Port Stanvac	South Control
Number of sites	5	10	5
Number of samples	50	100	50
Annelida	45.2	53.9	50.3
Arthropoda	40.2	34.4	28.9
Echinodermata	6.7	4.2	5.9
Mollusca	2.1	1.6	4.8
Nematoda	2.9	2.5	4.2
Nemertea	1.3	2.2	3.7
Sipuncula	0.8	0.3	1.4
Others	0.8	0.9	0.8

Table 17Number of sites and samples collected with the percent abundance of major phyla of
macrofauna at North Control, Port Stanvac and South Control for Survey 2.

Analyses of the number of individuals (A), number of taxonomic groups (S), Shannon-Wiener diversity (H) and Pielou's evenness (J) for macrofauna separately indicated no significant differences between the control locations and Port Stanvac or between the two control locations (Table 18). Only small-scale variation between sites within each location was significant (Table 18).

Table 18PERMANOVA results for abundance (A), number of taxonomic groups (S), Shannon-
Wiener diversity (H') and Pielou's evenness (J) of macrofauna between Treatment
(Control and Port Stanvac) with Locations (Port Stanvac, North Control and South
Control) nested within Treatment and Sites nested within Locations for Survey 2.
Significant differences (p < 0.05) are in bold.

Number of individuals (A)				
Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	2400.70	12.8360	0.2038
Location(Treatment)	1	132.14	0.4226	0.5201
Site(Location(Treatment))	17	314.57	8.2493	0.0001
Residual	177	38.13		
Number of taxonomic grou	ıps (S)			
Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	191.290	2.3264	0.4492
Location(Treatment)	1	61.397	1.2811	0.2779
Site(Location(Treatment))	17	48.223	9.1441	0.0001
Residual	177	5.274		
Shannon-Wiener Diversity	(H')			
Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	4.717	1.5988	0.5196
Location(Treatment)	1	2.253	1.5881	0.2295
Site(Location(Treatment))	17	1.427	6.1337	0.0001
Residual	177	0.233		
Pielou's evenness (J')				
Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	0.1531	5.2823	0.1697
Location(Treatment)	1	0.0201	1.5125	0.2410
Site(Location(Treatment))	17	0.0133	2.7587	0.0042
Residual	177	0.0048		

Mean macrofaunal abundances were variable across sites at all locations ranging from 3.3 individuals per core at Site SC05 to 24.1 individuals per core at PS05 (Figure 13a). Mean abundances at control locations ranged from 3.8 ± 0.9 (mean \pm SE) to 6.3 ± 0.7 individuals for North Control sites and 3.3 ± 0.5 to 16.9 ± 3.6 individuals for South Control sites (Figure 13a). At Port Stanvac sites, the mean abundances ranged from 5.2 ± 1.1 to 24.1 ± 3.4 individuals (Figure 13a). The lowest mean number of taxonomic groups was recorded at Sites NC04 and NC05 and the highest was at Site SC03 (Figure 13b). Mean number of taxonomic groups at Port Stanvac sites were between 3.3 ± 0.6 and 9.1 ± 0.8 , while North Control sites were between 2.7 ± 0.4 and 5.2 ± 0.6 and South Control sites were between 3.1 ± 0.5 and 10.3 ± 1.4 (Figure 13b). Most sites had highly diverse assemblages with the Shannon-Wiener diversity index greater than one (Figure 14a). The lowest diversity was recorded at Site NC04 and the highest at

Site SC03. There was generally an even distribution of taxa across all sites with Pielou's evenness greater than 0.8 (Figure 14b). Mean values for evenness for the control locations ranged from 0.91 ± 0.05 to 0.96 ± 0.01 for North Control sites and 0.94 ± 0.02 to 1.00 ± 0.01 for South Control sites. Port Stanvac had evenness ranging from 0.85 ± 0.03 to 0.95 ± 0.02 (Figure 14b).



Figure 13 Mean (a) abundance *A* (individuals per core) and (b) number of taxonomic groups *S*, with SE bars (n=10 except n=9 for PS09, NC04 and SC05) of macrofauna for each of the 20 sites sampled at North Control (NC), Port Stanvac (PS) and South Control (SC) for Survey 2.







PERMANOVA analysis of all replicate samples indicated significant difference in macrofaunal assemblage structure between Port Stanvac and the two control locations and variations between sites within a location (Table 19). The nMDS ordination using mean abundance per site yielded a two-dimensional plot with a high stress value of

0.18 (meaning the plot is useful but not in the details) showing some separation of the three locations (Figure 15).

Table 19PERMANOVA results of comparisons of macrofaunal assemblage structure between
Treatment (Control and Port Stanvac) with Location (Port Stanvac, North Control and
South Control) nested within Treatment and Site nested within Location for Survey 2.
Significant differences (p < 0.05) are in bold.

Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	28602	3.2640	0.0249
Location(Treatment)	1	6602	0.8552	0.5700
Site(Location(Treatment))	17	7752	2.6547	0.0001
Residual	177	2920		



Figure 15 Two-dimensional nMDS ordination plot of square-root transformed mean abundance data of benthic macrofaunal assemblages at Port Stanvac, North Control and South Control for Survey 2.

The within-location similarities as indicated by SIMPER analysis showed that they were approximately 50% for all locations (Table 20). Within each location, 12 taxonomic groups variously contributed to ~60% of the similarity, of which only four were found across all three locations (Table 20). The crustacean order Tanaidacea and polychaete family Lumbrineridae were the top two highest contributors to similarity for Port Stanvac sites. High contributors to similarity for North Control sites were Tanaidacea

and polychaete family Syllidae, while South Control had the polychaete family Lumbrineridae and the crustacean order Gammaridea (Table 20).

The between-location SIMPER analysis showed that dissimilarity between Port Stanvac and North Control was 44%, between Port Stanvac and South Control was 46% and between the two control locations was 44% (Table 21). There were 14 discriminating taxonomic groups contributing cumulatively to ~50% of the dissimilarity between Port Stanvac and North Control and 15 groups between Port Stanvac and South Control (Table 21). Sixteen groups contributed to the dissimilarity between North and South Control. The crustacean order Tanaidacea and polychaete family Syllidae cumulatively contributed ~12% to the dissimilarity between Port Stanvac and each of the two control locations (Table 21). For the dissimilarity between North and South Control, the contributing taxa were crustacean order Gammaridea, polychaete family Capitellidae and phylum Nemertea (Table 21).

Table 20	Macrofaunal taxonomic groups listed in order of contribution to a cumulative
	percentage of ~60% of overall within-location similarities at North Control, Port
	Stanvac and South Control for Survey 2 (taxa in italic are unique to that location).

	Within-location similarity			
47.6	51.3	52.5		
North Control	Port Stanvac	South Control		
Tanaidacea	Tanaidacea	Lumbrineridae		
Spionidae	Lumbrineridae	Gammaridea		
Lumbrineridae	Gammaridea	Tanaidacea		
Gammaridea	Capitellidae	Syllidae		
Capitellidae	Nemertea	Spionidae		
Phoxocephalidae	Spionidae	Phoxocephalidae		
Magelonidae	Ampharetidae	Magelonidae		
	Phyllodocidae	Nemertea		
		Holothuroidea		

Table 21	Macrofaunal taxonomic groups listed in order of contribution to a cumulative
	percentage of ~50% of the dissimilarity between each pair of locations (North Control,
	Port Stanvac and South Control) for Survey 2.

