Table S1: Macroinvertebrate taxonomic groupings for abundance estimates. Amphipod taxa were defined as in Takhteev & Didorenko, 2015; mollusk taxa were defined as in Sitnikova, 2012.

Amphipoda	**Mollusca**	**Other**
Brandtia latissima intermida (Dorogostaiskii 1930)	Acroloxidae	Asellidae
Brandtia latissima lata (Dybowsky 1874)	Baicaliidae	Caddisflies
Brandtia latissima latior (Dybowsky 1874)	Benedictidate	Hirudinea
Brandtia latissima latissima (Gerstfeldt 1858)	Maackia	Planaria
Brandtia parasitica parasitica (Dybowsky 1874)	Planorbidae	
Cryptoropus inflatus (Dybowsky 1874)	Valvatidae	
Cryptoropus pachytus (Dybowsky 1874)		
Cryptoropus rugosus (Dybowsky 1874)		
Eulimnogammarus capreolus (Dybowsky 1874)		
Eulimnogammarus cruentes (Dorogostaiskii 1930)		
Eulimnogammarus cyaneus (Dybowsky 1874)		
Eulimnogammarus grandimanus (Bazikalova 1945)		
Eulimnogammarus maacki (Gerstfeldt 1858)		
Eulimnogammarus marituji (Bazikalova 1945)		
Eulimnogammarus verucossus (Gerstfeldt 1858)		
Eulimnogammarus viridis viridis (Dybowsky 1874)		
Eulimnogammarus vittatus (Dybowsky 1874)		
Pallasea brandtia brandita (Dybowsky 1874)		
Pallasea brandtii tenera (Sovinskii 1930)		

Pallasea cancelloides (Gerstfeldt 1858)		
Pallasea cancellus (Pallas 1776)		
Pallasea viridis (Garjajev 1901)		
Poekilogammarus crassimus (Sovinskii 1915)		
Poekilogammarus ephippiatus (Dybowsky 1874)		
Poekilogammarus megonychus perpolitus (Takhteev 2002)		
Poekilogammarus pictus (Dybowsky 1874)		

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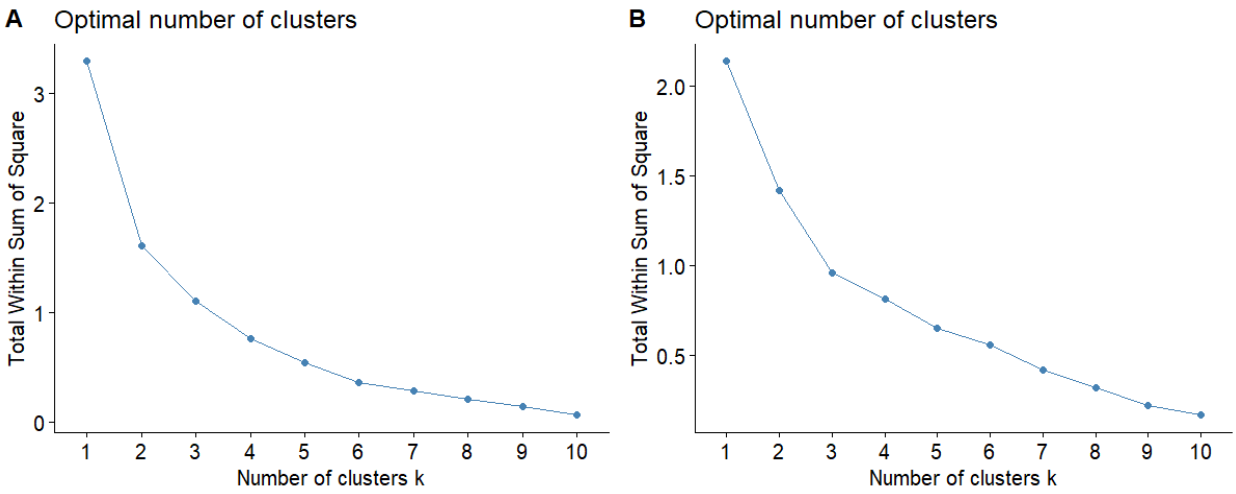

Figure S1: With-group-sum-of-squares (wss) for increasing number of k-mediod clusters for periphyton (A) and invertebrate (B) community data. In the case of periphyton data, wss decreases most markedly with three clusters, whereas invertebrate community abundance is best described by potential two or three clusters.

