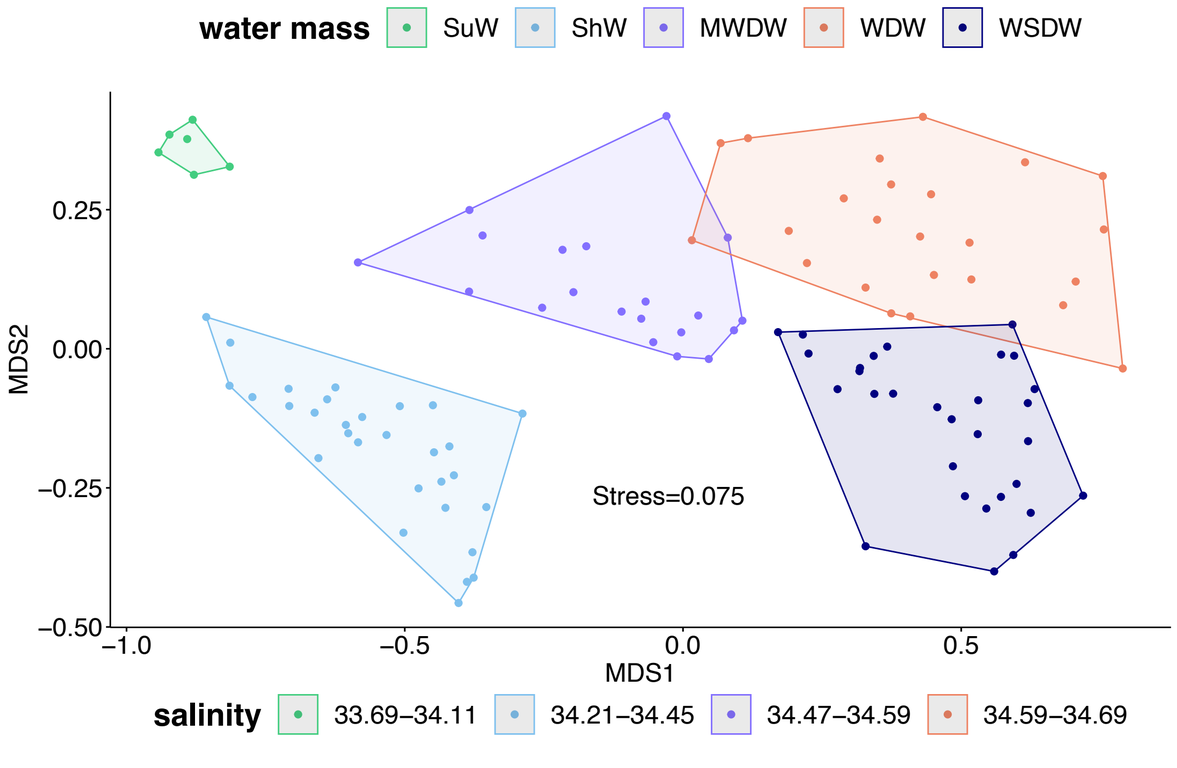
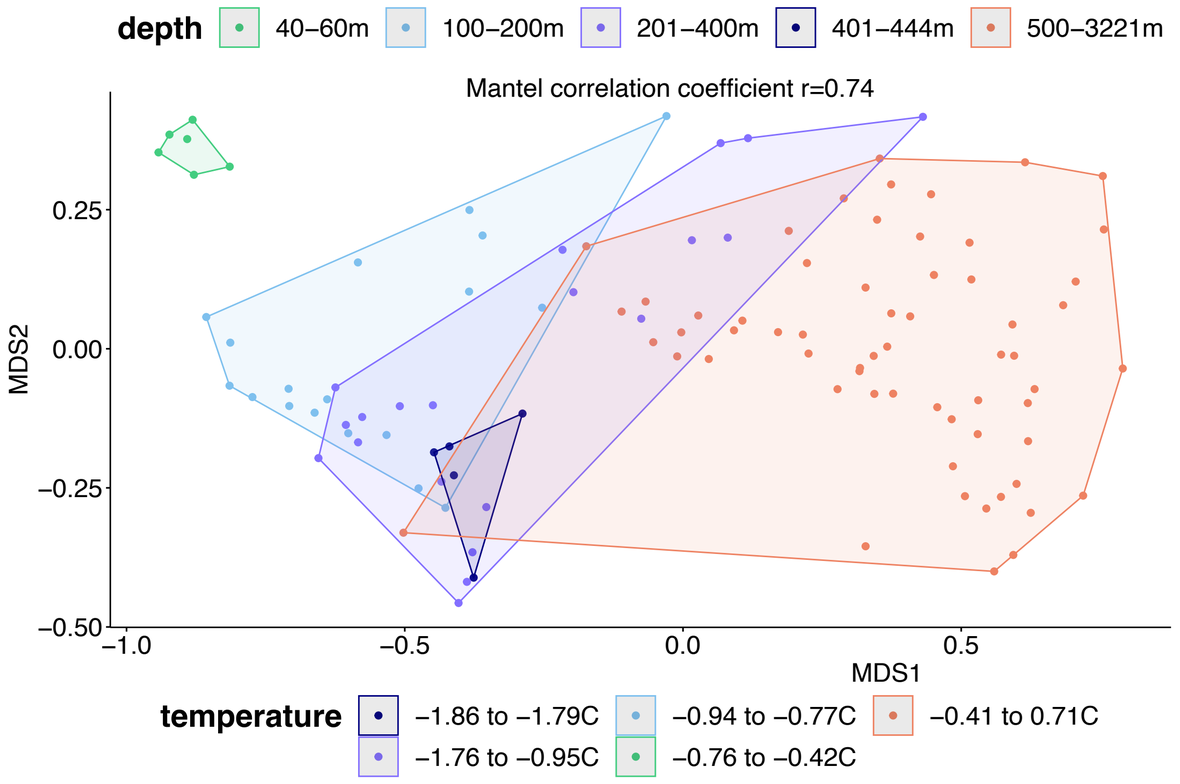
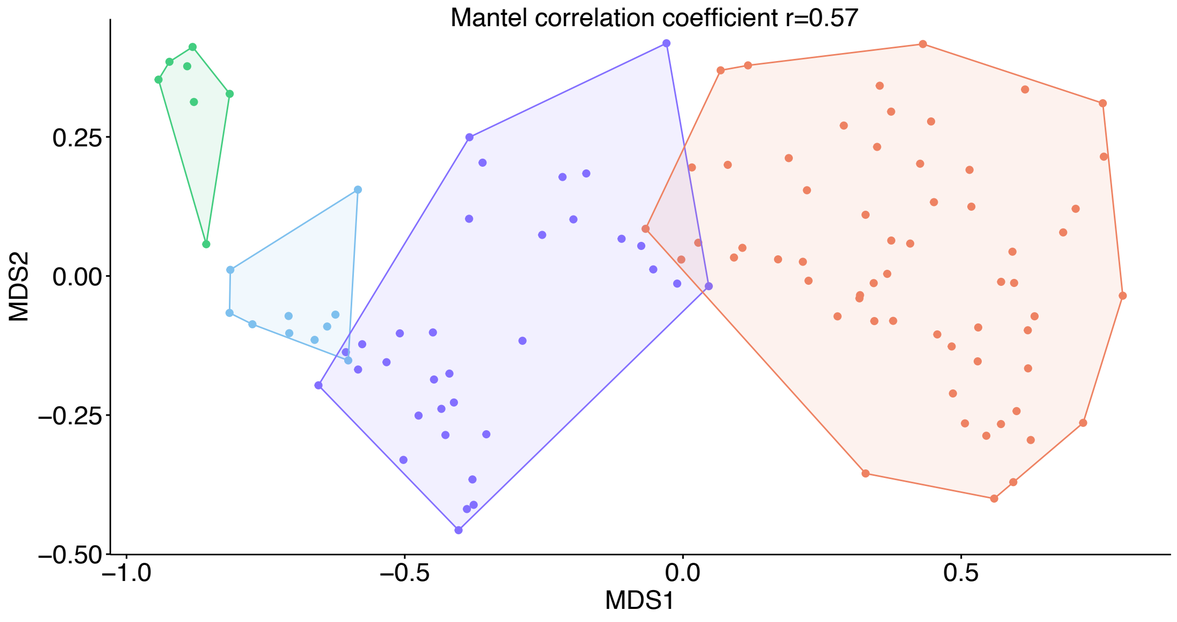
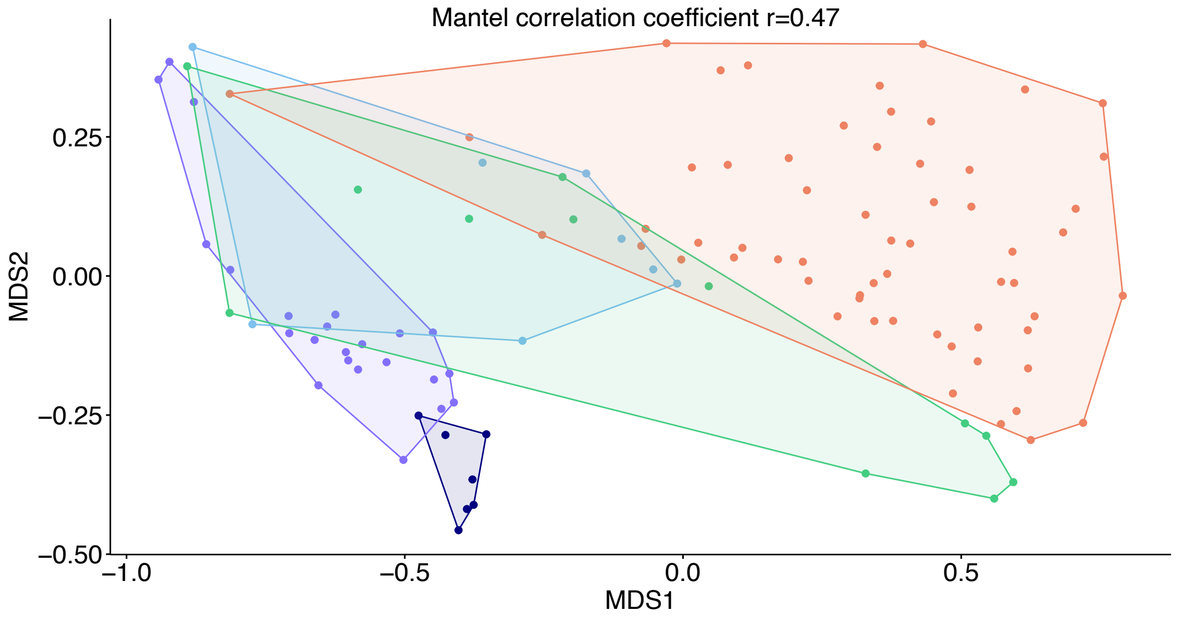
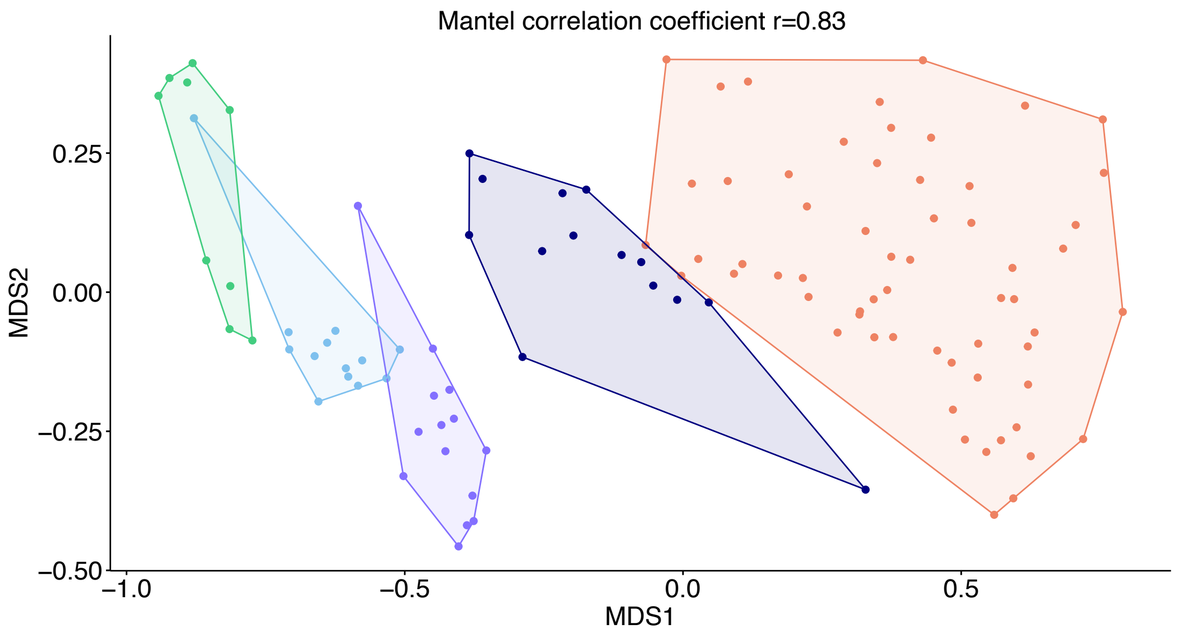
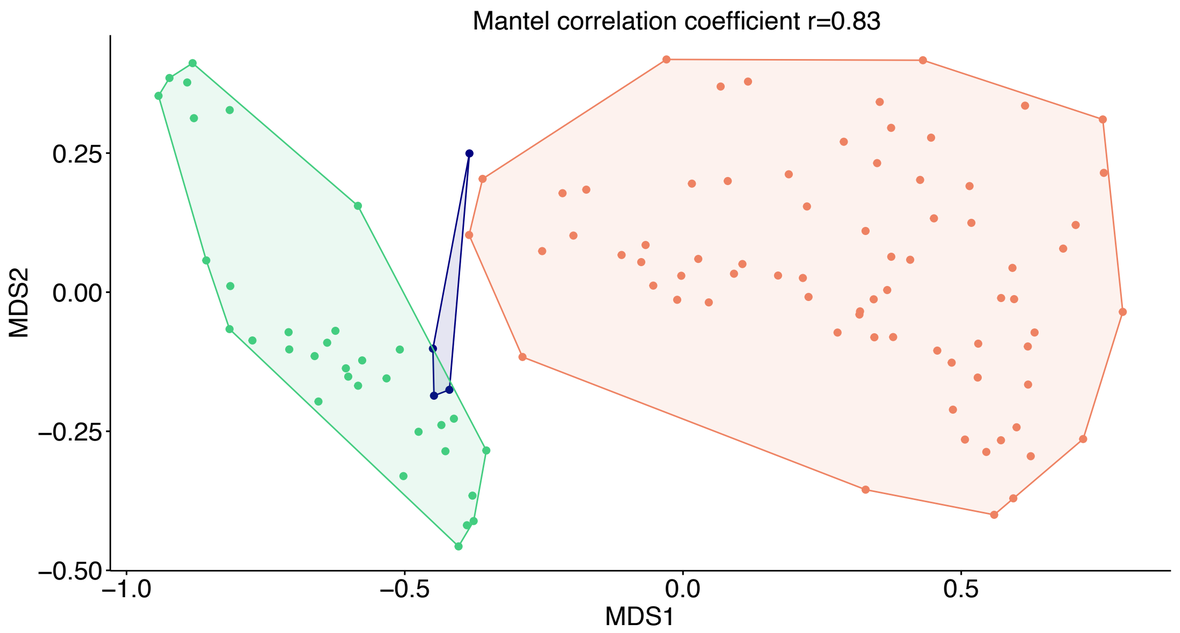