	Between-location dissimilarity			
44.2	45.5	44.0		
Port Stanvac North Control	Port Stanvac South Control	North Control South Control		
Tanaidacea	Tanaidacea	Gammaridea		
Syllidae	Syllidae	Capitellidae		
Ampharetidae	Ampharetidae	Nemertea		
Dorvilleidae	Dorvilleidae	Tanaidacea		
Gammaridea	Phyllodocidae	Ophiuroidea		
Nemertea	Hesionidae	Nematoda		
Capitellidae	Nematoda	Ostracoda		
Hesionidae	Capitellidae	Bivalvia		
Phyllodocidae	Gammaridea	Lumbrineridae		
Lumbrineridae	Nephtyidae	Dorvilleidae		
Nephtyidae	Spionidae	Syllidae		
Ophiuroidea	Bivalvia	Phyllodocidae		
Nematoda	Urohaustoriidae	Ampharetidae		
Urohaustoriidae	Paraonidae	Flabelligeridae		
	Lumbrineridae	Urohaustoriidae		
		Spionidae		

3.2.3 Meiofauna

A total of 11,866 individuals from 30 taxonomic groups and nine phyla of meiofauna were collected for Survey 2 in September 2020. The phylum Nematoda accounted for 66% of the overall abundance. Arthropoda (Crustacea) was the next most abundant at 28% and Annelida (Polychaeta) at 4% of overall abundance. The remaining six phyla contributed less than 1.5% to the overall abundance. A list and total abundance of meiofauna at each location are provided in Appendix 4.

Annelida meiofauna was dominated by the polychaete family Syllidae with 48% of the total Annelida abundance. Polychaete juvenile contributed 32% and family Capitellidae contributed 18%, with the remaining 11 families contributing 11%. The crustacean meiofauna was dominated by copepods (81%). The other abundant crustaceans were Crustacean nauplii (12%). A summary of percent abundance of meiofauna at each of the three locations, North Control, Port Stanvac and South Control is given in Table 22.

Key Taxa	North Control	Port Stanvac	South Control
Number of sites	5	10	5
Number of samples	50	100	50
Annelida	2.07	3.77	5.87
Arthropoda	22.30	27.62	32.40
Mollusca			0.006
Nematoda	72.23	66.34	58.83
Nemertea	1.04	1.39	1.51
Sipuncula	2.34	0.86	1.33
Others	0.02	0.02	0.06

Table 22Number of sites and samples collected with the percent abundance of major phyla of
meiofauna at North Control, Port Stanvac and South Control for Survey 2.

Analyses of each of the univariate measures indicated only small-scale significant differences between sites within each location for all measures. There was no significant difference between Port Stanvac sites and either of the control sites (Table 23).

Mean meiofaunal abundances (*A*) for each site were most variable at Port Stanvac, having both highest and lowest mean abundance (Figure 16a). Site PS09 at Port Stanvac had the highest mean abundance with 103.2 ± 9.0 individuals while Site PS03 had the lowest with 25.5 ± 2.5 . Mean abundances at North Control sites were less variable with values ranging from 35.3 ± 4.1 to 55.1 ± 5.8 , while sites at South Control had higher abundances with means ranging from 49.4 ± 3.7 to 61.9 ± 8.4 . Port Stanvac sites had the highest and lowest mean number of taxonomic groups across all locations ranging from 5.8 ± 0.3 to 10.8 ± 0.3 (Figure 16b). North Control sites had mean number of taxonomic groups ranging between 7.3 ± 0.5 and 10.1 ± 0.6 , while sites at South Control had a higher range between 7.5 ± 0.6 and 10.8 ± 0.4 .

The Shannon-Wiener diversity index across all sites from the three locations were generally low with nine site having values <1 and the remaining sites with values <1.5, indicating that the meiofaunal assemblages were not diverse (Figure 17a). Port Stanvac sites had both the lowest and highest mean diversity across all sites ranging from 0.47 ± 0.04 to 1.50 ± 0.03 . North Control sites had lower diversity ranging from 0.66 ± 0.06 to 1.11 ± 0.05 , while South Control sites had diversity >1.0 for all sites except for Site SC04 (Figure 17a). The meiofaunal assemblages were not evenly distributed with values for Pielou's evenness (*J*') averaging 0.5 (Figure 17b). Port Stanvac sites had values ranging from 0.23 ± 0.02 to 0.61 ± 0.05 and South Control sites had lower evenness with values from 0.33 ± 0.03 to 0.50 ± 0.05 and South Control sites had values from 0.33 ± 0.02 to 0.59 ± 0.03 .

PERMANOVA results for the meiofaunal assemblages showed significant variations for sites within a location but no differences between control locations or between Port Stanvac and control locations (Table 24). The nMDS ordination plot of the sites showed no distinct separation of the three locations, with sites scattered across the plot (Figure 18).

Table 23PERMANOVA results for comparisons of mean abundance (A), number of taxonomic
groups (S), Shannon-Wiener diversity (H) and Pielou's evenness (J) of meiofauna
between Treatment (Control and Port Stanvac) with Locations (Port Stanvac, North
Control and South Control) nested within Treatment and Sites nested within Locations for
Survey 2. Significant differences (p < 0.05) are in bold.

Abundance (A)				
Source	Df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	18280	4.657	0.3293
Location(Treatment)	1	2840	0.911	0.3594
Site(Location(Treatment))	17	3116	6.390	0.0001
Residual	180	488		
Number of taxonomic group	os (S)			
Source	Df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	52.020	1.837	0.4874
Location(Treatment)	1	23.040	1.006	0.3316
Site(Location(Treatment))	17	22.904	11.991	0.0001
Residual	180	1.910		
Shannon-Wiener Diversity (Ή')			
Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	0.828	0.965	0.6227
Location(Treatment)	1	0.980	0.829	0.3680
Site(Location(Treatment))	17	1.183	44.730	0.0001
Residual	180	0.026		
Pielou's evenness (J')				
Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	0.099	0.884	0.6398
Location(Treatment)	1	0.141	0.803	0.3785
Site(Location(Treatment))	17	0.175	34.861	0.0001
Residual	180	0.005		





Figure 16 Mean (a) abundance *A* (individuals per core) and (b) number of taxonomic groups *S*, with SE bars (n=10) of macrofauna for each of the 20 sites sampled at North Control (NC), Port Stanvac (PS) and South Control (SC) for Survey 2.



Figure 17 Mean (a) Shannon-Wiener diversity *H*' and (b) Pielou's evenness *J*', with SE bars (n=10) of macrofauna for each of the 20 sites sampled at North Control (NC), Port Stanvac (PS) and South Control (SC) for Survey 2.

Table 24PERMANOVA results of comparisons of meiofaunal assemblage structure between
Treatment (Control and Port Stanvac) with Locations (Port Stanvac, North Control and
South Control) nested within Treatment and Sites nested within Locations for Survey 2.
Significant differences (p < 0.05) are in bold.

Source	df	MS	Pseudo-F	<i>p</i> (perm)
Treatment	1	3246	1.063	0.5311
Location(Treatment)	1	3122	0.901	0.4315
Site(Location(Treatment))	17	3464	14.394	0.0001
Residual	180	241		



Figure 18 Two-dimensional nMDS ordination plot of square-root transformed mean abundance data of benthic meiofaunal assemblages from Port Stanvac, North Control and South Control for Survey 2.