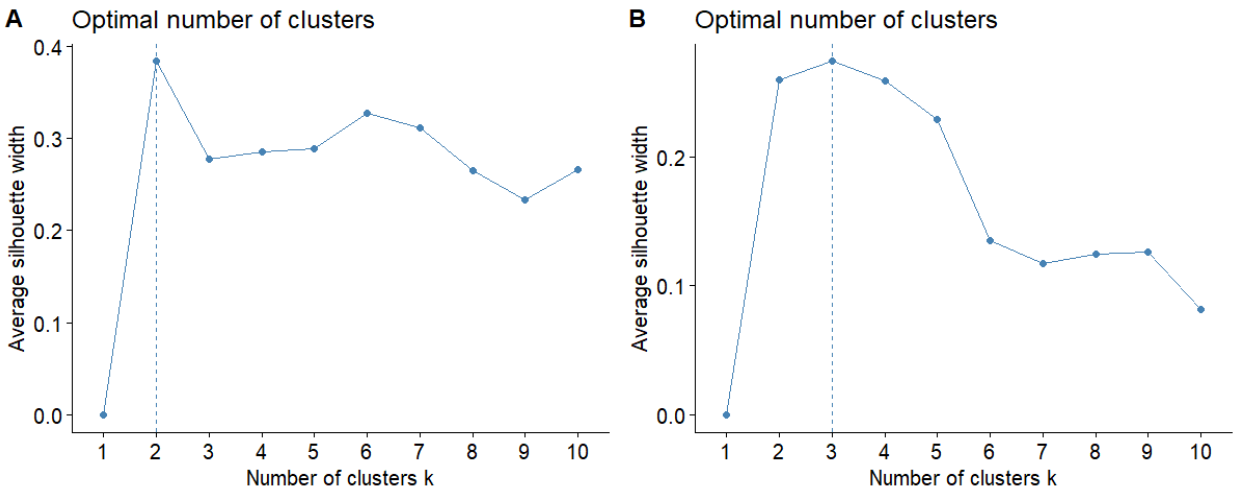

Figure S2: Average silhouette width for increasing number of k-mediod clusters for periphyton (A) and invertebrate (B) community data. In the case of periphyton data, average silhouette width decreases most markedly with three clusters, whereas invertebrate community abundance is best described by two or three clusters as the average silhouette width for both two and three clusters was highest before beginning to decrease.