water mass
SuW
ShW
MWDW
WDW
WSDW
Stress=0.075
MDS1
MDS2
salinity
33.69–34.11
34.21–34.45
34.47–34.59
34.59–34.69

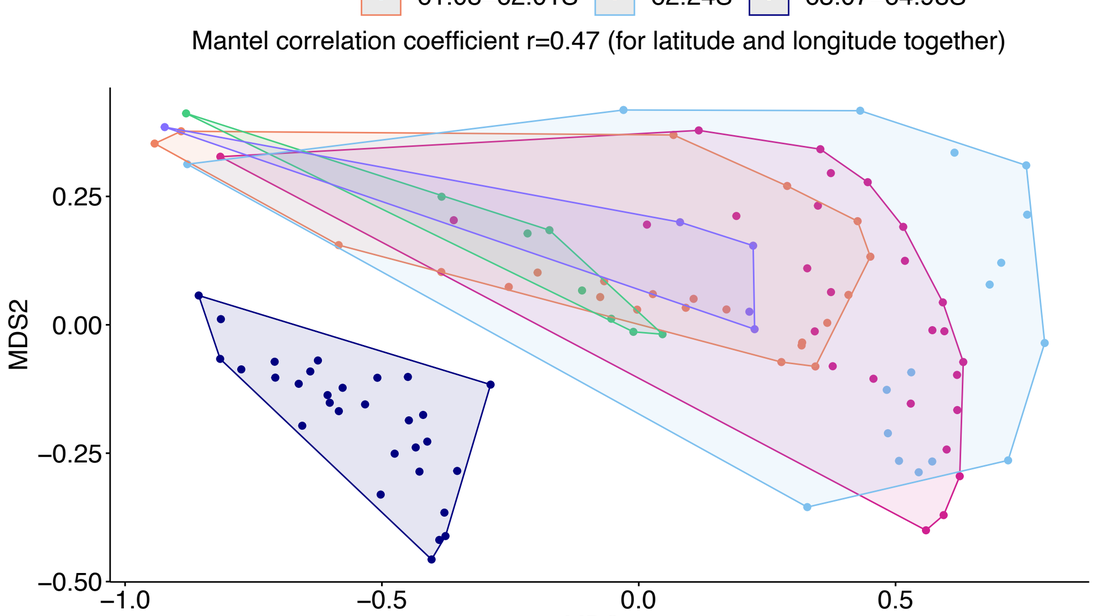

depth
40–60m
100–200m
201–400m
401–444m
500–3221m
Mantel correlation coefficient r=0.74
MDS1
MDS2
temperature
−1.86 to −1.79C
−1.76 to −0.95C
−0.94 to −0.77C
−0.76 to −0.42C
−0.41 to 0.71C