There was high within-location similarity for all locations indicated by SIMPER analyses, with within similarity for North Control at 87%, Port Stanvac at 70% and South Control at 79% (Table 25). Nematoda, Copepoda and Crustacean nauplii dominated at all location, accounting for ~70% of similarity within each location. For Port Stanvac, Ostracoda, Sipuncula, Syllidae and Nemertea contributed further up to ~90% of within-location similarity. North Control had contributions from Nemertea, Sipuncula, Syllidae and Polychaeta juvenile, while South Control had Syllidae, Sipuncula, Polychaeta juvenile and Ostracoda (Table 25). Dissimilarities between locations were all low (<30%), with similar discriminating taxa for all locations (Table

26). The top two discriminating taxa common to all locations were Nematoda and Copepoda (Table 26).

Table 25Meiofaunal taxonomic groups listed in order of contribution to a cumulative percentage
of ~80% of overall within-location similarities at North Control, Port Stanvac and South
Control for Survey 2 (taxa in italic are unique to that location).

Within-location similarity		
87.6	70.2	79.0
North Control	Port Stanvac	South Control
Nematoda	Nematoda	Nematoda
Copepoda	Copepoda	Copepoda
Crustacean nauplii	Crustacean nauplii	Crustacean nauplii
Ostracoda	Nemertea	Syllidae
Sipuncula		Sipuncula

Table 26Meiofaunal taxonomic groups listed in order of contribution to a cumulative percentage
of ~80% of the dissimilarity between each pair of locations (North Control, Port
Stanvac and South Control) for Survey 2.

	Between-location dissimilarity			
23.8	25.9	18.9		
Port Stanvac North Control	Port Stanvac South Control	North Control South Control		
Nematoda	Copepoda	Copepoda		
Copepoda	Nematoda	Nematoda		
Crustacean nauplii	Crustacean nauplii	Capitellidae		
Syllidae	Syllidae	Nemertea		
Ostracoda	Capitellidae	Capitellidae		
Polychaeta juvenile	Nemertea	Nemertea		
Sipuncula	Ostracoda	Syllidae		
Nemertea	Polychaeta juvenile	Crustacean nauplii		
	Halacaroidea	Polychaeta juvenile		
		Sipuncula		
		Halacaroidea		
		Ostracoda		

3.2 Infauna-sediment relationship

3.2.1 Survey 1

DISTLM analysis of macrofaunal assemblage and sediment grain size for Survey 1 yielded a model with three sediment grain size fractions giving the best adjusted R^2 value, with only very coarse sand and very fine sand fractions contributing significantly to explain 31% of the variation in macroinfaunal assemblage structure (Table 27). Visualising the model with a dbRDA plot, showed that the first two axes explained 32% of the total variation in macroinfaunal assemblage structure (Figure 19). Sites from North Control are clustered to the right of the plot, indicating that the macrofaunal assemblage structure was correlated to fine sand (right), while Port Stanvac and South Control sites were more variable, with sites scattered across the plot (Figure 19). The dbRDA plot was compared to the nMDS plot and there was little concordance between the two plots. Although the RELATE test was significant (p = 0.01), the Rho value was a low value of 0.49, indicating that sediment composition may not be a strong driver in structuring the macrofaunal assemblage.

Table 27Results of DISTLM sequential test for relationship between macrofaunal assemblage
structure and sediment grain size fractions from Survey 1, using step-wise procedure
and adjusted R^2 criteria with all fractions integrated in a multiple regression model.
Significant contributions (p < 0.05) are in bold.

Variable	Adjusted R ²	Pseudo-F	p	Proportion of explained variance (%)
Very coarse sand	0.1454	4.2335	0.0001	19.0
Very fine sand	0.2245	2.8348	0.0004	11.6
Fine sand	0.2494	1.5646	0.0649	6.2





DISTLM for meiofaunal assemblage structure and sediment from Survey 1 yielded a model with four variables which gave the best adjusted R^2 , but only coarse sand and very coarse sand fractions were significant contributors, explaining 49% of the variation in the structure of the meiofaunal assemblage (Table 28). The dbRDA plot showed that most sites were negatively correlated to coarse and very coarse sand and the first two axes explained 54% of the total variation in meiofaunal assemblage structure (Figure 20). In comparing the dbRDA plot to the nMDS plot, the clustering of sites was generally similar. The RELATE test was significant (p = 0.01) with a Rho value 0.641, suggesting that sediment grain size may have a role in structuring the meiofauna assemblage structure.

Table 28Results of DISTLM sequential test for relationship between meiofaunal assemblage
structure and sediment grain size fractions for Survey 1, using step-wise procedure
and adjusted R² criteria with all fractions integrated in a multiple regression model.
Significant contributions (p < 0.05) are in bold.

Variable	Adjusted R ²	Pseudo-F	p	Proportion of explained variance (%)
Coarse sand	0.3693	12.1270	0.0001	40.3
Very coarse sand	0.4301	2.9196	0.0178	8.8
Very fine sand	0.4586	1.8830	0.0957	5.4
Gravel	0.1433	1.5596	0.1684	4.3



Figure 20 dbRDA ordination of meiofaunal assemblage as predicted by the DISTLM model showing the relationship between sediment grain size fractions that best explain the variation in meiofaunal assemblage at North Control, Port Stanvac and South Control sampled for Survey 1. The vectors indicate the strength and direction of the effect of sediment grain size fractions on meiofaunal assemblage.

3.2.2 Survey 2

DISTLM analysis of the macrofaunal and sediment grain size data for Survey 2 yielded a model with seven sediment grain size fractions with the best R² value, but only very coarse sand, silt and medium sand fractions contributed significantly to explain 40% of the variation in macroinfaunal assemblage structure (Table 29). The dbRDA plot of the model showed that the first two axes explained 34% of the total variation in macrofaunal assemblage structure with sites clustering based on the three significant sediment fractions (Figure 21). When the dbRDA plot was compared to the nMDS plot, there was no concordance between the two plots. Although the RELATE test was significant (p = 0.0001), the Rho value of 0.51 was low, indicating that sediment composition may not be a strong driver in structuring the macrofaunal assemblage.

Results of DISTLM sequential test for relationship between macrofaunal assemblage
structure and sediment grain size fractions for Survey 2, using step-wise procedure
and adjusted R ² criteria with all fractions integrated in a multiple regression model.
Significant contributions ($p < 0.05$) are in bold.

Variable	Adjusted R ²	Pseudo-F	p	Proportion of explained variance (%)
Very coarse sand	0.2125	4.8578	0.0001	21.3
Silt	0.3186	2.6459	0.0100	10.6
Medium sand	0.3954	2.0331	0.0076	7.7
Clay	0.4409	1.2210	0.2495	4.6
Gravel	0.4803	1.0603	0.4043	3.9
Fine sand	0.5145	0.9161	0.5644	3.4
Very fine sand	0.5372	0.5893	0.8634	2.3



Figure 21 dbRDA ordination of macrofaunal assemblage as predicted by the DISTLM model showing the relationship between sediment grain size fractions that best explain the variation in macrofaunal assemblage at North Control, Port Stanvac and South Control sampled for Survey 2. The vectors indicate the strength and direction of the effect of sediment grain size fractions on macrofaunal assemblage.