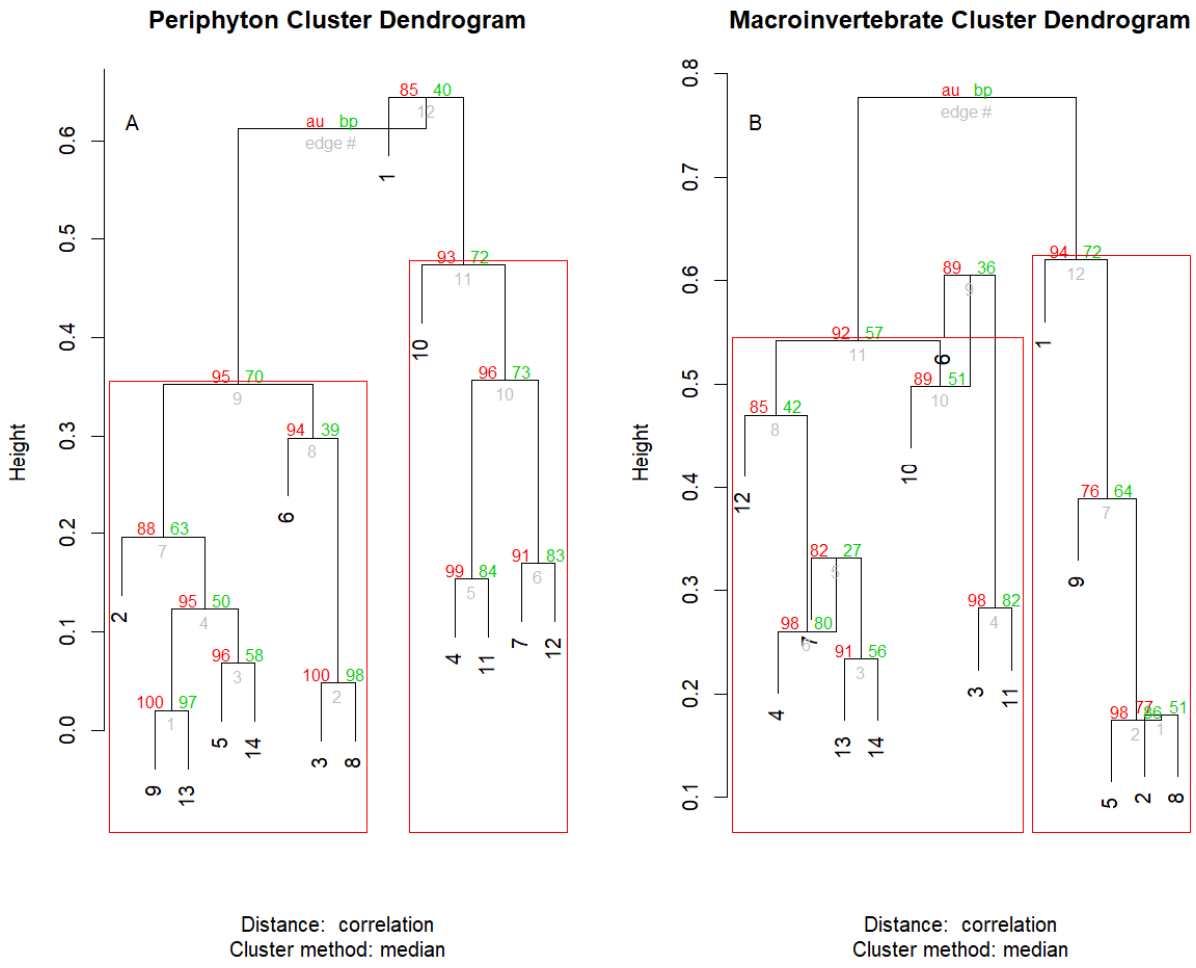

Figure S3: Weighted Pair-Group Centroid Clustering (WPGMC) for periphyton (A) and macroinvertebrate (B) community compositions. Approximately unbiased (au) p-values are computed by multiscale bootstrap resampling, and displayed in red on the left side of each node. Bootstrapped probabilities (bp) are displayed in green on the right side of each node. Unlike k-mediods, WPGMC uses a hierarchical approach to assign clusters, which are bootstrapped in order to generated a probability of group membership. This technique suggested that both periphyton and macroinvertebrates could be grouped in two clusters. Grouping macroinvertebrates into three clusters was possible; however, three clusters resulted in 8 of the

14 sampling locations being assigned to a group. In contrast, two groups enabled 13 of the 14 sampling locations to be assigned to a cluster.

