

Table S1: List of barcode tags used to demultiplex the pyrosequencing library

<i>Sample ID</i>	<i>Barcode</i>
DIS-NDW	CTATAT
DIS-BWI	CTATCA
DIS-LCL	CTACTG
ATL-NDW	TGATAT
ATL-BWI	TGATCA
ATL-UCL1	TGACTG
ATL-UCL2	TGACAC
ATL-LCL	TGAGCG

Table S2: Spearman's rank correlation matrix between measured environmental variables, cell density and depth in the 8 samples. The pairs of variables with positive correlation coefficients and P values below 0.050 tend to increase together. For the pairs with negative correlation coefficients and P values below 0.050, one variable tends to decrease while the other increases. For pairs with P values greater than 0.050, there is no significant relationship between the two variables.

	<b>Fe</b>	<b>Mn</b>	<b>SO4</b>	<b>PO4</b>	<b>NO3</b>	<b>NH4</b>	<b>NO2</b>	<b>Cl</b>	<b>Cu</b>	<b>Si</b>	<b>Temperature</b>	<b>Salinity</b>	<b>TOC</b>	<b>IC</b>	<b>Cell Density</b>	
<b>Depth</b>	0.846	0.903	-0.905	0.299	0.167	0.881	0.91	0.791	0.119	0.929	0.97	0.97	-0.405	-0.833	-0.548	
<i>P Values</i>	0.00178	2E-07	2E-07	0.423	0.662	2E-07	2E-07	0.0149	0.749	2E-07	0.0000002	2E-07	0.29	0.00526	0.139	
<b>Fe</b>	0.643	-0.873	0.521	0.273	0.846	0.878	0.969	0.355	0.627	0.741	0.851	-0.655	-0.764	-0.873		
<i>P Values</i>	0.0716	2E-07	0.16	0.498	0.00178	2E-07	2E-07	0.353	0.086	0.0287	0.00178	0.0716	0.0212	0.0000002		
<b>Mn</b>		-0.83	0.135	0.317	0.708	0.761	0.531	0.195	0.976	0.957	0.884	-0.366	-0.659	-0.317		
<i>P Values</i>		0.00526	0.705	0.423	0.0374	0.0212	0.16	0.619	2E-07	0.0000002	2E-07	0.353	0.0588	0.423		
<b>SO4</b>			-0.539	-0.333	-0.857	-0.838	-0.846	-0.286	-0.786	-0.85	-0.874	0.595	0.833	0.643		
<i>P Values</i>			0.139	0.387	0.00178	0.00526	0.00178	0.46	0.0149	0.00178	2E-07	0.102	0.00526	0.0716		
<b>PO4</b>				-0.12	0.192	0.139	0.549	0.635	0.0958	0.169	0.181	-0.79	-0.228	-0.743		
<i>P Values</i>				0.749	0.619	0.705	0.139	0.0716	0.794	0.662	0.619	0.0149	0.537	0.0287		
<b>NO3</b>					0.286	0.287	0.218	0.262	0.167	0.275	0.204	-0.0476	-0.143	-0.143		
<i>P Values</i>					0.46	0.46	0.578	0.498	0.662	0.46	0.578	0.885	0.705	0.705		
<b>NH4</b>						0.97	0.873	-0.143	0.714	0.802	0.922	-0.262	-0.952	-0.5		
<i>P Values</i>						2E-07	2E-07	0.705	0.0374	0.0096	2E-07	0.498	2E-07	0.182		
<b>NO2</b>							0.851	-0.0479	0.778	0.843	0.964	-0.323	-0.922	-0.539		
<i>P Values</i>							0.00178	0.885	0.0149	0.00526	2E-07	0.387	2E-07	0.139		
<b>Cl</b>								0.218	0.518	0.659	0.796	-0.573	-0.791	-0.846		
<i>P Values</i>								0.578	0.16	0.0588	0.0149	0.12	0.0149	0.00178		
<b>Cu</b>									0.0952	0.132	0.0359	-0.786	0.214	-0.643		
<i>P Values</i>									0.794	0.705	0.885	0.0149	0.578	0.0716		
<b>Si</b>										0.97	0.898	-0.286	-0.69	-0.286		
<i>P Values</i>										0.0000002	2E-07	0.46	0.0474	0.46		
<b>Temperature</b>											0.928	-0.299	-0.731	-0.419		
<i>P Values</i>											2E-07	0.423	0.0287	0.26		
<b>Salinity</b>												-0.395	-0.874	-0.515		
<i>P Values</i>												0.29	2E-07	0.16		
<b>TOC</b>													0.262	0.81		
<i>P Values</i>													0.498	0.0096		
<b>IC</b>														0.405		
<i>P Values</i>														0.29		

Table S3: Pearson correlation between the alpha-diversity metrics

	<i>Bacteria</i>				<i>Archaea</i>			
	Chao1	Observed Species	Shannon	Simpson	Chao1	Observed Species	Shannon	Simpson
Chao1	1				1			
Observed Species	0.97	1			0.95	1		
Shannon	0.64	0.57	1		-0.03	-0.09	1	
Simpson	0.40	0.32	0.93	1	-0.21	-0.26	0.97	1

Table S4: Marginal effects and conditional effects of the environmental as per their ability to explain variation in the bacterial genera. LambdaA is the amount of variance explained. P is the probability value and F refers to the F statistics. a) The marginal effect refers to the amount of variation explained by the respective parameter independent of other factors b) whereas the conditional effect refers to the variation explained after other parameters are added in the order of the variable column.

Marginal Effects		Conditional Effects		
Variable	Lambda1	LambdaA	P	F
Temperature	0.35	0.35	0.008	3.27
Salinity	0.32	0.09	0.474	0.75
SO4	0.32	0.12	0.37	1.15
Mn	0.22	0.23	0.106	3.35
Si	0.19	0.08	0.404	1.12

Table S5: Output from the DCA analysis generated using CANOCO for Windows showing variance explained by the first four axis. The length of the gradient is below 3 and so a linear model (RDA analysis) is more appropriate.

	<i>Bacteria</i>				<i>Archaea</i>			
Axes	1	2	3	4	1	2	3	4
Eigenvalues	0.448	0.219	0.016	0.009	0.442	0.154	0.017	0.007
Lengths of gradient	1.749	2.11	0.493	0.416	1.946	1.066	0.577	0.646
Species-environment correlations	1	0.939	0.659	0.878	1	0.999	0.997	0.992
Cumulative percentage variance of species data	34.8	51.9	53.1	53.8	33.2	44.8	46.1	46.6
Cumulative percentage variance of species-environment relation	44.4	62.9	0	0	31	41	0	0