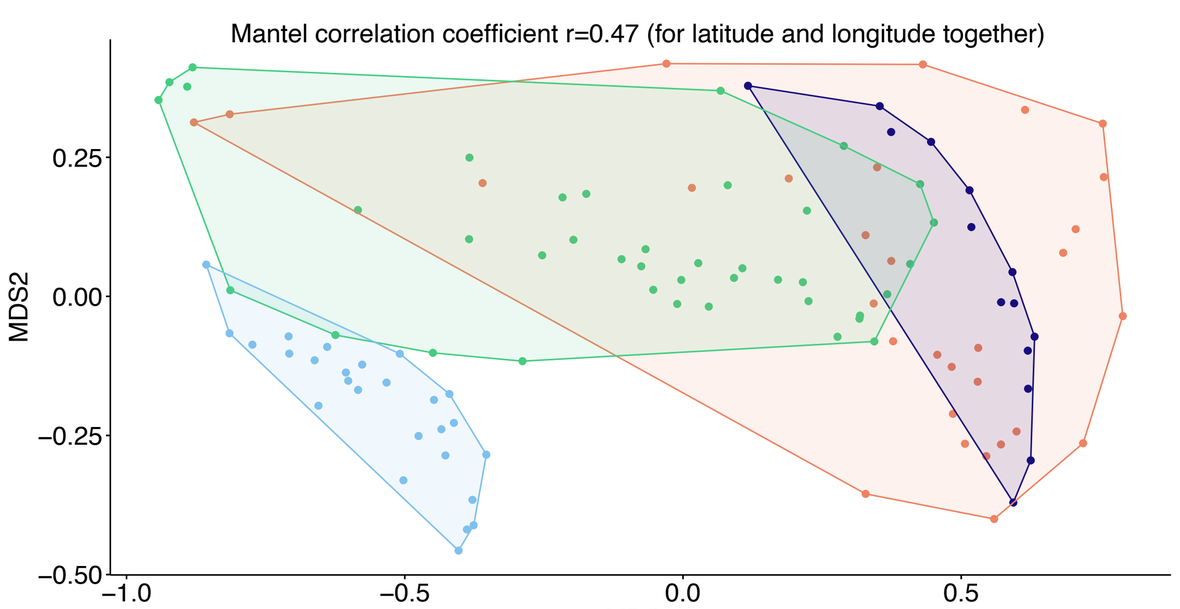

Mantel correlation coefficient r=0.57
MDS1
MDS2
oxygen
208–250
254–280
285–304
304–322
323–336

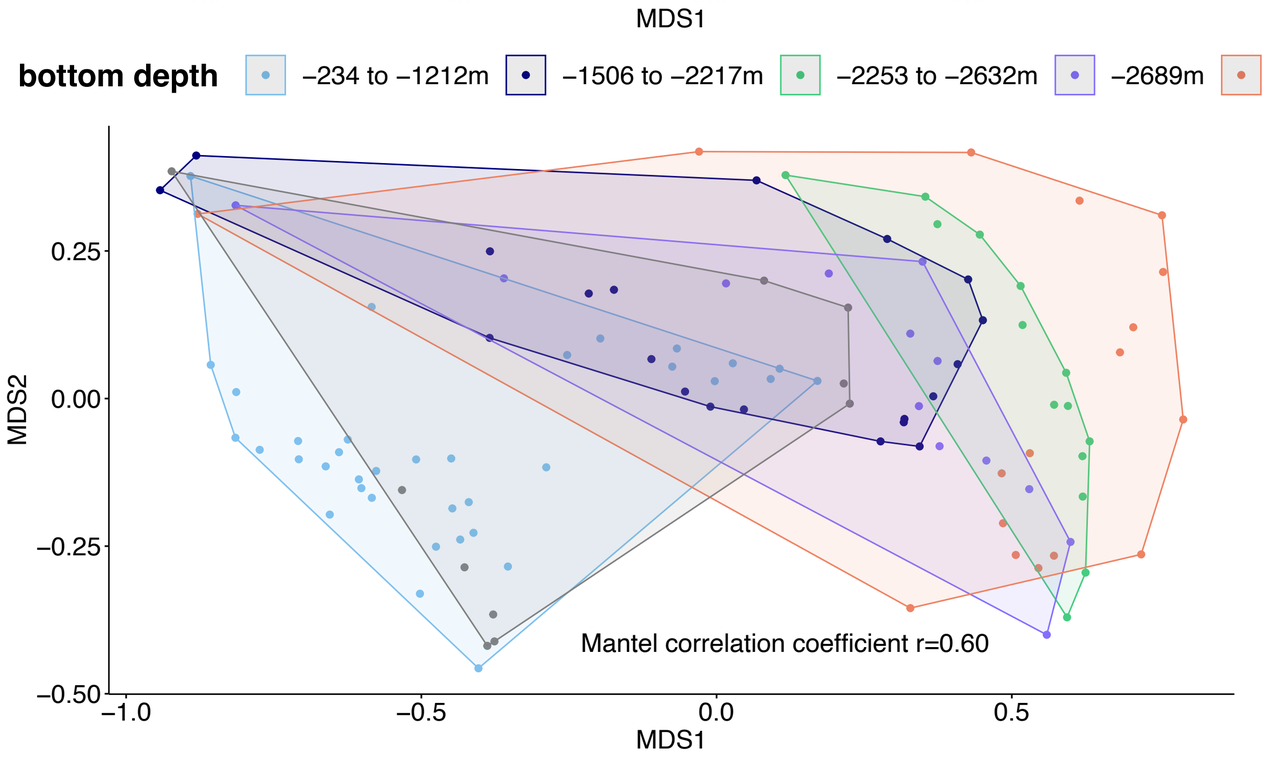

Mantel correlation coefficient r=0.47
MDS1
MDS2
oxygen saturation
58.8–76.5%
76.6–77.6%
77.8–91.0%

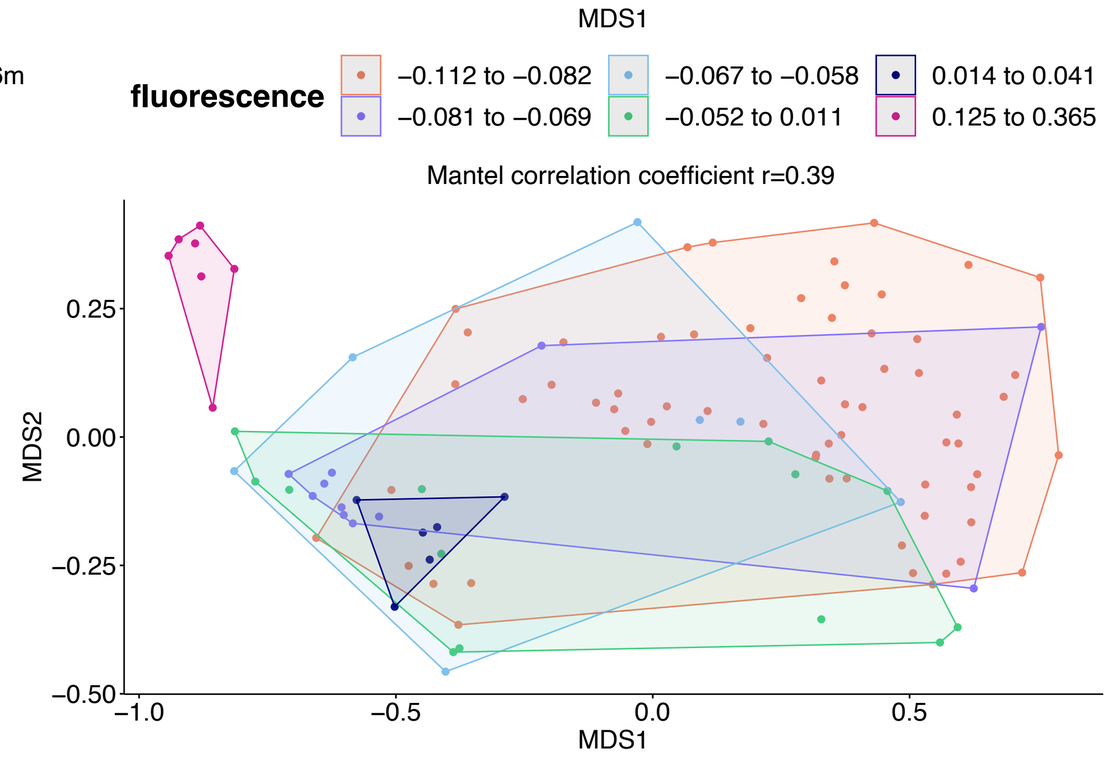

Mantel correlation coefficient r=0.83
MDS1
MDS2
latitude
60.84–60.85S
61.08–62.01S
62.02S
62.24S
62.76S
63.07–64.98S


Mantel correlation coefficient r=0.83
MDS1
MDS2
longitude
47.90–48.20W
49.59–51.43W
51.52–54.98W
55.68–57.78W


Mantel correlation coefficient r=0.47 (for latitude and longitude together)
MDS1
MDS2
bottom depth
−234 to −1212m
−1506 to −2217m
−2253 to −2632m
−2689m
−3286m

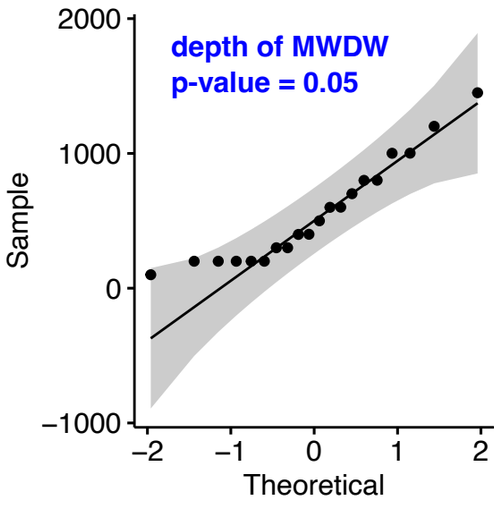

Mantel correlation coefficient r=0.47 (for latitude and longitude together)
MDS1
MDS2
fluorescence
−0.112 to −0.082
−0.081 to −0.069
−0.067 to −0.058
−0.052 to 0.011
0.014 to 0.041
0.125 to 0.365