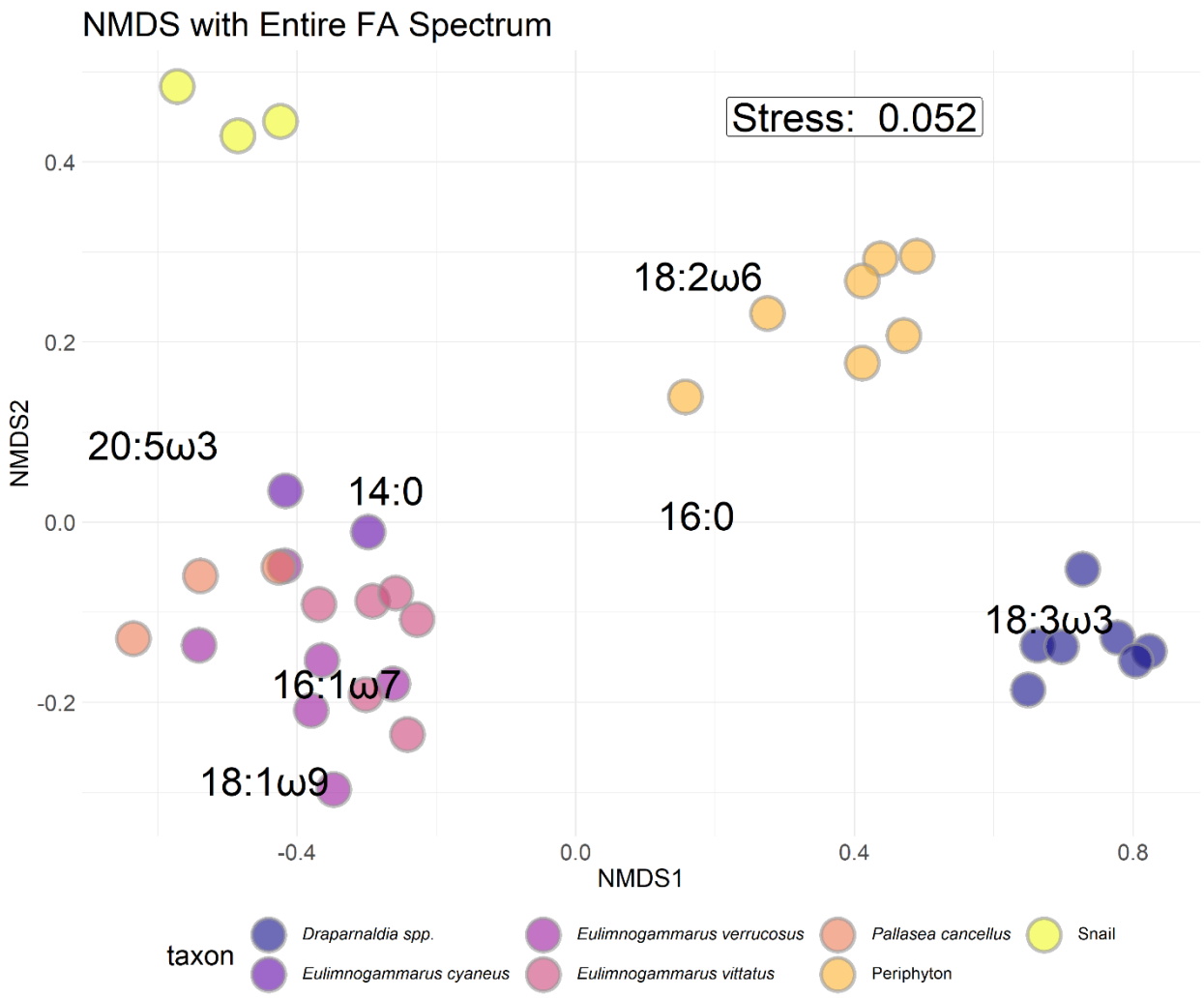

Figure S2: NMDS with Bray-Curtis dissimilarity of proportional fatty acid compositions for each macroinvertebrate and primary producer collected. *Eulimnogammarus* and *Pallasea* are endemic amphipod genera. *Draparnaldia* spp. are endemic filamentous algae that are large and form very dense mats easily collected where it occurs. *Draparnaldia* spp. occurred in large, visible colonies, allowing us to sample and analyze just the *Draparnaldia* spp. fatty acids. Because *Draparnaldia* spp.fatty acids were dominated by 18:3ω3 more so than periphyton, they formed their own cluster. Snails were not identified to species prior to fatty acid analysis. Interspecific variation in fatty acid composition tended to be larger than intraspecific variation, implying that fatty acid signatures were largely species-specific and not environmentally driven.