A model with seven sediment grain size fractions for best adjusted R² value was the result of the DISTLM analysis of meiofaunal assemblage and sediment fractions for Survey 2, with five of the fractions contributing significantly (Table 30). The first two axes in the dbRDA ordination plot accounted for 70% of the total variation in meiofaunal assemblage structure (Figure 22). The dbRDA plot had some match to the results of the nMDS of meiofaunal assemblage. The RELATE test indicated a significant

correlation between meiofauna and sediment (Rho = 0.486, p = 0.0001), indicating that sediment composition may be a structuring force for the meiofaunal assemblage.

Table 30Results of DISTLM sequential test for relationship between meiofaunal assemblage
structure and sediment grain size fractions for Survey 2, using step-wise procedure
and adjusted R² criteria with all fractions integrated in a multiple regression model.
Significant contributions (p < 0.05) are in bold.

Variable	Adjusted R ²	Pseudo-F	p	Proportion of explained variance (%)
Coarse sand	0.3686	10.5090	0.001	36.8
Silt	0.4749	3.4399	0.007	10.6
Very fine sand	0.6111	5.6038	0.001	13.6
Very coarse sand	0.6746	2.9265	0.025	6.3
Clay	0.7271	2.6945	0.028	5.3
Fine sand	0.7528	1.3942	0.253	2.6
Gravel	0.7728	1.0601	0.386	2.0



Figure 22 dbRDA ordination of meiofaunal assemblage as predicted by the DISTLM model showing the relationship between sediment grain size fractions that best explain the variation in meiofaunal assemblage at North Control, Port Stanvac and South Control sampled for Survey 2. The vectors indicate the strength and direction of the effect of sediment grain size fractions on meiofaunal assemblage.

3.3 Comparison between surveys in 2020

3.3.1 Sediment Grain Size

PERMANOVA analysis of the sediment composition showed that changes between the two surveys were different between sites, indicating that small-scale variability in changes over time. As there were no significant differences over time between locations within a treatment, it meant that the two control locations had little or consistent overall changes (Table 31). These changes are visualised in the PCA plot, with PC1 accounting for 64% of the variability, differentiating sites with fine/very fine sand from sites with very coarse sand/gravel (left to right), and PC2 accounting for a further 26%, differentiating sites with medium/coarse sand from sites with fine/very fine sand (top to bottom, Figure 23). The changes between surveys were not consistent for all locations with shifts in different directions. Post Stanvac had more variable changes, whilst most sites for the two control locations had smaller to no changes (Figure 23).

2020. Significant differences ($p < 0.05$) are in bold.				
Source	df	MS	Pseudo F	<i>p</i> (perm)
Survey	1	846	1.1172	0.5693
Treatment	1	34762	1.0326	0.5574
Location(Treatment)	1	25804	2.4338	0.0915
Survey*Treatment	1	346	0.7854	0.6690
Site(Location(Treatment))	17	10634	83.6580	0.0001
Survey*Location(Treatment)	1	1023	0.5961	0.4855
Survey*Site(Location(Treatment))	17	1723	13.5580	0.0001
Residual	359	127		

Table 31 PERMANOVA results for comparison of sediment composition from Survey 1 and 2 in 2020. Significant differences (p < 0.05) are in bold.



Figure 23 PCO plot of sediment grain size for the sites at North Control, Port Stanvac and South Control for Survey 1 (open symbols) and Survey 2 (filled symbols) in 2020 with superimposed vectors of sediment fractions. Vector length reflects the correlation between each fraction in PC1 and PC2, with the circle representing the vector length for a correlation of 1. Arrows indicate the shift between surveys for each site.

3.3.2 Macrofauna

The overall abundance of macrofauna decreased from 3038 individuals in Survey 1 (February 2020) to 1889 in Survey 2 (September 2020). PERMANOVA carried out to assess any changes in the macrofaunal assemblage structure indicated that there were site differences within each location, but the changes were not consistent between the two surveys (Table 32). There were significant changes between the two control locations, but the overall changes were also different for the two surveys (Table 32). No significant differences were detected between Port Stanvac and the control locations. These changes in macroinfaunal assemblages between surveys is shown in the PCO plot, with all sites moving in different directions (Figure 24).

Source	df	MS	Pseudo-F	<i>p</i> (perm)
Survey	1	21999	1.6934	0.2180
Treatment	1	46625	2.2020	0.1273
Location(Treatment)	1	15649	1.5092	0.1532
Survey*Treatment	1	6269	0.6200	0.8260
Site(Location(Treatment))	17	10394	3.8931	0.0001
Survey*Location(Treatment)	1	9557	2.0515	0.0452
Survey*Site(Location(Treatment))	17	4665	1.7472	0.0001
Residual	357	2670		

Table 32PERMANOVA results for comparison of macrofaunal assemblages between Survey 1
and 2 in 2020. Significant differences (p < 0.05) are in bold.



Figure 24 PCO plot of square-root transformed mean abundance data of macrofaunal assemblages for the sites at North Control, Port Stanvac and South Control from Survey 1 (open symbols) and Survey 2 (filled symbols) in 2020. Arrows indicate the change for each site between the two surveys.

3.3.3 Meiofauna

The overall abundance of meiofauna increased marginally from a total of 11516 individuals in Survey 1 to 11866 individuals in Survey 2. There was no significant difference between the two surveys, but the Year by Site interaction indicated that individual sites varied inconsistently over years (Figure 25).

Table 33	PERMANOVA results for comparison of meiofaunal assemblages between Survey 1 and
	2 in 2020. Significant differences ($p < 0.05$) are in bold.

Source	df	MS	Pseudo-F	<i>p</i> (perm)
Survey	1	4176	3.3057	0.1131
Treatment	1	5867	1.1701	0.4990
Location(Treatment)	1	4675	0.9983	0.3695
Survey*Treatment	1	2588	2.3112	0.2149
Site(Location(Treatment))	17	4686	16.2110	0.0001
Survey*Location(Treatment)	1	1064	0.4828	0.7344
Survey*Site(Location(Treatment))	17	2205	7.6294	0.0001
Residual	360	289		



Figure 25 PCO plot of square-root transformed mean abundance data of meiofaunal assemblages for the sites at North Control, Port Stanvac and South Control from Survey 1 (open symbols) and Survey 2 (filled symbols) in 2020. Arrows indicate the change for each site between the two surveys.
3.4 Comparison between years

3.4.1 Macrofauna

The total site mean abundance of macrofauna for the major phyla at each location (North Control, Port Stanvac and South Control) for all monitoring years is given in Table 34. The abundances provided by AdelaideAqua for the 2017 survey are anomalously low compared with those from the 2013 and 2020 surveys to an extent which requires clarification before any further analysis. As such, comparison of macrofauna assemblage was only carried out between the February 2013 and 2020 surveys.

There was a decrease in total site mean abundance of macrofauna from 106,265 individuals in the 2013 survey to 93,307 in the 2020 survey. Annelida and Arthropoda dominated at all locations in both years (Table 34). Results of PERMANOVA carried out to assess any changes between the 2013 and 2020 surveys indicated significant difference between years and differences between the two control sites but there was no interaction between these two factors (Table 35). There was no difference between Port Stanvac and the two control locations, with individual sites varying inconsistently over years as indicated by the Year by Site interaction (Table 35). The differences in macroinfaunal assemblages between the two monitoring years is shown in the PCO plot, with distinct separation of years (Figure 26a) but not of locations (Figure 26b).