Mantel correlation coefficient r=0.60
MDS1
MDS2

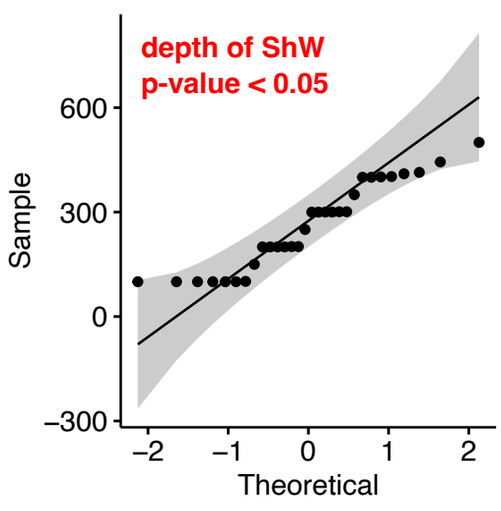

Mantel correlation coefficient r=0.39
MDS1
MDS2

Suppl. Fig. 1. Two-dimensional NMDS plots illustrating pairwise Bray-Curtis distances between pico-nano eukaryotic communities in the Western Weddell Sea. All NMDS plots are identical (with a stress value = 0.075 is shown in panel **A**), but the samples are clustered in different ways as described below. The water masses are mapped on the NMDS plot in the upper left corner, along with the environmental variables measured in this study and geographical coordinates. Boundary points on gradients of those variables (where pico-nano eukaryotic community composition is significantly different across the boundary) were identified using a split moving-window analysis of ecological differentiation based on a Z-score cutoff of 1.2 , and samples were clustered according to these boundary points. The clusters are colored and marked with polygons. The intervals of the variable corresponding to the clusters are shown in the legends on top of each plot. Mantel correlation coefficients (calculated for a matrix of Bray-Curtis distances between the pico-nano eukaryotic communities and for a matrix of Bray-Curtis distances between the samples based on a variable) are shown for each continuous variable.