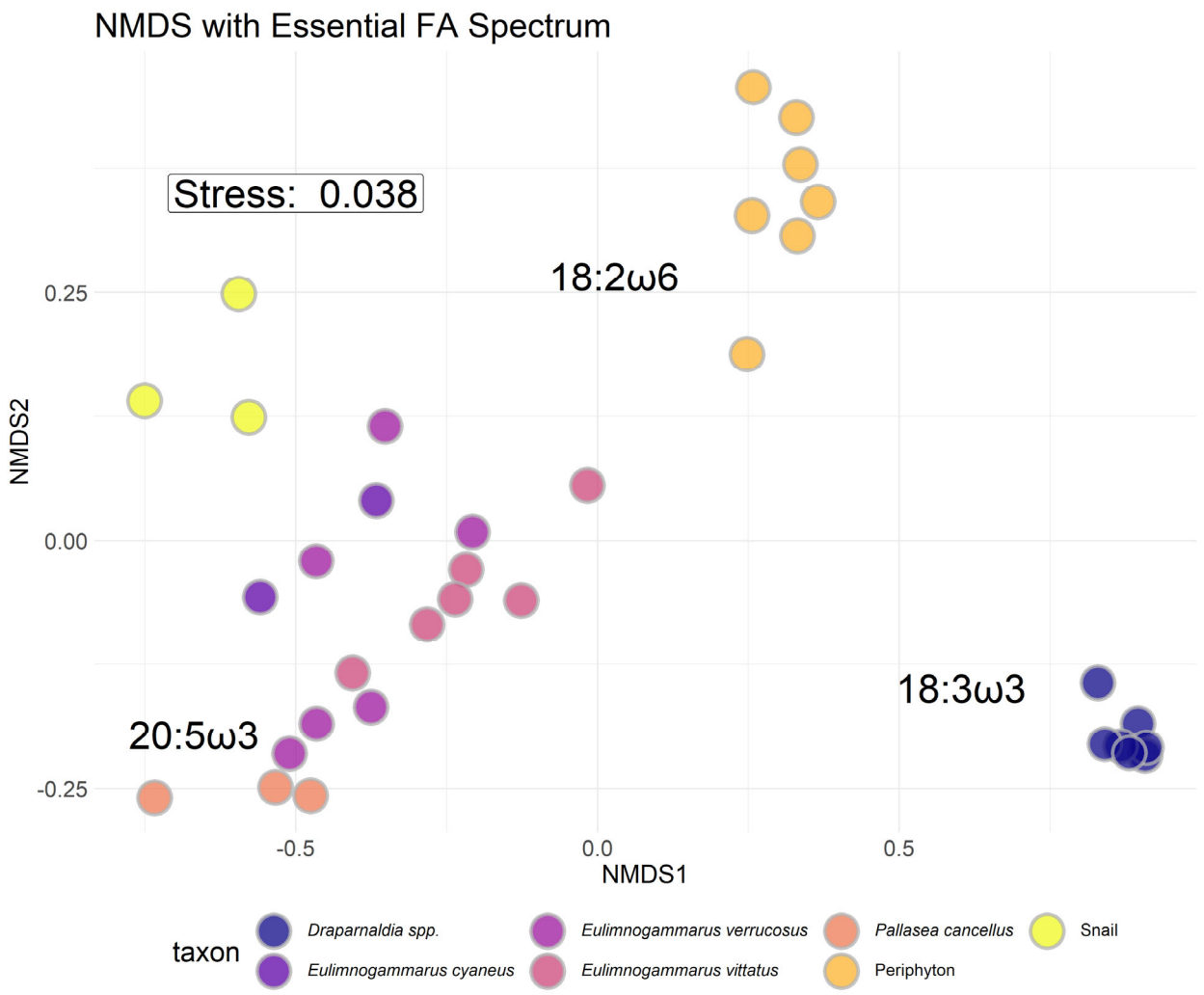

Figure S3: NMDS with Bray-Curtis dissimilarity of proportional biologically essential fatty acid compositions for each macroinvertebrate and primary producer collected. *Eulimnogammarus* and *Pallasea* are endemic amphipod genera. *Draparnaldia* spp. are endemic filamentous algae that are large and form very dense mats easily collected where it occurs. *Draparnaldia* spp. occurred in large, visible colonies, allowing us to sample and analyze just the *Draparnaldia* spp. fatty acids. Because *Draparnaldia* spp. fatty acids were dominated by 18:3ω3 more so than periphyton, they formed their own cluster. Snails were not identified to species prior to fatty acid analysis. Interspecific variation in fatty acid composition tended to be larger than intraspecific

variation, implying that fatty acid signatures were largely species-specific and not environmentally driven.

Table S2: Fatty acid groupings used in this analysis	
Fatty Acid Group	Fatty acids considered
Branched	a-15:0, i-15:0, a-17:0, i-17:0
SAFA	12:0, 14:0, 15:0, 16:0, 17:0, 18:0, 20:0, 22:0, 24:0
MUFA	14:1ω5, 15:1ω7, 17:1n7, 16:1ω5, 16:1ω6, 16:1ω7, 16:1ω8, 16:1ω9, 18:1ω7, 18:1ω9, 20:1ω7, 20:1ω9, 22:1ω7, 22:1ω9
SCPUFA	16:2ω4, 16:2ω6, 16:2ω7, 16:3ω3, 16:3ω4, 16:3ω6, 16:4ω1, 16:4ω3, 18:2ω6, 18:2ω6t, 18:3ω3, 18:3ω6, 18:4ω3, 18:4ω4, 18:5ω3
LCPUFA	20:2ω5(11), 20:2ω5(13), 20:2ω6, 20:3ω3, 20:3ω6, 20:4ω3, 20:4ω6, 20:5ω3, 22:2ω6, 22:3ω3, 22:4ω3, 22:4ω6, 22:5ω3, 22:5ω6, 22:6ω3

