Supplemental Material

Environmental impacts on skin microbiomes of sympatric high Arctic salmonids

Supplemental Tables

Table S1. SIMPER analysis, showing Arctic char skin microbial ASVs labelled to the lowest assigned taxonomic rank along with their respective phyla, in brackets, corresponding to the ASVs responsible for the top 30% of dissimilarity (or alternatively the top 20 ASVs if there are more than 20 taxa in the top 30%) between pairwise-comparisons of seasonal habitats.

Salinity (Overall Average Dissimilarity 99.2%)					
Taxa	Saline (%)	Fresh (%)	Average Dissimilarity	Contribution (%)	Cumulative (%)
Photobacterium (Proteobacteria)	19.2	0.03	9.6	9.7	9.7
Tychonema CCAP 1459-11B (Cyanobacteria)	9.9	0.0001	5	5	14.7
Rivularia PCC-7116 (Cyanobacteria)	6.6	0.004	3.3	3.3	18
Carnobacterium maltaromaticum (Firmicutes)	5.2	0.04	2.6	2.6	20.7
Psychrobacter (Proteobacteria)	3.1	0.9	1.9	1.9	22.6
Aliivibrio (Proteobacteria)	3.3	0.001	1.6	1.6	24.2
Cyanobium PCC-6307 (Cyanobacteria)	2.8	0.04	1.4	1.4	25.6
Staphylococcus (Firmicutes)	0.9	1.6	1.2	1.2	26.8
Escherichia-Shigella (Proteobacteria)	0	2.3	1.1	1.1	27.9
Psychrobacter (Proteobacteria)	1	1.2	1.1	1.1	29
Oxalobacteraceae (Proteobacteria)	0.08	1.7	0.9	0.9	29.9
Autumn Saline – Autumn Fresh (Overall Average Dissimilarity 98.8%)					
Taxa	Autumn Saline (%)	Autumn Fresh (%)	Average Dissimilarity	Contribution (%)	Cumulative (%)

Taxa					
Photobacterium (Proteobacteria)	19.2	0.05	9.6	9.7	9.7
Tychonema CCAP 1459-11B (Cyanobacteria)	9.9	0	5.0	5	14.7
Escherichia-Shigella (Proteobacteria)	0	6.8	3.4	3.4	18.2
Rivularia PCC-7116 (Cyanobacteria)	6.6	0.003	3.3	3.4	21.5
Carnobacterium maltaromaticum (Firmicutes)	5.2	0.06	2.6	2.7	24.2
Psychrobacter (Proteobacteria)	3.1	2.3	2.5	2.5	26.7
Cyanobacteria	0	4.2	2.1	2.1	28.8
Aliivibrio (Proteobacteria)	3.3	0.002	1.6	1.7	30.4

Autumn Saline – Winter Fresh (Overall Average Dissimilarity 99.2%)

Taxa	Autumn Saline (%)	Winter Fresh (%)	Average Dissimilarity	Contribution (%)	Cumulative (%)
Photobacterium (Proteobacteria)	19.2	0.04	9.6	9.7	9.7
Tychonema CCAP 1459-11B (Cyanobacteria)	9.9	0	5.0	5	14.7
Staphylococcus (Firmicutes)	0.05	7.3	3.6	3.7	18.3
Rivularia PCC-7116 (Cyanobacteria)	6.6	0	3.3	3.3	21.7
Planoglabratella opercularis (Cyanobacteria)	0	6.5	3.2	3.3	25.0
Psychrobacter (Proteobacteria)	1	5.03	2.9	2.9	27.8
Carnobacterium maltaromaticum (Firmicutes)	5.2	0.04	2.6	2.6	30.5

Autumn Saline – Spring Fresh (Overall Average Dissimilarity 99.5%)

Taxa	Autumn Saline (%)	Spring Fresh (%)	Average Dissimilarity	Contribution (%)	Cumulative (%)
Photobacterium (Proteobacteria)	19.2	0.008	9.6	9.7	9.7
Tychonema CCAP 1459-11B (Cyanobacteria)	9.9	0.0003	5.0	5	14.6
Rivularia PCC-7116 (Cyanobacteria)	6.6	0.006	3.3	3.3	18.0
Carnobacterium maltaromaticum (Firmicutes)	5.2	0.01	2.6	2.6	20.6
Oxalobacteraceae (Proteobacteria)	0.08	3.6	1.8	1.8	22.4
Aliivibrio (Proteobacteria)	3.3	0.001	1.6	1.6	24.03
Psychrobacter (Proteobacteria)	3.1	0.05	1.6	1.6	25.6
Cyanobium PCC-6307 (Cyanobacteria)	2.8	0.01	1.4	1.4	27.01
Staphylococcus (Firmicutes)	0.9	1.8	1.3	1.3	28.3
Aquabacterium (Proteobacteria)	0.006	2.5	1.3	1.3	29.6
Massilia (Proteobacteria)	0.009	1.9	0.9	0.9	30.5