Table 34Number of sites sampled with the total site mean abundance of major phyla of
macrofauna at North Control, Port Stanvac and South Control for the February 2013,
2017 and 2020 surveys. Data standardised to per m² with means calculated from n= 8
for 2013 and n=10 for 2017 and 2020 surveys.

Location	North Control	Port Stanvac	South Control
Number of sites sampled	5	10	5
Key Phylum			
2013 February Survey			
Annelida	10749	31596	19080
Arthropoda	10481	17545	8446
Echinodermata	115	77	38
Mollusca	230	1075	154
Nematoda	1958	1804	1728
Nemertea	77	499	499
Sipuncula		38	38
Others	38		
2017 February Survey			
Annelida	266	1014	437
Arthropoda	404	722	525
Echinodermata	31	8	10
Mollusca	293	379	253
Nematoda	4		0.4
Nemertea			
Sipuncula	6	0.4	7
Others	4	6	2
2020 February Survey			
Annelida	4453	31143	6296
Arthropoda	13176	22267	3962
Echinodermata	1014	1229	491
Mollusca	676	891	215
Nematoda	737	1781	1597
Nemertea	799	1474	768
Sipuncula	61	123	31
Others	31	31	61

Source	df	MS	Pseudo-F	<i>p</i> (perm)				
Year	1	10288	9.0617	0.0364				
Treatment	1	3042	0.6269	0.6792				
Location(Treatment)	1	4377	5.4505	0.0013				
Year*Treatment	1	1837	1.7739	0.3130				
Site(Location(Treatment))	17	811	1.4827	0.0271				
Year*Location(Treatment)	1	966	0.8778	0.4740				
Year*Site(Location(Treatment))	10	1101	2.0124	0.0022				
Residual	257	547						

Table 35 PERMANOVA results for comparison of macrofaunal assemblages between the February 2013 and 2020 surveys. Significant differences (p < 0.05) are in bold.



Figure 26 PCO plot of fourth-root transformed site mean abundance data showing changes in the benthic macrofaunal assemblages between the 2013 and 2020 surveys, with (a) plot labelled by year and (b) plot labelled by locations. The plot is superimposed with vectors of contributing taxa and the vector length reflects the taxa that separate the two years and locations.

3.4.2 Meiofauna

Comparison of meiofauna assemblage was carried out for all the three years of surveys. The total site mean abundance of meiofauna for the major phyla at each location (North Control, Port Stanvac and South Control) is given in Table 36.

Table 36Number of sites sampled with the total site mean abundance of major phyla of
meiofauna at North Control, Port Stanvac and South Control for the February 2013,
2017 and 2020 surveys. Data standardised to per cm² with means calculated from
n=8 for 2013 and n=10 for 2017 and 2020 surveys.

Location	North Control	Port Stanvac	South Control	
Number of sites sampled	5	10	5	
Key Phylum				
2013 February Survey				
Annelida	13.59	14.78	11.29	
Arthropoda	39.70	75.21	27.04	
Echinodermata				
Mollusca	0.03	0.04		
Nematoda	189.69	621.59	180.41	
Nemertea	2.81	4.40	1.46	
Sipuncula	0.14	1.56	0.87	
Others	0.04	0.28	0.03	
2017 February Survey				
Annelida	4.1	15.3	3.6	
Arthropoda	294.5	524.0	360.9	
Echinodermata		1.5		
Mollusca	24.8	58.2	37.1	
Nematoda	82.3	161.6	88.4	
Nemertea		3.5		
Sipuncula	0.3	1.9		
Others	3.0	18.3	10.0	
2020 February Survey				
Annelida	4.08	36.78	13.48	
Arthropoda	38.19	239.81	80.31	
Echinodermata	0.01		0.04	
Mollusca		0.1	0.07	
Nematoda	179.68	389.88	146.81	
Nemertea	2.65	6.78	3.75	
Sipuncula	1.78	4.67	2.43	
Others	0.03	0.14	0.16	

The total site mean abundances for the three surveys in 2013, 2017 and 2020 were 1,185, 1,693 and 1,152 respectively. Nematoda dominated at the three locations for the 2013 and 2020 surveys, while Arthropoda dominated for the 2017 survey (Table 36).

PERMANOVA carried out to assess any changes between the years (2013, 2017 and 2020) indicated that the meiofaunal assemblage differed across all sites over time, but there was no difference between Port Stanvac and the two control locations (Table 37). Individual sites varied inconsistently over years as indicated by the Year by Site interaction (Table 37). The differences in meiofaunal assemblages between the three years is shown in the PCO plot, with distinct separation of years (Figure 27a), but not of locations (Figure 27b), indicating no difference between Port Stanvac and the control locations. The difference between 2013 and 2017 was characterised by the dominance of major phyla, Nematoda for 2013 and Arthropoda for 2017.

are in bold.	iy 2013, 2017 ali	u 2020. Signin	icant unierences	(<i>p</i> < 0.05)
Source	df	MS	Pseudo-F	<i>p</i> (perm)
Year	2	59151	9.0617	0.0049
Treatment	1	2943	0.6269	0.3798
Location(Treatment)	1	2051	5.4505	0.1829
Year*Treatment	2	4529	1.7739	0.2517
Site(Location(Treatment))	17	1460	1.4827	0.0001
Year*Location(Treatment)	2	2170	0.8778	0.1576
Year*Site(Location(Treatment))	20	1344	2.0124	0.0001
Residual	374	342		

Table 37PERMANOVA results for comparison of meiofaunal assemblages among the three
surveys conducted in February 2013, 2017 and 2020. Significant differences (p < 0.05)
are in bold.



Figure 27 PCO plot of square-root transformed site mean abundance data showing differences in the benthic meiofaunal assemblages for the February 2013, 2017 and 2020 surveys, with (a) plot labelled by year and (b) plot labelled by locations. The plot is superimposed with vectors of contributing taxa and the vector length reflects the taxa that separate the three years and locations.

4 DISCUSSION

The potential effects of desalination plants have been widely investigated and can influence marine organisms in aspects such as the development of species, survival of larva and breeding and reproductive traits (Mauguin and Corsin 2005, Miri and Chouikhi 2005, Missimer and Maliva 2018, Naser 2013, Riera *et al.* 2011). (Del Pilar Ruso *et al.* 2008, Del Pilar Ruso *et al.* 2009, Fernández-Torquemada *et al.* 2005, Lattemann and Höpner 2008, Miri and Chouikhi 2005). There have also been studies that show no detectable effects of desalination discharges (Danoun 2007, Pérez Talavera and Quesada Ruiz 2001, Raventos *et al.* 2006, Tsiourtis 2001). The environmental impact statement for the ADP acknowledged the ecological sensitivity of marine organisms to brine discharges but found that measurable adverse impacts of the ADP on the marine environment within Gulf St Vincent would be unlikely (SA Water 2008).

In general, there were no significant differences in macrofauna or meiofauna abundance, diversity measures or community structure between Port Stanvac and the control locations for the surveys in February and September 2020, except for the macrofaunal assemblage in September 2020. Significant difference between the two control locations was only detected for macrofaunal assemblage in February 2020. At a finer spatial scale, significant differences in all measures were invariably detected between sites within each location for both surveys.