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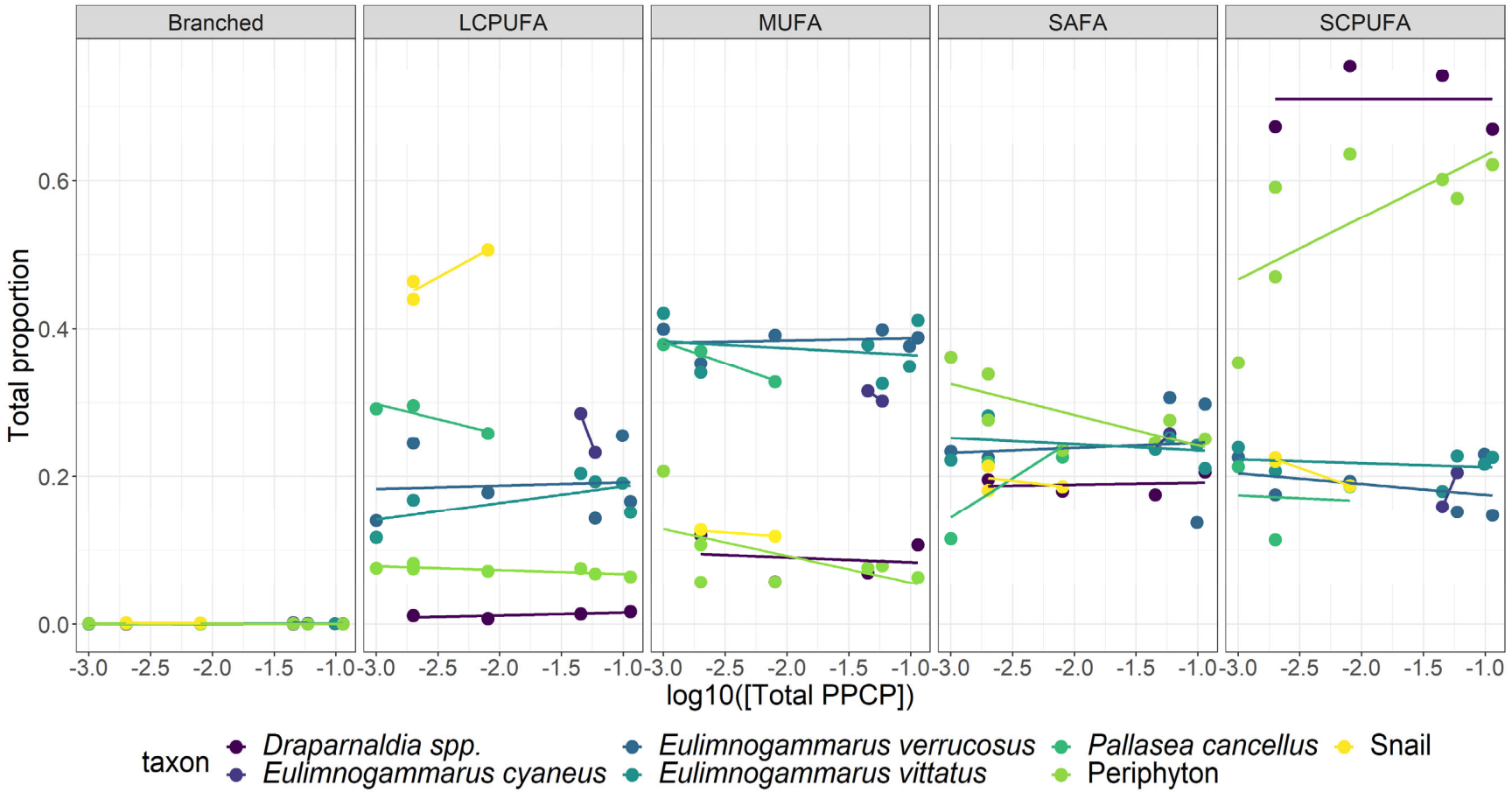

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1250 Figure S4: Proportions of major fatty aid groups (as defined in Table S2) across the sewage gradient. Primary producers

1251 (*Draparnaldia* spp. and periphyton) were largely characterized by SCPUFAs, amphipods were largely associated with high MUFA

1252 abundance, and snails were generally characterized with high LCPUFA abundance. Across the sewage gradient, periphyton SCPUFA