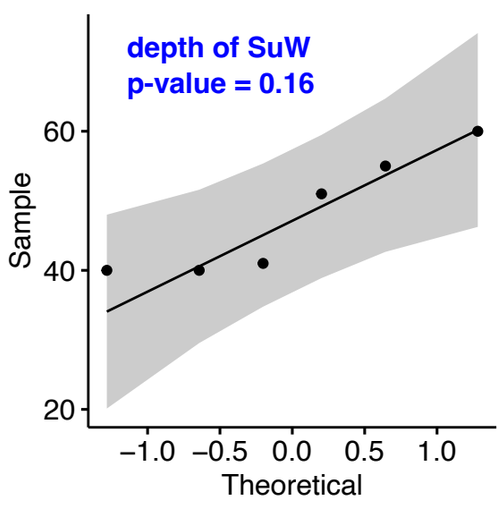
depth of MWDW
p-value = 0.05



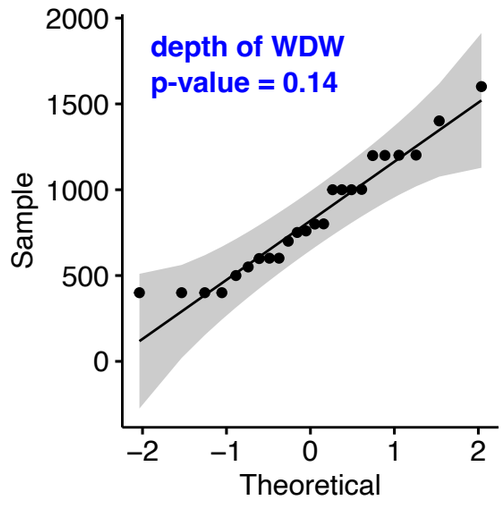
depth of ShW
p-value < 0.05



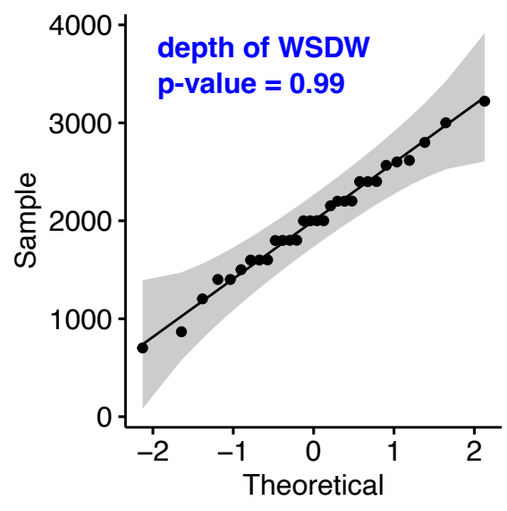
depth of SuW
p-value = 0.16



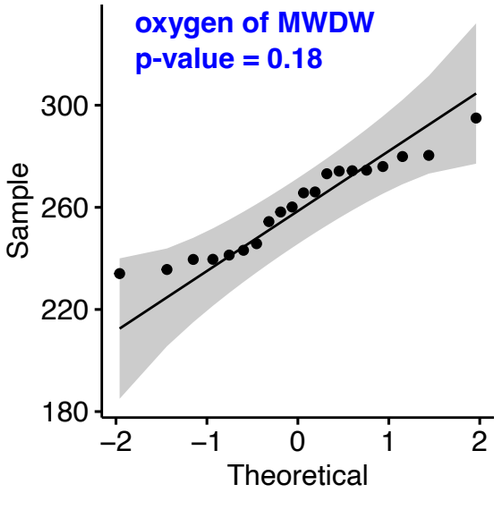
depth of WDW
p-value = 0.14



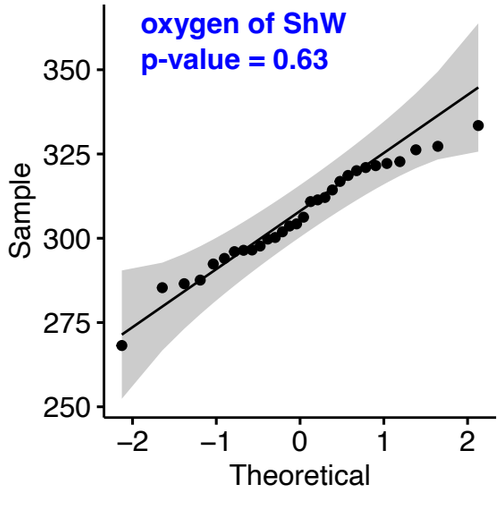
depth of WSDW
p-value = 0.99



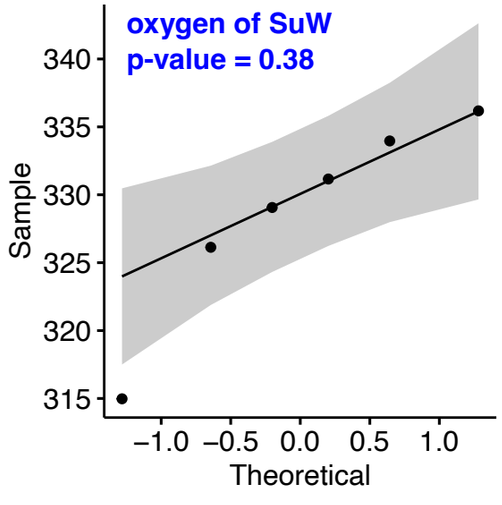
oxygen of MWDW
p-value = 0.18



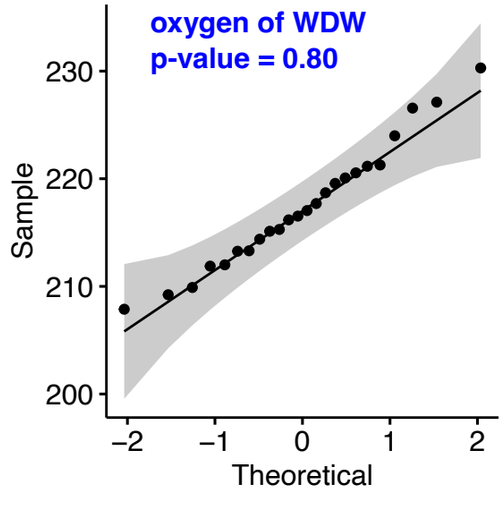
oxygen of ShW
p-value = 0.63



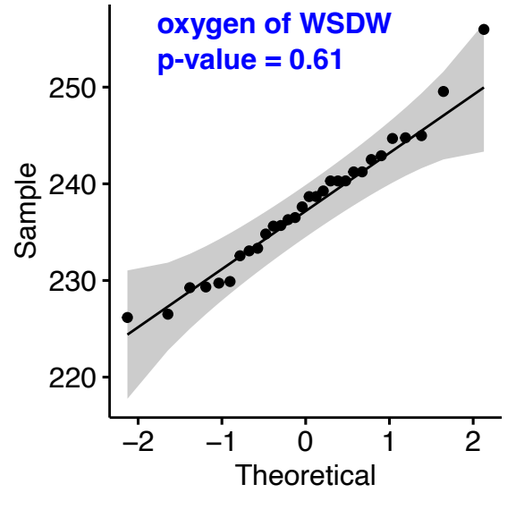
oxygen of SuW
p-value = 0.38



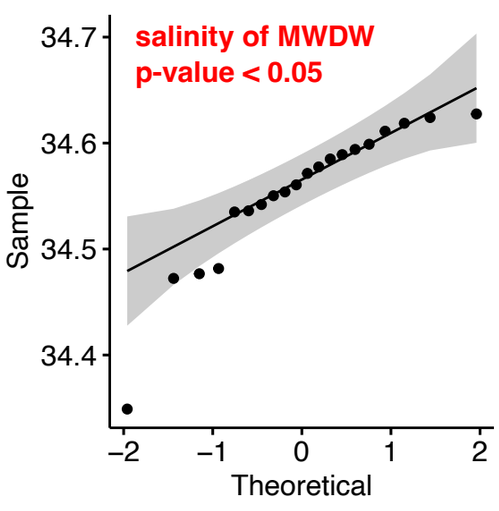
oxygen of WDW
p-value = 0.80



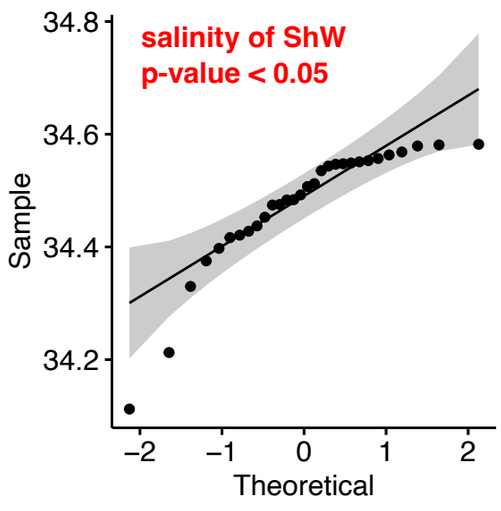
oxygen of WSDW
p-value = 0.61



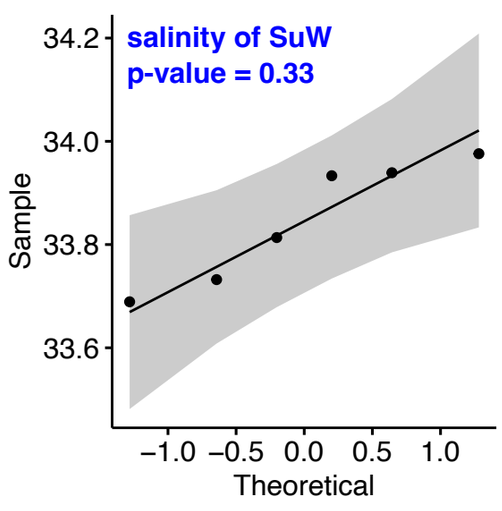
salinity of MWDW
p-value < 0.05



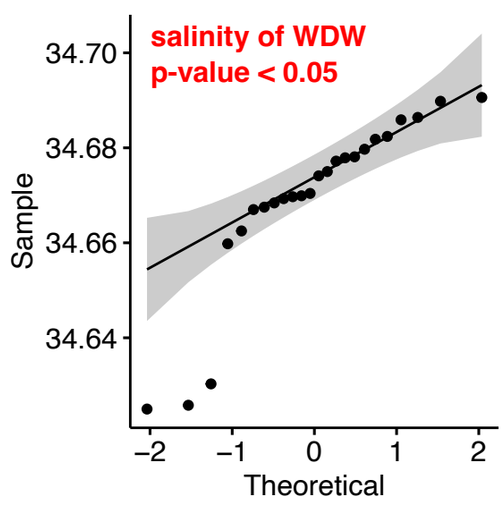
salinity of ShW
p-value < 0.05