Brine discharges over soft sediment habitats have the potential to change the structure and diversity of infaunal assemblages with increased dominance of nematodes and reduced diversity and abundance of polychaetes (Del Pilar Ruso *et al.* 2009, Riera *et al.* 2011). However, the macrofaunal assemblages at Port Stanvac and the control locations were dominated by polychaetes (and crustaceans) for both surveys, and nematode abundances in the meiofaunal assemblages were the same for Port Stanvac and control locations (~60% of total abundance) in both surveys. The overall macrofauna and meiofauna community structure between surveys were not significantly different with individual sites varying inconsistently over the two surveys.

The sediment grain size composition between Port Stanvac and the two control locations or between the two control locations were not significantly different. There was only small-scale difference between sites within a location. Consequently, the correlation between sediment grain size composition and the macroinfaunal and meiofaunal assemblages did not show consistent correlation between the two surveys.

Some polychaete species are useful bioindicators, being opportunistic and responsive to environmental perturbations (Del Pilar Ruso *et al.* 2009, Grassle and Grassle 1974). Syllidae are considered a good quality area indicator (Elias *et al.* 2004) while Capitellidae indicate a polluted area (Pocklington and Wells 1992). Contrary to this

indicator paradigm described, the dominant polychaete species found in both years (2013 and 2020) were not indicative of an impact of brine discharge from the ADP. Syllidae and Capitellidae dominated in 2013, while Syllidae (and Dorvilleidae) dominated in 2020. Comparison of the macrofaunal assemblage between 2013 and 2020 showed differences between years and between the two control locations but this was not consistent between years. Individual sites varied inconsistently for the two years with no difference detected between Port Stanvac and the control locations.

For the meiofaunal assemblage comparisons of the 2013, 2017 and 2020 surveys, differences were detected across all sites over time, but there was no difference between Port Stanvac and the control locations. These differences were characterised by the dominance of major phyla with Arthropoda (mostly copepods) for 2017 and Nematoda for 2013, while 2020 sites were more variable.

Sediment composition were not consistent for any of the survey years and consequently, correlation with meiofaunal assemblages were either weak or none (Dittmann *et al.* 2017, Loo *et al.* 2014).

All the surveys were carried out while the ADP was operational. However, the monthly discharge of brine was variable over time (Figure 28). Discharge was at similar levels during the February surveys for 2013 and 2020, but minimal for the 2017 survey, adding additional weight to the comparisons between 2017 and 2020 for interpreting the potential impact of the desalination plant.



Figure 28 The monthly discharge of brine (ML) from 2012 to 2020, with the red lines indicating the surveys carried out in 2013, 2017 and 2020.

5 CONCLUSION

In addition to the general lack of significant difference between the Port Stanvac and control locations for the 2020 surveys (with the exception of the September 2020 macrofaunal assemblage), there were no significant interactions between treatment (Port Stanvac and control locations) and year in the comparisons made of macrofauna and meiofauna abundance, diversity measures or community structure. Furthermore, there was no evidence of differences in indicator species between Port Stanvac and the control locations. The overall results suggest that the desalination plant brine discharge is not impacting the infaunal assemblages at Port Stanvac. However, it should be acknowledged that there is a high level of variation and inconsistency in trends among sites, which undermines the ability to draw conclusions from the comparisons between Port Stanvac and the control locations.

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List and total abundance* of macrofaunal taxonomic groups sampled from all sites at (a) Port Stanvac, (b) North Control and (c) South Control for Survey 1 in February 2020

Phylum Class Order Suborder Family**	North	Port	South				
Filylulli	Class	Order	Suborder	ranniy	Control	Stanvac	Control
ANNELIDA	POLYCHAETA			CAPITELLIDAE	14	102	25
ANNELIDA	POLYCHAETA			MALDANIDAE		2	
ANNELIDA	POLYCHAETA			OPHELIIDAE		3	3
ANNELIDA	POLYCHAETA			ORBINIIDAE	3	1	5
ANNELIDA	POLYCHAETA			PARAONIDAE		20	5
ANNELIDA	POLYCHAETA			SACCOCIRRIDAE		123	1
ANNELIDA	POLYCHAETA			SCALIBREGMATIDAE		3	
ANNELIDA	POLYCHAETA	AMPHINOMIDA		AMPHINOMIDAE		1	
ANNELIDA	POLYCHAETA	CANALIPALPATA	PHYLLODOCIDA	SIGALIONIDAE	3	14	6
ANNELIDA	POLYCHAETA	CANALIPALPATA	SABELLIDA	OWENIIDAE	1	1	1
ANNELIDA	POLYCHAETA	CANALIPALPATA	SABELLIDA	SABELLIDAE	3	14	1
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	MAGELONIDAE	16	14	10
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	POECILOCHAETIDAE	3	10	5
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	SPIONIDAE	42	88	36
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	AMPHARETIDAE	9	20	4
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	CIRRATULIDAE	5	10	6
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	FLABELLIGERIDAE	3	9	
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	PECTINARIIDAE		2	
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	TEREBELLIDAE	2	14	3
ANNELIDA	POLYCHAETA	EUNICIDA		DORVILLEIDAE	1	169	9
ANNELIDA	POLYCHAETA	EUNICIDA		EUNICIDAE		5	1
ANNELIDA	POLYCHAETA	EUNICIDA		LUMBRINERIDAE	11	108	6
ANNELIDA	POLYCHAETA	EUNICIDA		OENONIDAE	2		
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	APHRODITIFORMIA	POLYNOIDAE		1	1

Appendix 1 continued

Dhylum	Class	Ordor	Subordor	Eamily**	North Port	South	
Fliyium	Class	Uldel	Suburuer	ranny	Control	Stanvac	Control
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	GLYCERIFORMIA	GLYCERIDAE	2	17	10
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	GLYCERIFORMIA	GONIADIDAE	3	9	3
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	HESIONIDAE	2	25	2
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	NEREIDIDAE		1	
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	SYLLIDAE	15	148	44
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	PHYLLODOCIFORMIA	PHYLLODOCIDAE	4	20	13
ANNELIDA	POLYCHAETA	PHYLLODOCIDA		NEPHTYIDAE	3	58	5
ARTHROPODA	MALACOSTRACA	AMPHIPODA	AMPHILOCHIDEA	STEGOCEPHALIDAE	1		
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA		75		
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA			158	20
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA	LEUCOTHOIDAE		1	
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA	LYSIANASSIDAE		2	1
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA	OEDICEROTIDAE	8	4	20
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA	PHOXOCEPHALIDAE	29	33	36
ARTHROPODA	MALACOSTRACA	AMPHIPODA		CAPRELLIDAE		7	1
ARTHROPODA	MALACOSTRACA	AMPHIPODA		KAMAKIDAE	1		
ARTHROPODA	MALACOSTRACA	AMPHIPODA		UROHAUSTORIIDAE	35		
ARTHROPODA	MALACOSTRACA	AMPHIPODA		UROHAUSTORIIDAE		8	5
ARTHROPODA	MALACOSTRACA	CUMACEA				6	2
ARTHROPODA	MALACOSTRACA	DECAPODA	DENDROBRANCHIATA		1	3	1
ARTHROPODA	MALACOSTRACA	DECAPODA	PLEOCYEMATA		2	6	2
ARTHROPODA	MALACOSTRACA	DECAPODA	PLEOCYEMATA	MAJOIDEA		4	
ARTHROPODA	MALACOSTRACA	DECAPODA	PLEOCYEMATA	PAGUROIDEA		3	
ARTHROPODA	MALACOSTRACA	DECAPODA	PLEOCYEMATA	MAJIDAE			1
ARTHROPODA	MALACOSTRACA	DECOPODA	PLEOCYEMATA	HYMENOSOMATIDAE	1		
ARTHROPODA	MALACOSTRACA	ISOPODA	CYMOTHOIDA	ANTHUROIDEA	19	5	1
ARTHROPODA	MALACOSTRACA	ISOPODA	FLABELLIFERA		3	2	2
ARTHROPODA	MALACOSTRACA	STOMATOPODA					1