Autumn Fresh – Winter Fresh (Overall Average Dissimilarity 98.7%)

Taxa	Autumn Fresh (%)	Winter Fresh (%)	Average Dissimilarity	Contribution (%)	Cumulative (%)
Staphylococcus (Firmicutes)	0.009	7.3	3.6	3.7	3.7
Escherichia-Shigella (Proteobacteria)	6.8	0	3.4	3.4	7.1
Planoglabratella opercularis (Cyanobacteria)	0.002	6.5	3.2	3.3	10.4
Psychrobacter (Proteobacteria)	0.6	5.03	2.7	2.8	13.2
Cyanobacteria	4.2	0.006	2.08	2.1	15.3
Staphylococcus (Firmicutes)	0.3	3.3	1.7	1.7	17

Acinetobacter (Proteobacteria)	0	3	1.5	1.5	18.5
Gemmataceae (Planctomycetota)	1.2	1.9	1.4	1.4	19.9
Psychrobacter (Proteobacteria)	2.3	0.5	1.3	1.3	21.2
Carnobacterium inhibens (Firmicutes)	2.5	0.08	1.3	1.3	22.5
Psychrobacter (Proteobacteria)	0.02	1.9	1	1	23.5
Cthoniobacter (Verrucomicrobiota)	1.7	0.07	0.9	0.9	24.4
Acinetobacter (Proteobacteria)	0.3	1.4	0.8	0.8	25.2
Psychrobacter (Proteobacteria)	0.2	1.4	0.7	0.8	26
Cyanobacteria	0	1.5	0.7	0.8	26.7
Luteolibacter (Verrucomicrobiota)	1.3	0.3	0.7	0.7	27.4
Cyanobium PCC-6307 (Cyanobacteria)	1.3	0.02	0.7	0.7	28.07
Luteolibacter (Verrucomicrobiota)	0.8	0.5	0.6	0.6	28.7
Cyanobacteria	1.2	0.006	0.6	0.6	29.3
Cyanobium PCC-6307 (Cyanobacteria)	1.2	0.002	0.6	0.6	29.9

Autumn Fresh – Spring Fresh (Overall Average Dissimilarity 97.9%)

Taxa	Autumn Fresh (%)	Spring Fresh (%)	Average Dissimilarity	Contribution (%)	Cumulative (%)
Escherichia-Shigella (Proteobacteria)	6.8	0	3.4	3.5	3.5
Cyanobacteria	4.2	0	2.07	2.1	5.6
Oxalobacteraceae (Proteobacteria)	0.06	3.6	1.8	1.8	7.4
Aquabacterium (Proteobacteria)	0.1	2.5	1.3	1.3	8.7
Carnobacterium inhibens (Firmicutes)	2.5	0.004	1.3	1.3	10
Psychrobacter (Proteobacteria)	2.3	0.05	1.2	1.2	11.2
Massilia (Proteobacteria)	0.05	1.9	0.9	1	12.2

Taxa					
Staphylococcus (Firmicutes)	0.3	1.8	0.9	0.9	13.1
Chthoniobacter (Verrucomicrobiota)	1.7	0.09	0.8	0.9	14
Massilia (Proteobacteria)	0.03	1.6	0.8	0.8	14.8
Gemmataceae (Planctomycetota)	1.2	1	0.8	0.8	15.7
Rhodoferax (Proteobacteria)	0.8	1.4	0.8	0.8	16.5
Cyanobium PCC-6307 (Cyanobacteria)	1.3	0.05	0.7	0.7	17.2
Streptococcus (Firmicutes)	0.3	1	0.6	0.7	17.9
Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium (Proteobacteria)	0.05	1.2	0.6	0.6	18.5
Luteolibacter (Verrucomicrobiota)	1.3	0.1	0.6	0.6	19.1
Cyanobacteria	1.2	0.07	0.6	0.6	19.8
Novosphingobium (Proteobacteria)	0.06	1.1	0.6	0.6	20.4
Cyanobium PCC-6307 (Cyanobacteria)	1.2	0	0.6	0.6	21
Micrococcaceae (Actinobacteriota)	0.7	0.4	0.6	0.6	21.5