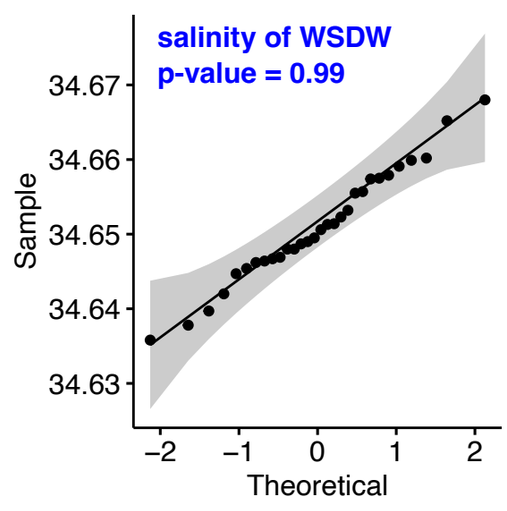
salinity of SuW
p-value = 0.33



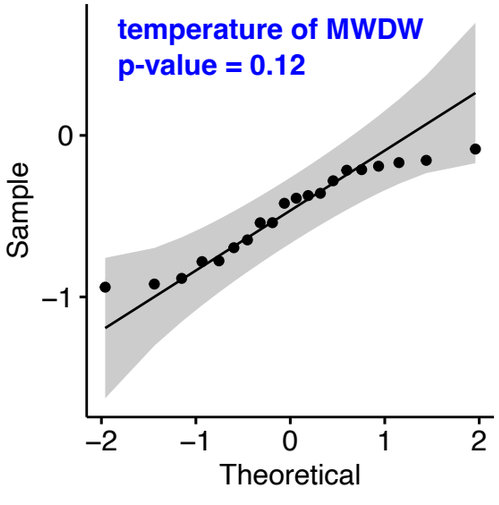
salinity of WDW
p-value < 0.05



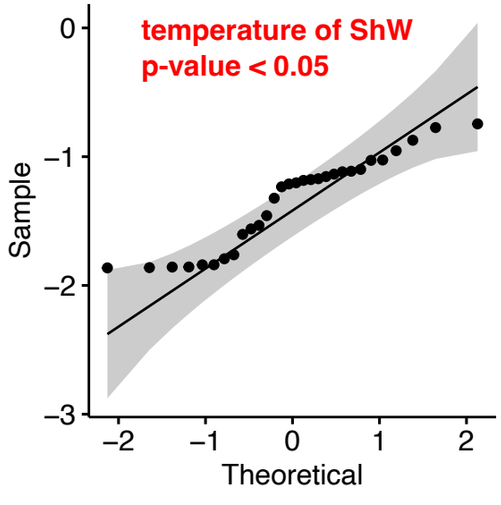
salinity of WSDW
p-value = 0.99



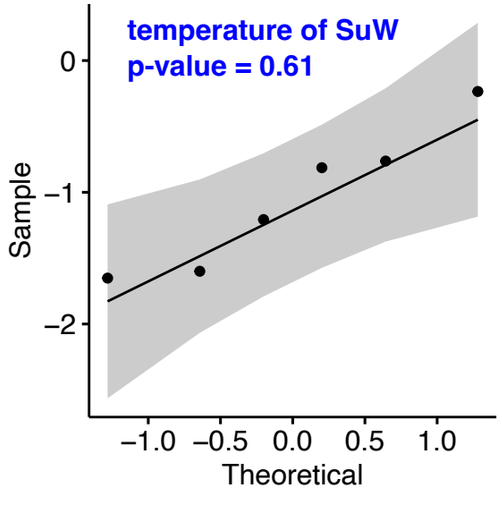
temperature of MWDW
p-value = 0.12



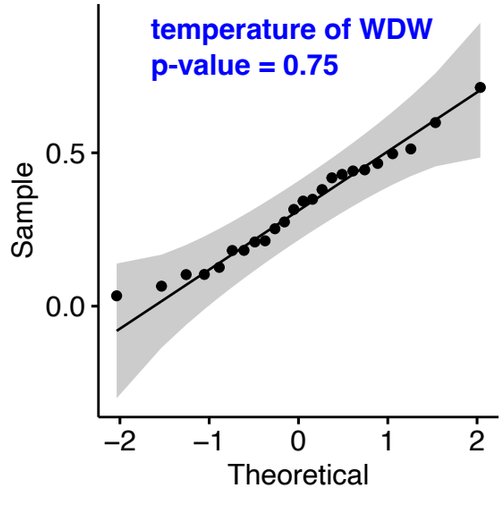
temperature of ShW
p-value < 0.05



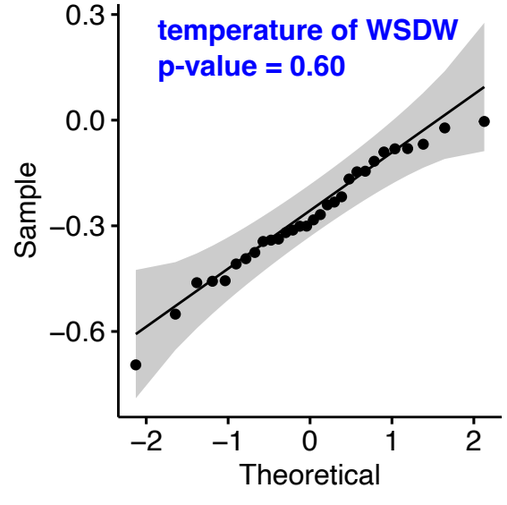
temperature of SuW
p-value = 0.61



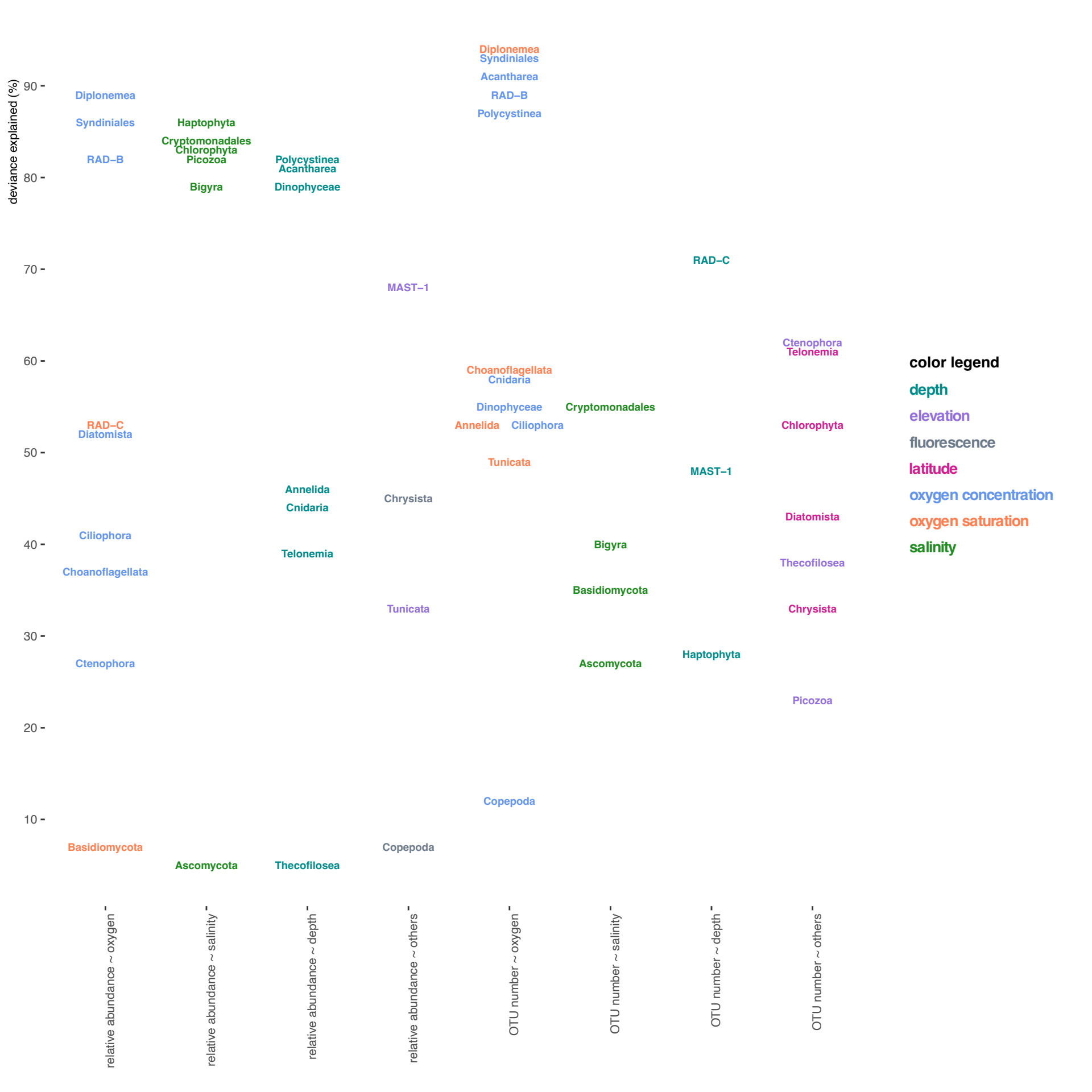
temperature of WDW
p-value = 0.75



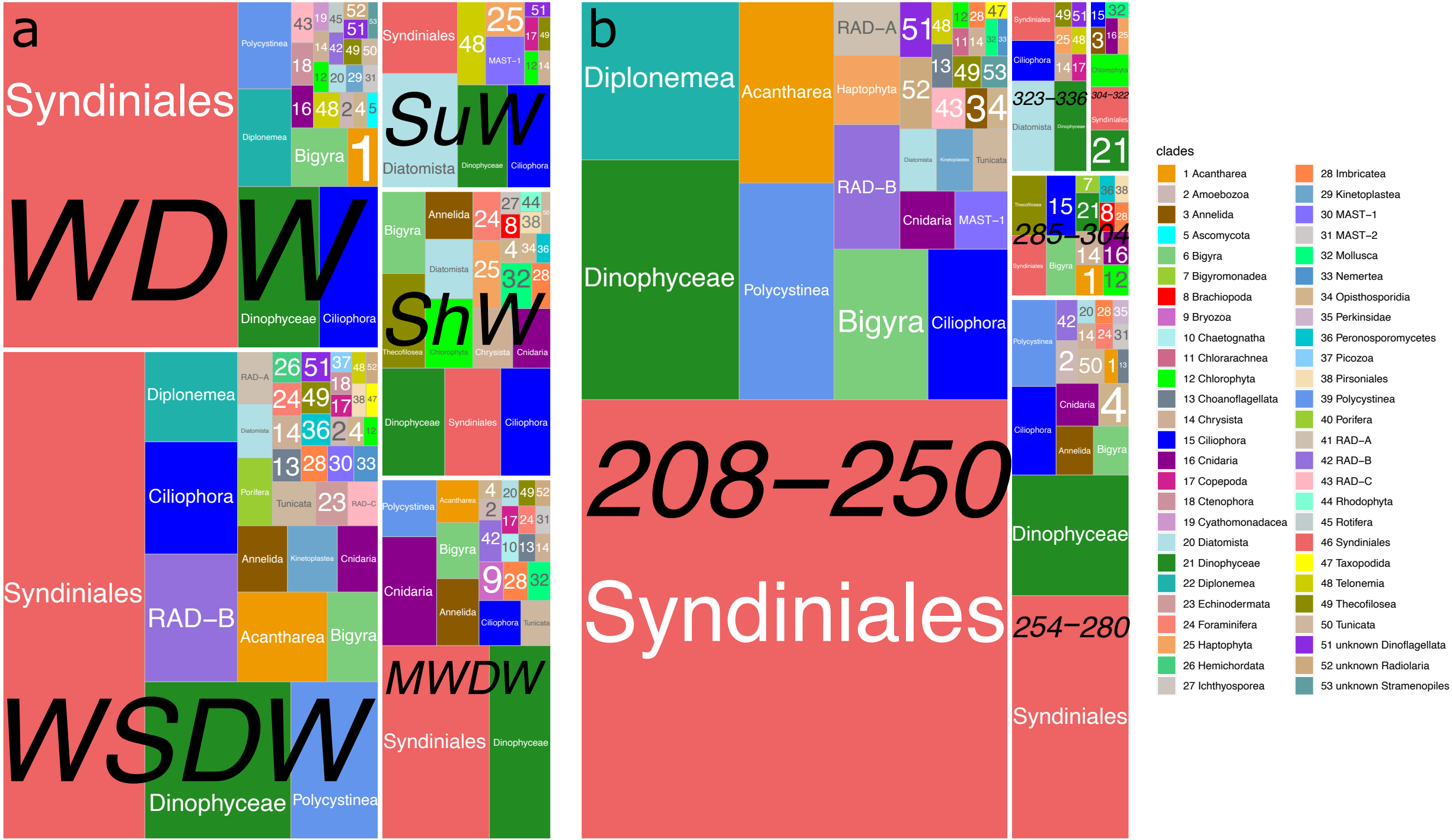
temperature of WSDW
p-value = 0.60



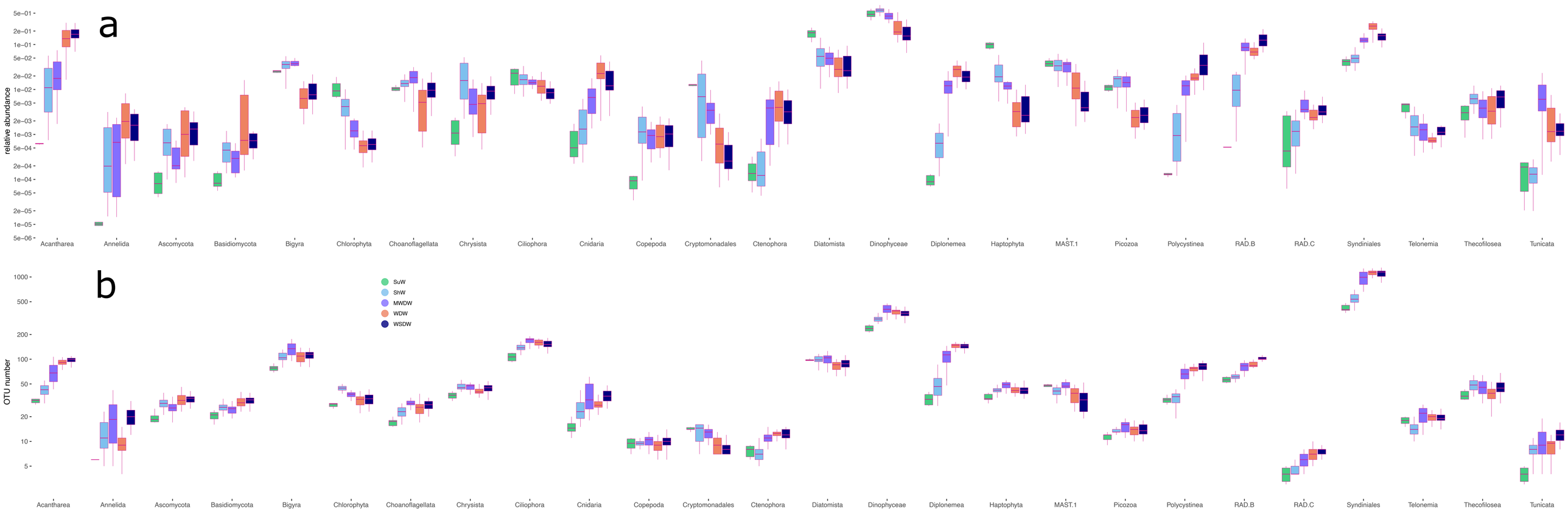
Suppl. Fig. 2. Normality test results for depth, oxygen concentration, salinity, and temperature across five water masses. Quantile-Quantile plots, confidence intervals and p-values of the Shapiro-Wilk test are shown.