Appendix 1 continued

Dhylum	Class	Ordor	Subordor	Eamily**	North Port	South	
Phylum	Class	Order	Suborder	Failing	Control	Stanvac	Control
ARTHROPODA	MALACOSTRACA	TANAIDACEA			235	469	34
ARTHROPODA	MAXILLOPODA	CALANOIDA			13	6	
ARTHROPODA	MAXILLOPODA	CYCLOPOIDA				1	
ARTHROPODA	MAXILLOPODA	HARPACTICOIDA			2	1	
ARTHROPODA	OSTRACODA				4	6	2
CHAETOGNATHA						1	
CHORDATA	LEPTOCARDII	AMPHIOXIFORMES		BRACHIOSTOMIDAE	1		
ECHINODERMATA	ECHINOIDEA				2	15	3
ECHINODERMATA	ECHINOIDEA	SPATANGOIDA			2	6	2
ECHINODERMATA	HOLOTHUROIDEA				5	8	5
ECHINODERMATA	OPHIUROIDEA				24	11	6
MOLLUSCA	BIVALVIA				12	19	5
MOLLUSCA	BIVALVIA			LIMIDAE		1	
MOLLUSCA	BIVALVIA	ADAPEDONTA		HIATELLIDAE	1		
MOLLUSCA	BIVALVIA	VENERIDA			2		
MOLLUSCA	BIVALVIA	VENERIDA		VENERIDAE		1	
MOLLUSCA	BIVALVIA	VENEROIDA		SOLENIDAE	3	2	1
MOLLUSCA	BIVALVIA			CORBULIDAE	1		
MOLLUSCA	CEPHALOPODA					1	
MOLLUSCA	GASTROPODA					3	
MOLLUSCA	GASTROPODA	NEOGASTROPODA		VOLUTIDAE	3		1
MOLLUSCA	GASTROPODA	NUDIBRANCHIA				1	
MOLLUSCA	SCAPHOPODA				1		
NEMATODA					24	58	52
NEMERTEA					26	48	25
SIPUNCULA					2	4	1

*Total abundance is the total number of animals from 100 core samples for Port Stanvac and 50 core samples for North Control and South Control ** Family also refers to lowest taxonomic group used for analysis that are not shown in the classification columns and include subclass and superfamily

List and total abundance* of meiofaunal taxonomic groups sampled from all sites at (a) Port Stanvac, (b) North Control and (c) South Control for Survey 1 in February 2020

Phylum	Class	Order	Suborder Eamily	North	Port	South	
Fliyiulli	Class	Order	Suborder	ranniy	Control	Stanvac	Control
ANNELIDA	POLYCHAETA			POLYCHAETA JUVENILE	110	588	210
ANNELIDA	POLYCHAETA			CAPITELLIDAE	2	14	21
ANNELIDA	POLYCHAETA			PARAONIDAE	1	3	9
ANNELIDA	POLYCHAETA			SACCOCIRRIDAE		4	1
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	MAGELONIDAE	2		
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	POECILOCHAETIDAE		1	
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	SPIONIDAE	5	1	2
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	CIRRATULIDAE		1	1
ANNELIDA	POLYCHAETA	EUNICIDA		DORVILLEIDAE		22	6
ANNELIDA	POLYCHAETA	EUNICIDA		LUMBRINERIDAE		8	12
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	HESIONIDAE		13	3
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	SYLLIDAE	132	832	502
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	PHYLLODOCIFORMIA	PHYLLODOCIDAE			1
ARTHROPODA	ARACHNIDA	TROMBIDIFORMES	PROSTIGMATA	HALACAROIDEA	8	144	58
ARTHROPODA	MALACOSTRACA			CRUSTACEAN NAUPLII	184	525	355
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA		7	45	2
ARTHROPODA	MALACOSTRACA	AMPHIPODA		UROHAUSTORIIDAE	1	1	
ARTHROPODA	MALACOSTRACA	CUMACEA				20	2
ARTHROPODA	MALACOSTRACA	ISOPODA				6	5
ARTHROPODA	MALACOSTRACA	ISOPODA	CYMOTHOIDA	ANTHURIDAE		1	
ARTHROPODA	MALACOSTRACA	ISOPODA	FLABELLIFERA		1		
ARTHROPODA	MALACOSTRACA	TANAIDACEA			26	24	33
ARTHROPODA	MAXILLOPODA			COPEPODA	1683	7397	3141
ARTHROPODA	OSTRACODA				209	1039	305

Appendix 2 continued

Dhylum	Class	Ordor	Subordor	Family	North Port Control Stanvac	South	
Phylum	Class	Order	Suboruer	Falliny	Control	Stanvac	Control
ECHINODERMATA	HOLOTHUROIDEA				1		2
ECHIURA						6	5
GASTROTRICHA						4	5
MOLLUSCA	BIVALVIA					5	3
MOLLUSCA	GASTROPODA				3		
NEMATODA					9499	17449	7535
NEMERTEA					138	304	173
ROTIFER					3	1	
SIPUNCULA					92	209	118

*Total abundance is the total number of animals from 100 core samples standardised to numbers per cm² for Port Stanvac and 50 core samples for North Control and South Control

** Family also refers to lowest taxonomic group used for analysis that are not shown in the classification columns and include subclass and superfamily

List and total abundance* of macrofaunal taxonomic groups sampled from all sites at (a) Port Stanvac, (b) North Control and (c) South Control for Survey 2 in September 2020

Phylum Class Order Suborder Famil	Familu**	North	Port	South			
Phylum	Class	Ulder	Suborder	Falliny	Control	Stanvac	Control
ANNELIDA	POLYCHAETA			CAPITELLIDAE	21	69	24
ANNELIDA	POLYCHAETA			MALDANIDAE		2	
ANNELIDA	POLYCHAETA			ORBINIIDAE	1	2	2
ANNELIDA	POLYCHAETA			PARAONIDAE		21	6
ANNELIDA	POLYCHAETA			SACCOCIRRIDAE	1	5	2
ANNELIDA	POLYCHAETA			SCALIBREGMATIDAE	2	1	
ANNELIDA	POLYCHAETA	CANALIPALPATA	PHYLLODOCIDA	CHRYSOPETALIDAE		1	
ANNELIDA	POLYCHAETA	CANALIPALPATA	PHYLLODOCIDA	SIGALIONIDAE	2	4	1
ANNELIDA	POLYCHAETA	CANALIPALPATA	SABELLIDA	OWENIIDAE	2	6	3
ANNELIDA	POLYCHAETA	CANALIPALPATA	SABELLIDA	SABELLIDAE		5	12
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	CHAETOPTERIDAE		1	
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	MAGELONIDAE	11	14	10
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	POECILOCHAETIDAE		4	1
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	SPIONIDAE	18	50	18
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	AMPHARETIDAE	4	52	8
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	CIRRATULIDAE	3	5	3
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	FLABELLIGERIDAE	7	13	2
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	TEREBELLIDAE	1	10	5
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	TRICHOBRANCHIDAE		2	
ANNELIDA	POLYCHAETA	EUNICIDA		DORVILLEIDAE	2	57	9
ANNELIDA	POLYCHAETA	EUNICIDA		EUNICIDAE		6	5
ANNELIDA	POLYCHAETA	EUNICIDA		LUMBRINERIDAE	10	85	34
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	APHRODITIFORMIA	POLYNOIDAE		2	
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	GLYCERIFORMIA	GLYCERIDAE	2	20	6