Winter Fresh – Spring Fresh (Overall Average Dissimilarity 98.4%)

Taxa	Winter Fresh (%)	Spring Fresh (%)	Average Dissimilarity	Contribution (%)	Cumulative (%)
Staphylococcus (Firmicutes)	7.3	0.2	3.7	3.8	3.8
Planoglabratella opercularis (Cyanobacteria)	6.5	0.8	3.3	3.4	7.1
Psychrobacter (Proteobacteria)	5.03	0.03	2.5	2.6	9.7
Staphylococcus (Firmicutes)	3.3	1.8	2.1	2.2	11.8
Oxalobacteraceae (Proteobacteria)	0.005	3.6	1.8	1.8	13.6

Acinetobacter (Proteobacteria)	3	0	1.5	1.5	15.2
Gemmataceae (Planctomycetota)	1.9	1	1.3	1.3	16.5
Aquabacterium (Proteobacteria)	0	2.5	1.3	1.3	17.7
Psychrobacter (Proteobacteria)	1.9	0.02	1.0	1.0	18.7
Massilia (Proteobacteria)	0	1.9	0.9	1.0	19.7
Massilia (Proteobacteria)	0.04	1.6	0.8	0.8	20.5
Cyanobacteria	1.5	0	0.7	0.8	21.3
Rhodoferax (Proteobacteria)	0	1.4	0.7	0.7	22.0
Psychrobacter (Proteobacteria)	1.4	0.07	0.7	0.7	22.7
Acinetobacter (Proteobacteria)	1.4	0	0.7	0.7	23.4
Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium (Proteobacteria)	0	1.2	0.6	0.6	24.0
Novosphingobium (Proteobacteria)	0.003	1.1	0.6	0.6	24.6
Streptococcus (Firmicutes)	0.04	1.04	0.5	0.5	25.2
Cyanobacteria	0	1.05	0.5	0.5	25.7
Psychrobacter (Proteobacteria)	0	1.03	0.5	0.5	26.2

Table S2. Core water sample microbiomes defined as ASVs comprising at least 0.1% abundance and present in at least 50% of samples from the specified group.

Phyla	Class	Order	Family	Genus	Species
Core Saline Water Microbiome					
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Psychrobacter*	
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Photobacterium*	

Cyanobacteria	Cyanobacteriia	Cyanobacteriales	Nostocaceae	*Rivularia* PCC-7116
Cyanobacteria	Cyanobacteriia	Phormidesmiales	Phormidesmiaceae	*Phormidesmis* ANT.LACV5.1
Cyanobacteria	Cyanobacteriia	Cyanobacteriales	Phormidiaceae	*Tychonema* CCAP 1459-11B
Cyanobacteria	Cyanobacteriia	Synechococcales	Cyanobiaceae	*Cyanobium* PCC-6307

Core Freshwater Microbiome

N/A

Core Autumn Saline Microbiome

Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	*Psychrobacter*
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	*Photobacterium*
Cyanobacteria	Cyanobacteriia	Cyanobacteriales	Nostocaceae	*Rivularia* PCC-7116
Cyanobacteria	Cyanobacteriia	Phormidesmiales	Phormidesmiaceae	*Phormidesmis* ANT.LACV5.1
Cyanobacteria	Cyanobacteriia	Cyanobacteriales	Phormidiaceae	*Tychonema* CCAP 1459-11B
Cyanobacteria	Cyanobacteriia	Synechococcales	Cyanobiaceae	*Cyanobium* PCC-6307

Core Autumn Fresh Microbiome

Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	*Polynucleobacter*
Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	*Chthoniobacter*
Planctomycetota	Planctomycetes	Gemmatales	Gemmataceae	
Cyanobacteria	Cyanobacteriia	Synechococcales	Cyanobiaceae	*Cyanobium* PCC-6307