deviance explained (%)
90
80
70
60
50
40
30
20
10
Diplonemea
Syndiniales
RAD–B
Haptophyta
Cryptomonadales
Chlorophyta
Picozoa
Bigyra
Polycystinea
Acantharea
Dinophyceae
Diplonemea
Syndiniales
Acantharea
RAD–B
Polycystinea
RAD–C
MAST–1
Ctenophora
Telonemia
Choanoflagellata
Cnidaria
Dinophyceae
Cryptomonadales
Annelida
Ciliophora
Chlorophyta
RAD–C
Diatomista
Tunicata
MAST–1
Annelida
Cnidaria
Chrysista
Diatomista
Ciliophora
Bigyra
Telonemia
Thecofilosea
Choanoflagellata
Basidiomycota
Tunicata
Chrysista
Haptophyta
Ctenophora
Ascomycota
Picozoa
Copepoda
Basidiomycota
Copepoda
Ascomycota
Thecofilosea
relative abundance ~ oxygen
relative abundance ~ salinity
relative abundance ~ depth
relative abundance ~ others
OTU number ~ oxygen
OTU number ~ salinity
OTU number ~ depth
OTU number ~ others
color legend
depth
elevation
fluorescence
latitude
oxygen concentration
oxygen saturation
salinity

Suppl. Fig. 3. A summary of GAM results showing influence of abiotic variables on relative abundance or OTU richness of 26 eukaryotic clades. Percentages of variance explained by GAM models are shown for clade/variable pairs on the y-axis. The environmental variables are coded by color and grouped into four categories: depth, oxygen, salinity, and the other variables. For relative abundance or OTU richness of each clade, only the highest variance explained across all the environmental variables is shown, hence each clade appears in one category only.

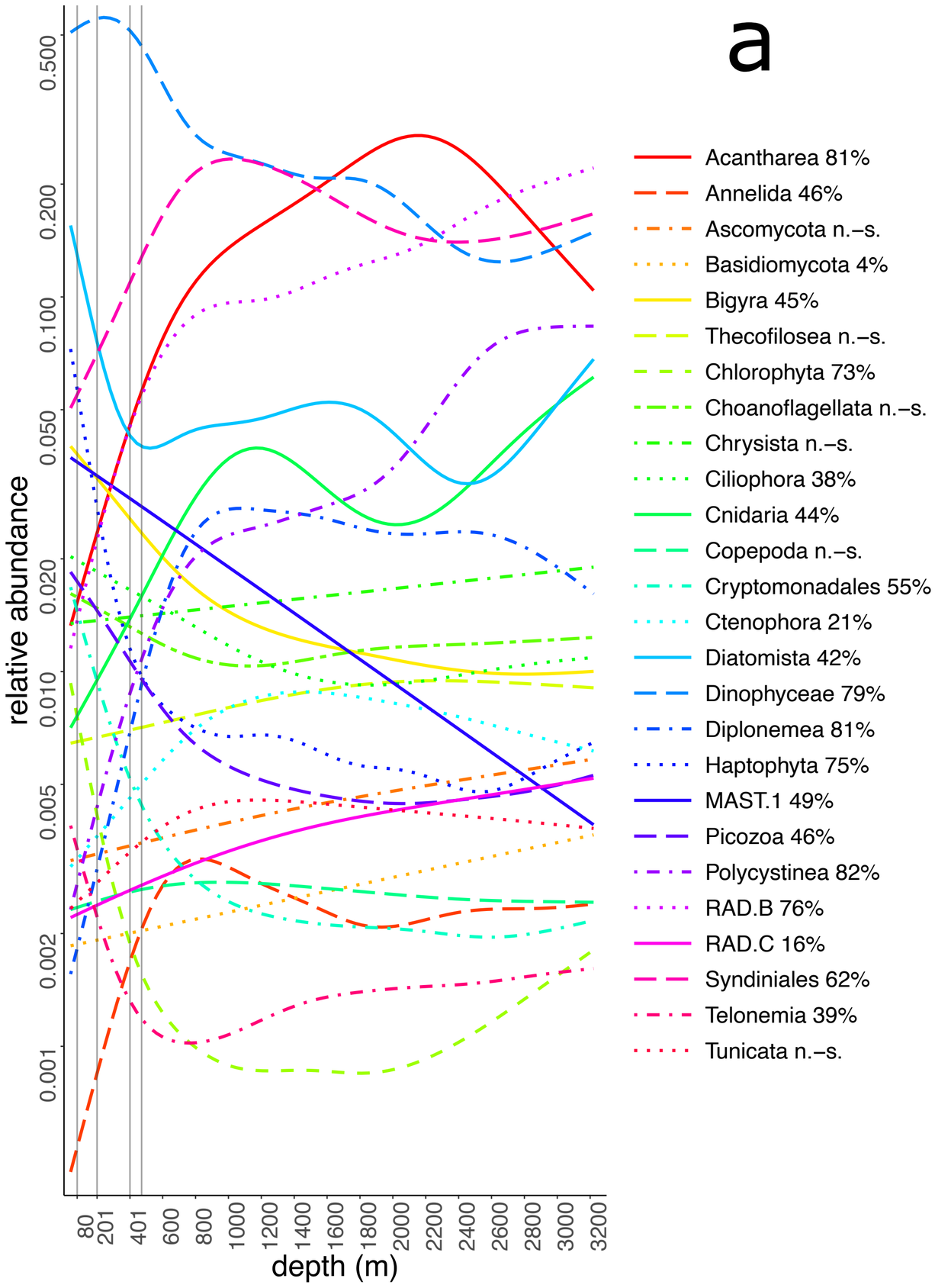

a
Syndiniales
WDW
Dinophyceae
Ciliophora
Polycystinea
Diplonemea
Bigyra
Syndiniales
SuW
Diatomista
Dinophyceae
Ciliophora
Syndiniales
ShW
Bigyra
Annelida
Diatomista
Thecofilosea
Chlorophyta
Chrysista
Cnidaria
Dinophyceae
Syndiniales
Ciliophora
Syndiniales
WSDW
Dinophyceae
Polycystinea
Diplonemea
Ciliophora
RAD–B
Acantharea
Bigyra
RAD–A
Diatomista
Porifera
Tunicata
RAD–C
Annelida
Kinetoplastea
Cnidaria
Polycystinea
Cnidaria
Acantharea
Bigyra
Annelida
Ciliophora
Tunicata
MWDW
Syndiniales
Dinophyceae
b
Diplonemea
Dinophyceae
Acantharea
Polycystinea
RAD–A
Haptophyta
RAD–B
Bigyra
Diatomista
Kinetoplastea
Tunicata
Cnidaria
MAST–1
Ciliophora
208–250
Syndiniales
Syndiniales
Ciliophora
323–336
Diatomista
Dinophyceae
304–322
Syndiniales
21
Thecofilosea
285–304
Syndiniales
Bigyra
Polycystinea
Cnidaria
Ciliophora
Dinophyceae
254–280
Syndiniales
clades
1 Acantharea
2 Amoebozoa
3 Annelida
5 Ascomycota
6 Bigyra
7 Bigyromonadea
8 Brachiopoda
9 Bryozoa
10 Chaetognatha
11 Chlorarachnea
12 Chlorophyta
13 Choanoflagellata
14 Chrysista
15 Ciliophora
16 Cnidaria
17 Copepoda
18 Ctenophora
19 Cyathomonadacea
20 Diatomista
21 Dinophyceae
22 Diplonemea
23 Echinodermata
24 Foraminifera
25 Haptophyta
26 Hemichordata
27 Ichthyosporea
28 Imbricatea
29 Kinetoplastea
30 MAST–1
31 MAST–2
32 Mollusca
33 Nemertea
34 Opisthosporidia
35 Perkinsidae
36 Peronosporomycetes
37 Picozoa
38 Pirsoniales
39 Polycystinea
40 Porifera
41 RAD–A
42 RAD–B
43 RAD–C
44 Rhodophyta
45 Rotifera
46 Syndiniales
47 Taxopodida
48 Telonemia
49 Thecofilosea
50 Tunicata
51 unknown Dinoflagellata
52 unknown Radiolaria
53 unknown Stramenopiles

Suppl. Fig. 4. Square pie charts illustrating taxonomy of OTUs that were identified as "indicators" for one of five water masses (panel **a**) or one of five intervals of oxygen concentration (panel **b**) separated by the ecological boundaries (Fig. 2). Taxonomic groups are labelled and numbered according to the legend. The water masses or oxygen concentration intervals are labelled in black.