Appendix 3 continued

Phylum	Class	Order	Suborder	Family**	North Control Port Stanvac 2 58 1 1 10 129 3 32 6 39 26 86 E 10 10 E 8 7 3 8 1 10 10 10 E 8 7 3 8 1 10 2 6 4 1 1 10 2 6 34 318 1 1 2 1 1 1 1	Port	South
Thylam	Class	order	Suboraci	T diffiny		Control	
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	GLYCERIFORMIA	GONIADIDAE		2	
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	HESIONIDAE	2	58	1
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	NEREIDIDAE		1	
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	SYLLIDAE	10	129	19
ANNELIDA	POLYCHAETA	PHYLLODOCIDA		NEPHTYIDAE	3	32	1
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	PHYLLODOCIFORMIA	PHYLLODOCIDAE	6	39	7
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA		26	86	32
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA	PHOXOCEPHALIDAE	10	10	11
ARTHROPODA	MALACOSTRACA	AMPHIPODA		CAPRELLOIDEA			7
ARTHROPODA	MALACOSTRACA	AMPHIPODA		UROHAUSTORIIDAE	8	7	6
ARTHROPODA	MALACOSTRACA	CUMACEA			3	8	4
ARTHROPODA	MALACOSTRACA	DECAPODA		LEUCOSIIDAE	1	2	
ARTHROPODA	MALACOSTRACA	DECAPODA	PLEOCYEMATA	HYMENOSOMATIDAE	1	1	3
ARTHROPODA	MALACOSTRACA	ISOPODA			10		1
ARTHROPODA	MALACOSTRACA	ISOPODA	CYMOTHOIDA		2	6	1
ARTHROPODA	MALACOSTRACA	ISOPODA	FLABELLIFERA			4	2
ARTHROPODA	MALACOSTRACA	NEBALIACEA					1
ARTHROPODA	MALACOSTRACA	TANAIDACEA			34	318	30
ARTHROPODA	MAXILLOPODA	HARPACTICOIDA			1		
ARTHROPODA	OSTRACODA					2	5
ARTHROPODA	PYCNOGONIDA	PANTOPODA			1		
CHORDATA	ASCIDIACEA				1	1	
CHORDATA	LEPTOCARDII	AMPHIOXIFORMES		BRACHIOSTOMIDAE		2	
CNIDARIA	ANTHOZOA	ACTINIARIA				1	2
ECHINODERMATA	ASTEROIDEA					1	
ECHINODERMATA	ECHINOIDEA					11	2
ECHINODERMATA	ECHINOIDEA	SPATANGOIDA				4	4
ECHINODERMATA	HOLOTHUROIDEA				3	24	7

Appendix 3 continued

Dhylum	Class	Ordor	Subordor	Family**	North	Port	South
Phylum	Class	Order	Suboruer	Failiny	NorthPortControlStanva131441555A11732	Stanvac	Control
ECHINODERMATA	OPHIUROIDEA				13	14	8
MOLLUSCA	BIVALVIA				4	15	12
MOLLUSCA	GASTROPODA					5	
MOLLUSCA	GASTROPODA			PATELLOGASTROPOD	A	1	4
MOLLUSCA	GASTROPODA						1
MOLLUSCA	SCAPHOPODA				1		
NEMATODA					7	32	15
NEMERTEA					3	29	13
PHORONIDA					1	7	1
SIPUNCULA					2	4	5

*Total abundance is the total number of animals from 100 core samples for Port Stanvac and 50 core samples for North Control and South Control ** Family also refers to lowest taxonomic group used for analysis that are not shown in the classification columns and include subclass and superfamily

List and total abundance* of meiofaunal taxonomic groups sampled from all sites at (a) Port Stanvac, (b) North Control and (c) South Control for Survey 2 in September 2020

Phylum	Class	Order	Suborder	Family	North	Port	South
					Control	Stanvac	Control
ANNELIDA	POLYCHAETA			POLYCHAETA JUVENILE	80	364	181
ANNELIDA	POLYCHAETA			CAPITELLIDAE	9	72	92
ANNELIDA	POLYCHAETA			PARAONIDAE		2	
ANNELIDA	POLYCHAETA			SACCOCIRRIDAE	1		
ANNELIDA	POLYCHAETA	CANALIPALPATA	PHYLLODOCIDA	SIGALIONIDAE		2	2
ANNELIDA	POLYCHAETA	CANALIPALPATA	SABELLIDA	SABELLIDAE		2	1
ANNELIDA	POLYCHAETA	CANALIPALPATA	SPIONIDA	SPIONIDAE	3	6	3
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	FLABELLIGERIDAE			1
ANNELIDA	POLYCHAETA	CANALIPALPATA	TEREBELLIDA	STERNASPIDAE		2	
ANNELIDA	POLYCHAETA	EUNICIDA		DORVILLEIDAE	3	3	4
ANNELIDA	POLYCHAETA	EUNICIDA		LUMBRINERIDAE		1	3
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	HESIONIDAE		1	8
ANNELIDA	POLYCHAETA	PHYLLODOCIDA	NEREIDIFORMIA	SYLLIDAE	147	524	241
ANNELIDA	POLYCHAETA	PHYLLODOCIDA		NEPHTYIDAE			2
ARTHROPODA	ARACHNIDA	TROMBIDIFORMES	PROSTIGMATA	HALACAROIDEA	15	114	43
ARTHROPODA	MALACOSTRACA			CRUSTACEAN NAUPLII	342	768	376
ARTHROPODA	MALACOSTRACA	AMPHIPODA	GAMMARIDEA		6	30	9
ARTHROPODA	MALACOSTRACA	CUMACEA			1		1
ARTHROPODA	MALACOSTRACA	ISOPODA					1
ARTHROPODA	MALACOSTRACA	ISOPODA	FLABELLIFERA			9	3
ARTHROPODA	MALACOSTRACA	TANAIDACEA				11	18
ARTHROPODA	MAXILLOPODA	HARPACTICOIDA		COPEPODA	1897	5422	3225
ARTHROPODA	OSTRACODA				259	289	177

Appendix 4 continued

Phylum	Class	Order	Suborder	Family	North	Port	South
					Control	Stanvac	Control
ECHINODERMATA	HOLOTHUROIDEA				2		
ECHIURA					2	3	5
GASTROTRICHA							1
MOLLUSCA	BIVALVIA						1
NEMATODA					8010	16629	7296
NEMERTEA					123	340	196
SIPUNCULA					270	227	165

*Total abundance is the total number of animals from 100 core samples for Port Stanvac and 50 core samples for North Control and South Control

** Family also refers to lowest taxonomic group used for analysis that are not shown in the classification columns and include subclass and superfamily