Actinobacteriota	Actinobacteria	Frankiales	Sporichthyaceae	hgcI clade	
Actinobacteriota	Acidimicrobiia				
Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	*Luteolibacter*	
Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	*Rhodoferax*	
Core Winter Fresh Microbiome					
Cyanobacteria	Cyanobacteriia	Chloroplast	Chloroplast	Chloroplast	*Planoglabratella opercularis*
Core Spring Fresh Microbiome					
Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	*Rhodoferax*	

Supplemental Figures
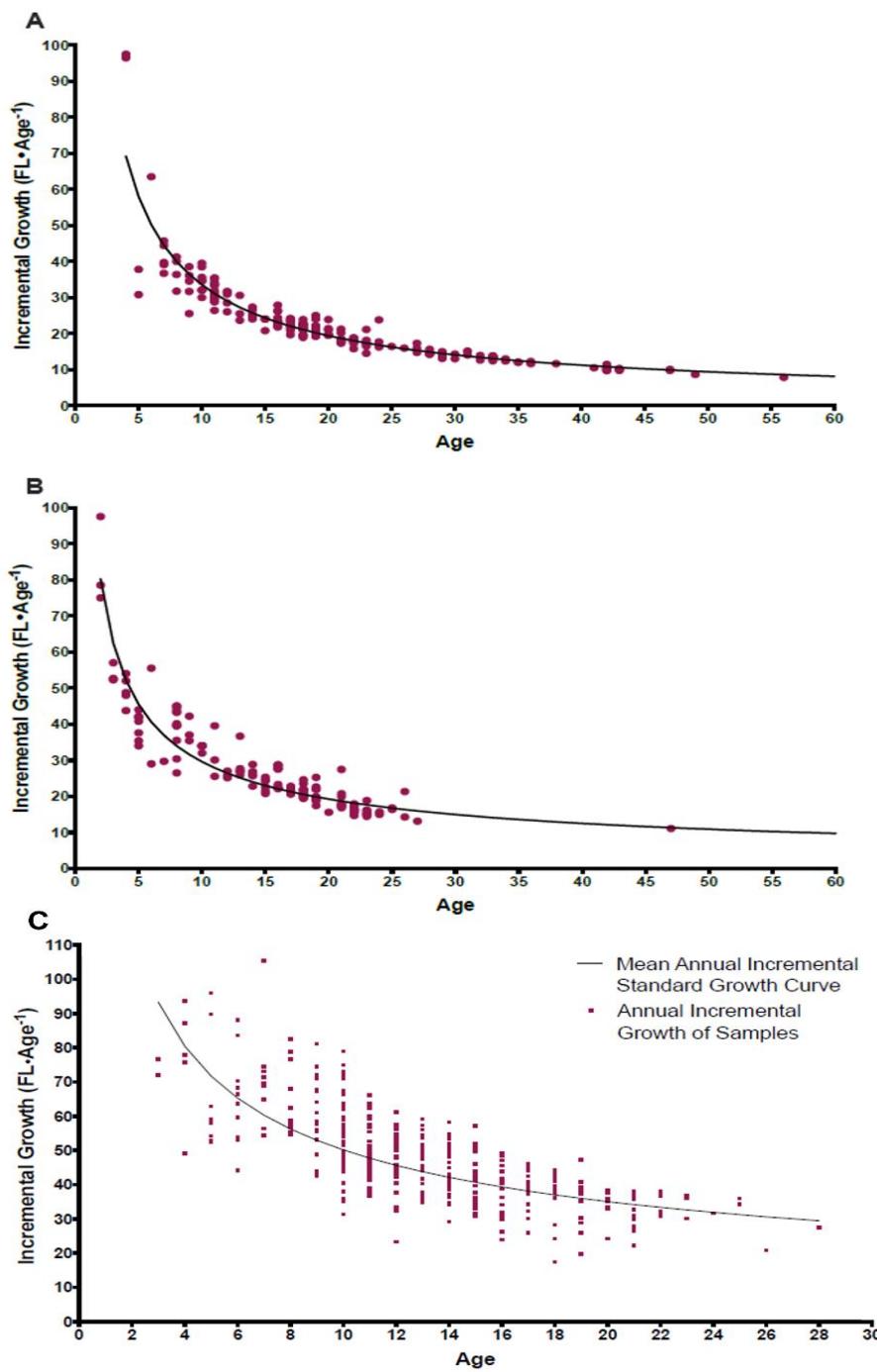