1253 tended to increase, which lead to more targeted analyses on which specific fatty acids were increasing. In contrast to periphyton, all
1254 other taxa remained consistent with respect to fatty acid proportions across the sewage gradient.
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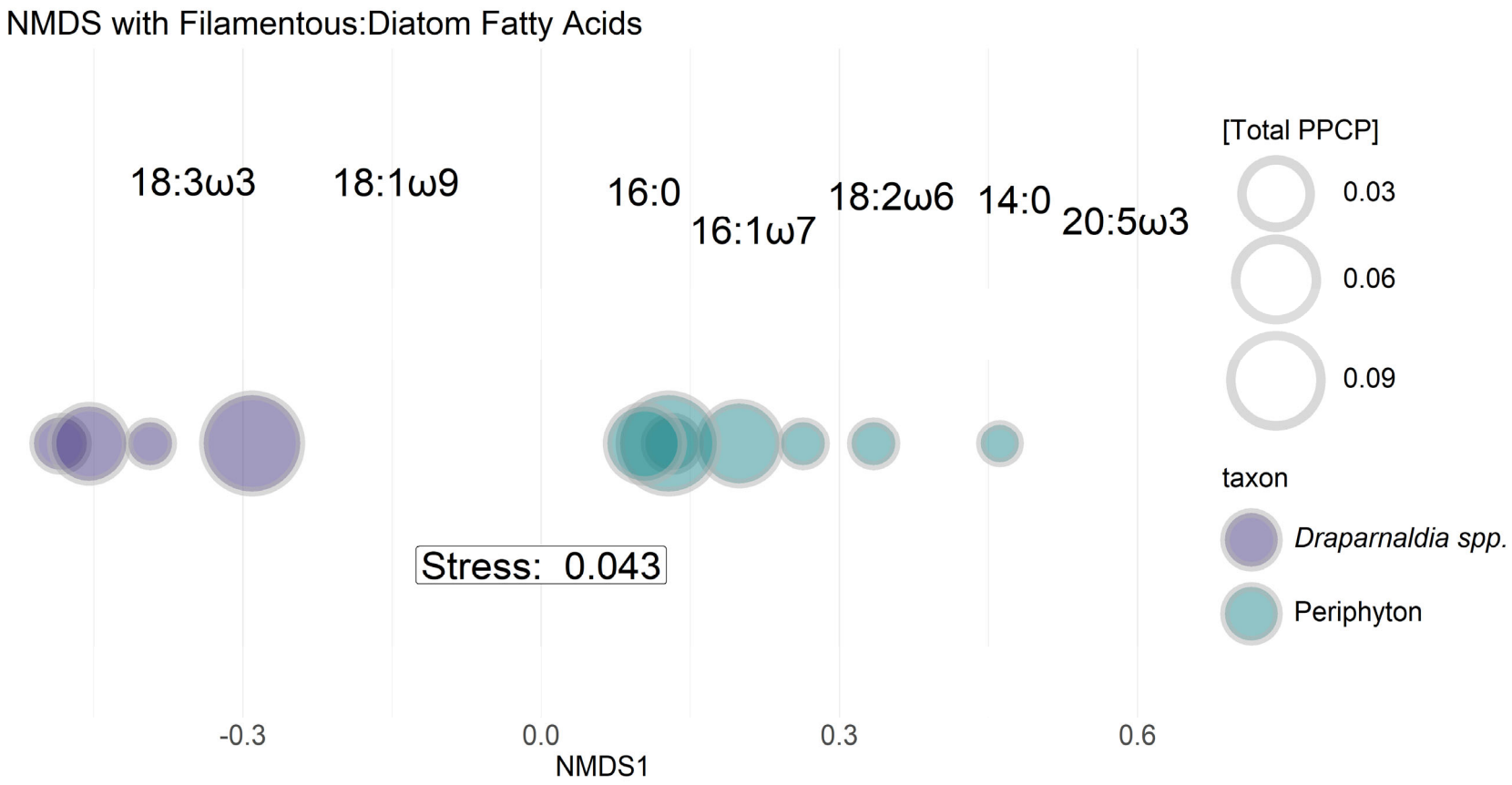

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1258 Figure S5: One-dimensional NMDS with Bray-Curtis similarity of seven targeted fatty acids of interest for primary producers. Fatty

1259 acid scores are placed above shapes. Shapes are sized by total PPCP concentration. Periphyton (blue-green) tend to increase in size

1260 from right-to-left, suggesting that periphyton tend to include more 18:3ω3 and 18:1ω9 (indicators of green algal taxa) with an

1261 increasing sewage signal. In contrast, *Draparnaldia* spp. (purple) fatty acids tend to remain consistent across the sewage gradient.