Figure S1. Annual incremental growth at age data against a growth standard curve for **(A)** lake whitefish using samples aged 4-43 (excluding outliers at ages 47, 49, and 56), **(B)** cisco using samples aged 2-27 (excluding outlier at ages 47), and **(C)** Arctic char samples aged 3-28. Note that the axes are adjusted for each salmonid type, individual data points are shown as dots, and that the data for lake whitefish and cisco (Hamilton et al., 2023) are presented here for convenience and comparison with the Arctic char growth standard curve.
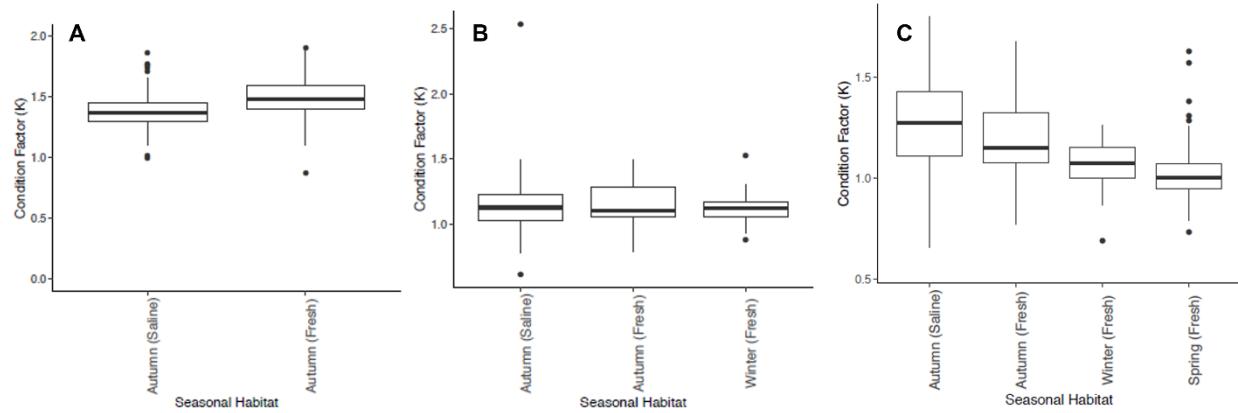
Figure S2. Condition factor (K) across seasonal habitats for (A) lake whitefish (B) cisco and (C) Arctic char. Note K data for lake whitefish and cisco (Hamilton et al., 2023) are presented here for comparison with the Arctic char K values.
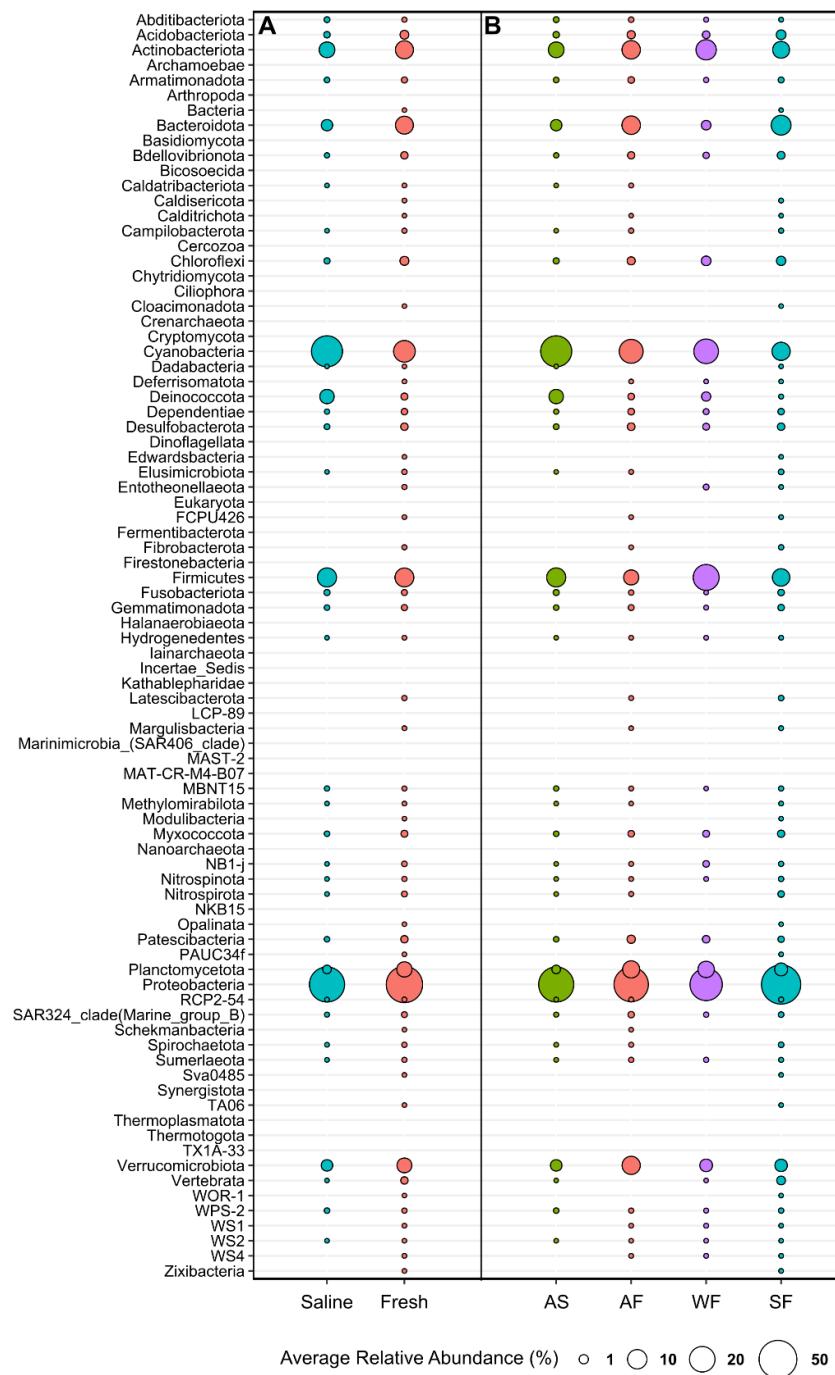
Figure S3. Bubble plots showing the average relative abundance of phyla in the skin microbiomes of Arctic char. **(A)** Phyla of saline water and freshwater caught fish. **(B)** Phyla of seasonal habitats in autumn saline (AS), autumn fresh (AF), winter fresh (WF), and spring fresh (SF) water.
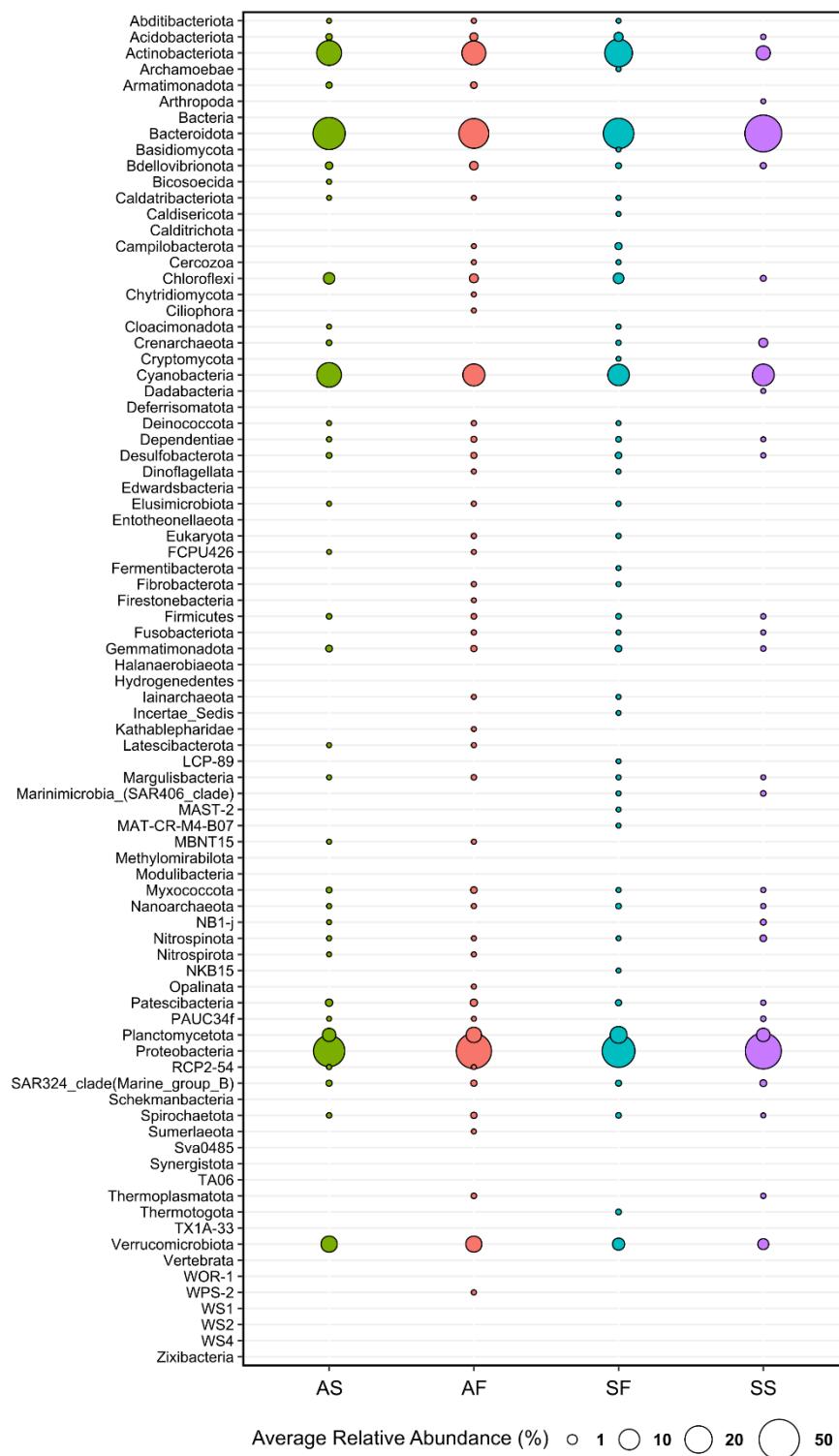
Figure S4. Bubble plots showing the average relative abundance of phyla in the water samples taken from autumn saline water (AS), autumn freshwater (AF), spring freshwater (SF), and spring saline water (SS).
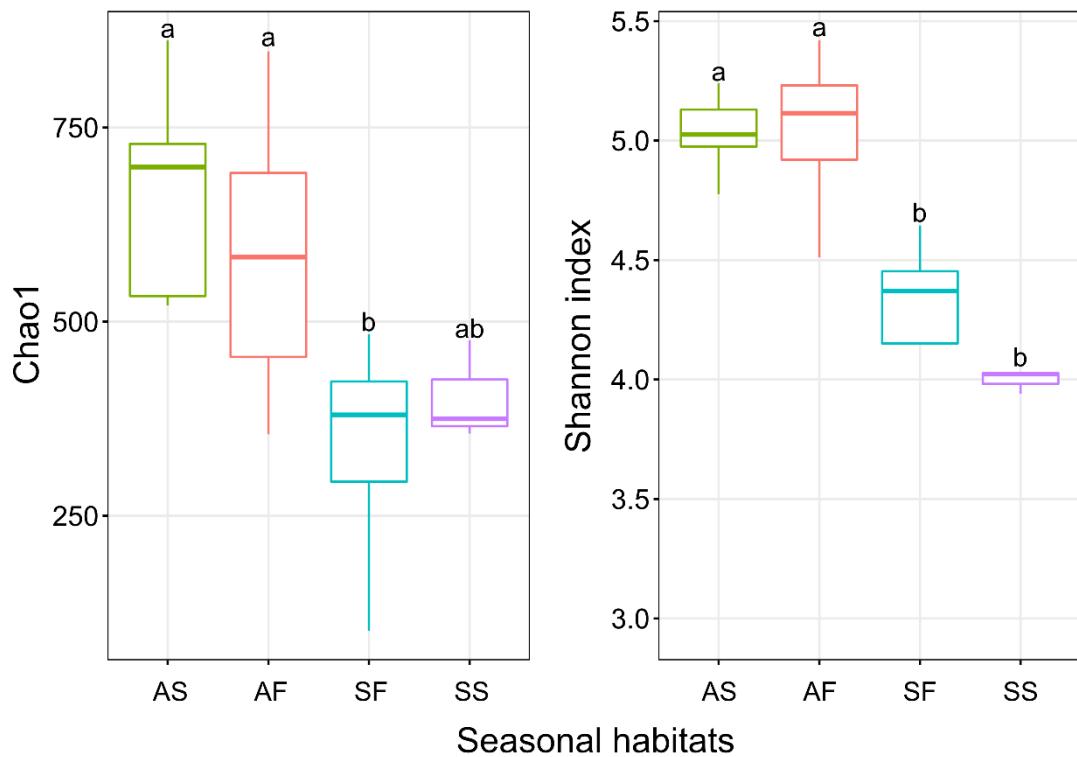
Figure S5. Alpha diversity metrics, Chao1 and Shannon diversity, measuring microbial community