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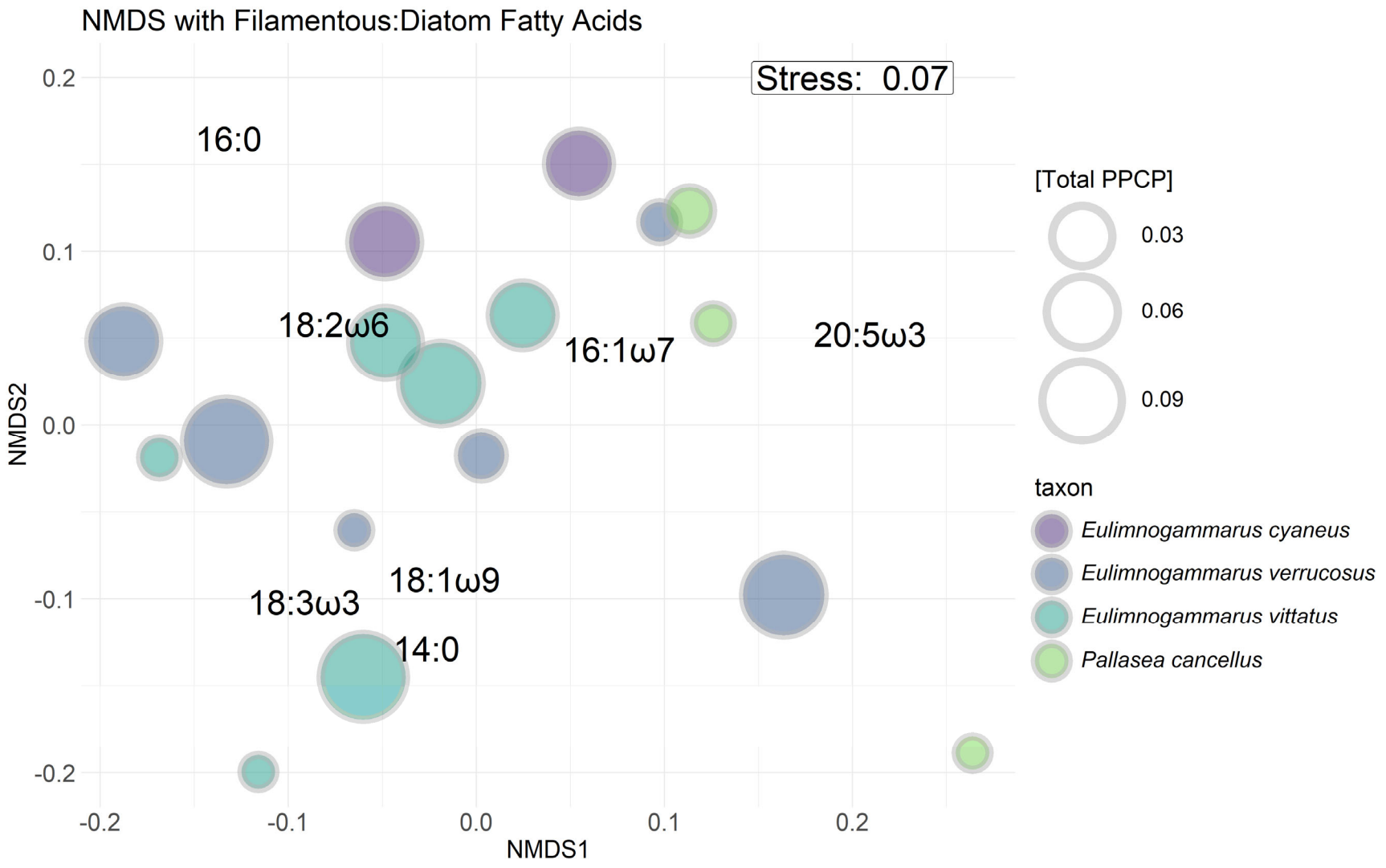
NMDS with Filamentous:Diatom Fatty Acids
Stress: 0.07
16:0
18:2ω6
16:1ω7
20:5ω3
18:1ω9
18:3ω3
14:0
NMDS1
NMDS2
0.2
0.1
0.0
-0.1
-0.2
[Total PPCP]
0.03
0.06
0.09
taxon
Eulimnogammarus cyaneus
Eulimnogammarus verrucosus
Eulimnogammarus vittatus
Pallasea cancellus

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Figure S6: NMDS with Bray-Curtis similarity of seven targeted fatty acids of interest for primary producers. Points are sized by total PPCP concentration. Visually, there appears to be no distinct separation among or within taxa unlike was observed with periphyton (Figure S5).

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