abundance and diversity, respectively, of water samples seasonal habitats autumn saline water (AS), autumn freshwater (AF), spring freshwater (SF), and spring saline water (SS). Lower case letters display significantly different ($p < 0.001$) groupings as determined by one-way ANOVA.
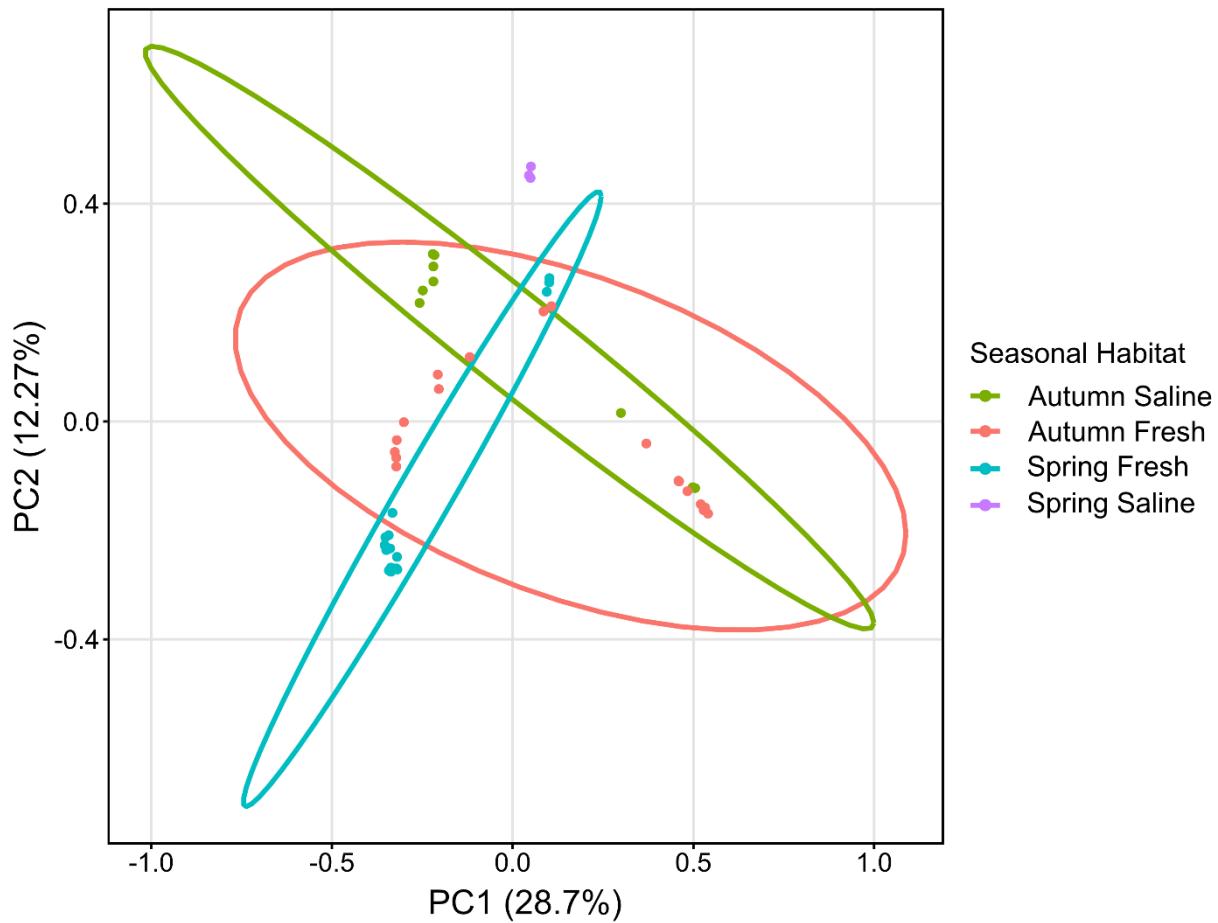
Figure S6. Principal coordinate analysis of water samples collected from different seasonal habitats (listed to the right of the graph) and showing water beta diversity using Bray-Curtis dissimilarity.