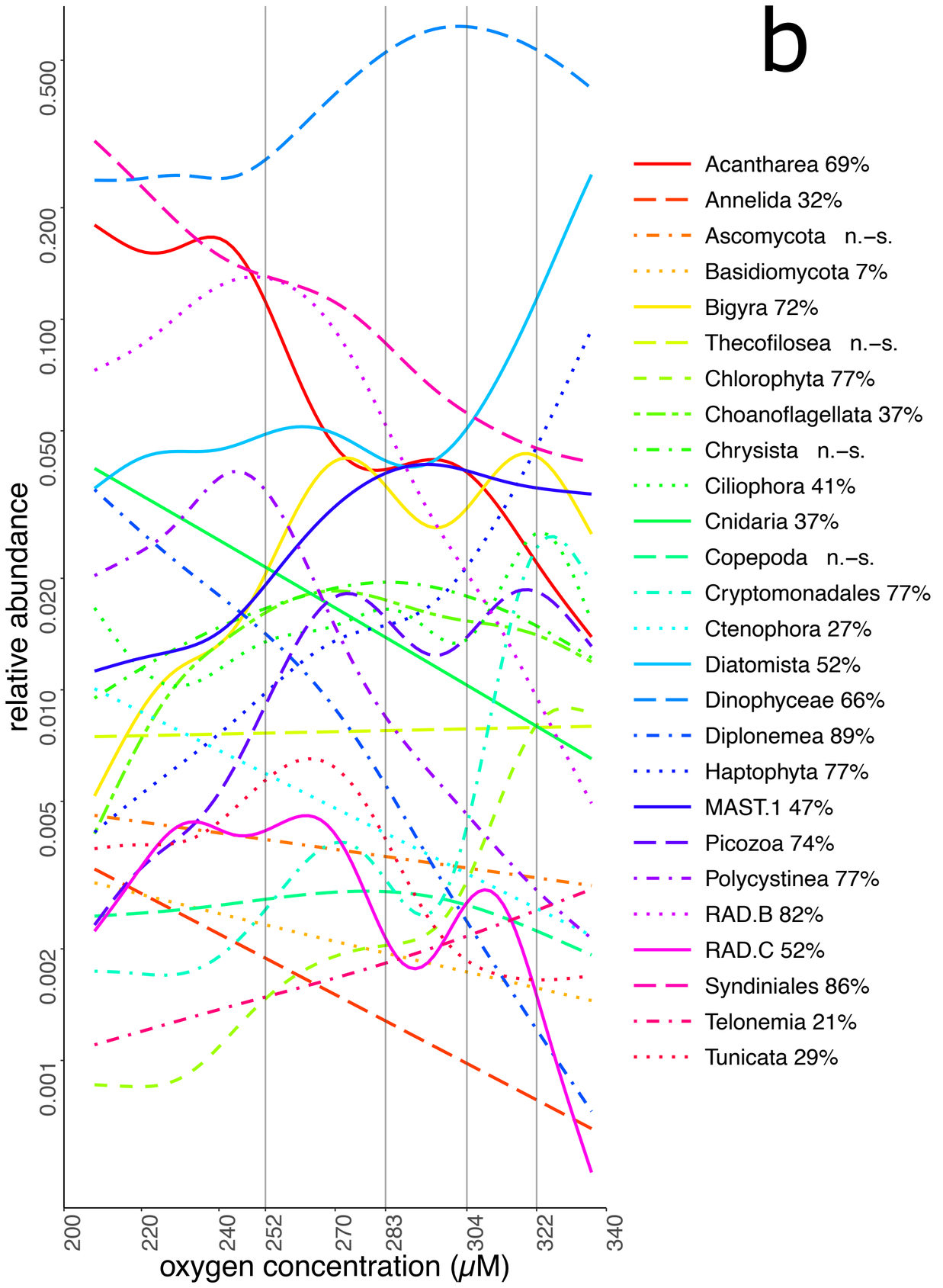

a
b
relative abundance
OTU number
5e−01
2e−01
1e−01
5e−02
2e−02
1e−02
5e−03
2e−03
1e−03
5e−04
2e−04
1e−04
5e−05
2e−05
1e−05
5e−06
1000
500
200
100
50
20
10
5
SuW
ShW
MWDW
WDW
WSDW
Acantharea
Annelida
Ascomycota
Basidiomycota
Bigyra
Chlorophyta
Choanoflagellata
Chrysista
Ciliophora
Cnidaria
Copepoda
Cryptomonadales
Ctenophora
Diatomista
Dinophyceae
Diplonemea
Haptophyta
MAST.1
Picozoa
Polycystinea
RAD.B
RAD.C
Syndiniales
Telonemia
Thecofilosea
Tunicata

Suppl. Fig. 5. Distribution of 26 eukaryotic taxonomic groups across the five water masses. Relative abundance (**a**) or OTU richness (**b**) values are shown in the form of boxplots. The y-axis scales are logarithmic.

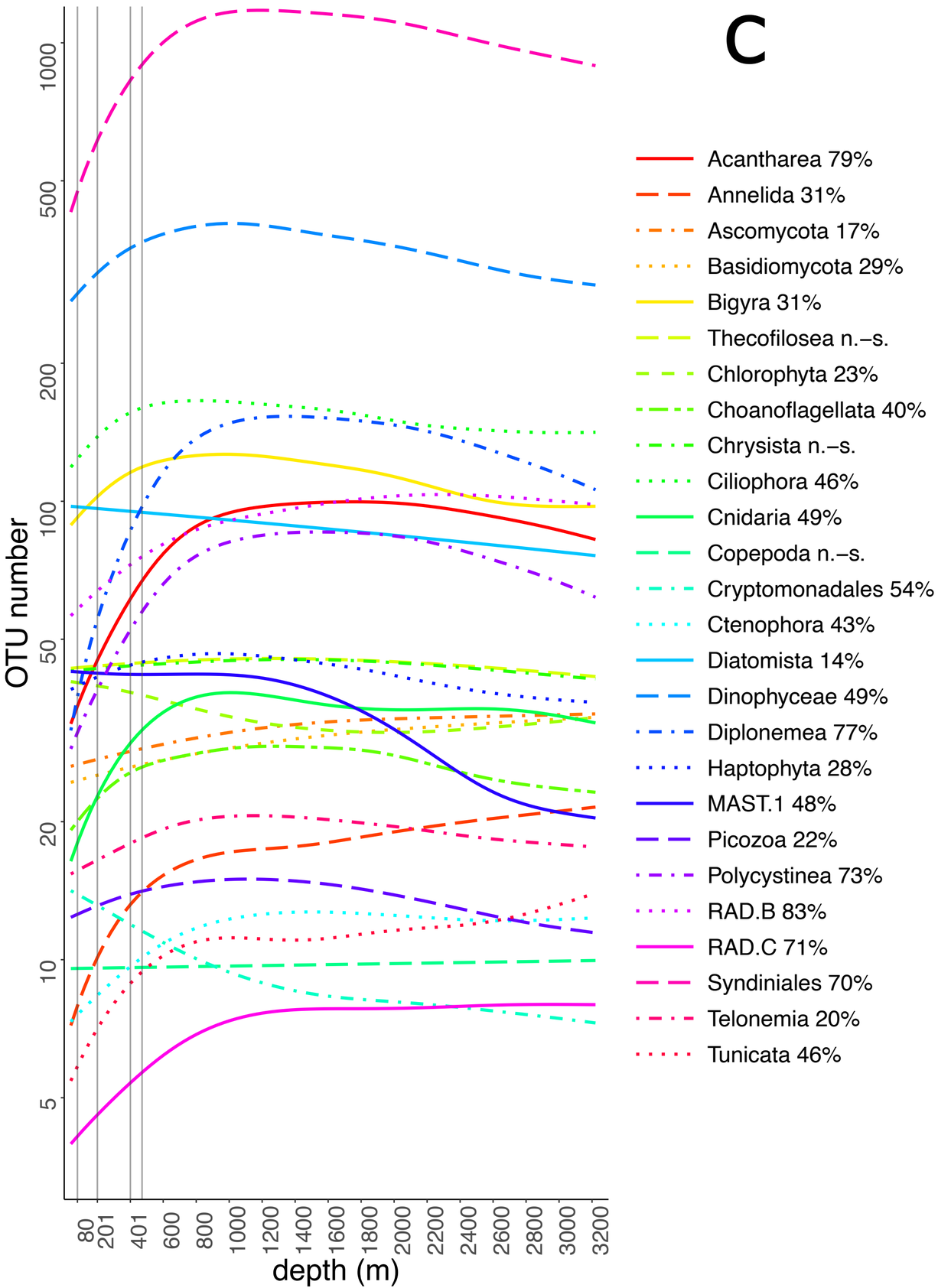
a


relative abundance
0.500
0.200
0.100
0.050
0.020
0.010
0.005
0.002
0.001
80
201
401
600
800
1000
1200
1400
1600
1800
2000
2200
2400
2600
2800
3000
3200
depth (m)
Acantharea 81%
Annelida 46%
Ascomycota n.–s.
Basidiomycota 4%
Bigyra 45%
Thecofilosea n.–s.
Chlorophyta 73%
Choanoflagellata n.–s.
Chrysista n.–s.
Ciliophora 38%
Cnidaria 44%
Copepoda n.–s.
Cryptomonadales 55%
Ctenophora 21%
Diatomista 42%
Dinophyceae 79%
Diplonemea 81%
Haptophyta 75%
MAST.1 49%
Picozoa 46%
Polycystinea 82%
RAD.B 76%
RAD.C 16%
Syndiniales 62%
Telonemia 39%
Tunicata n.–s.

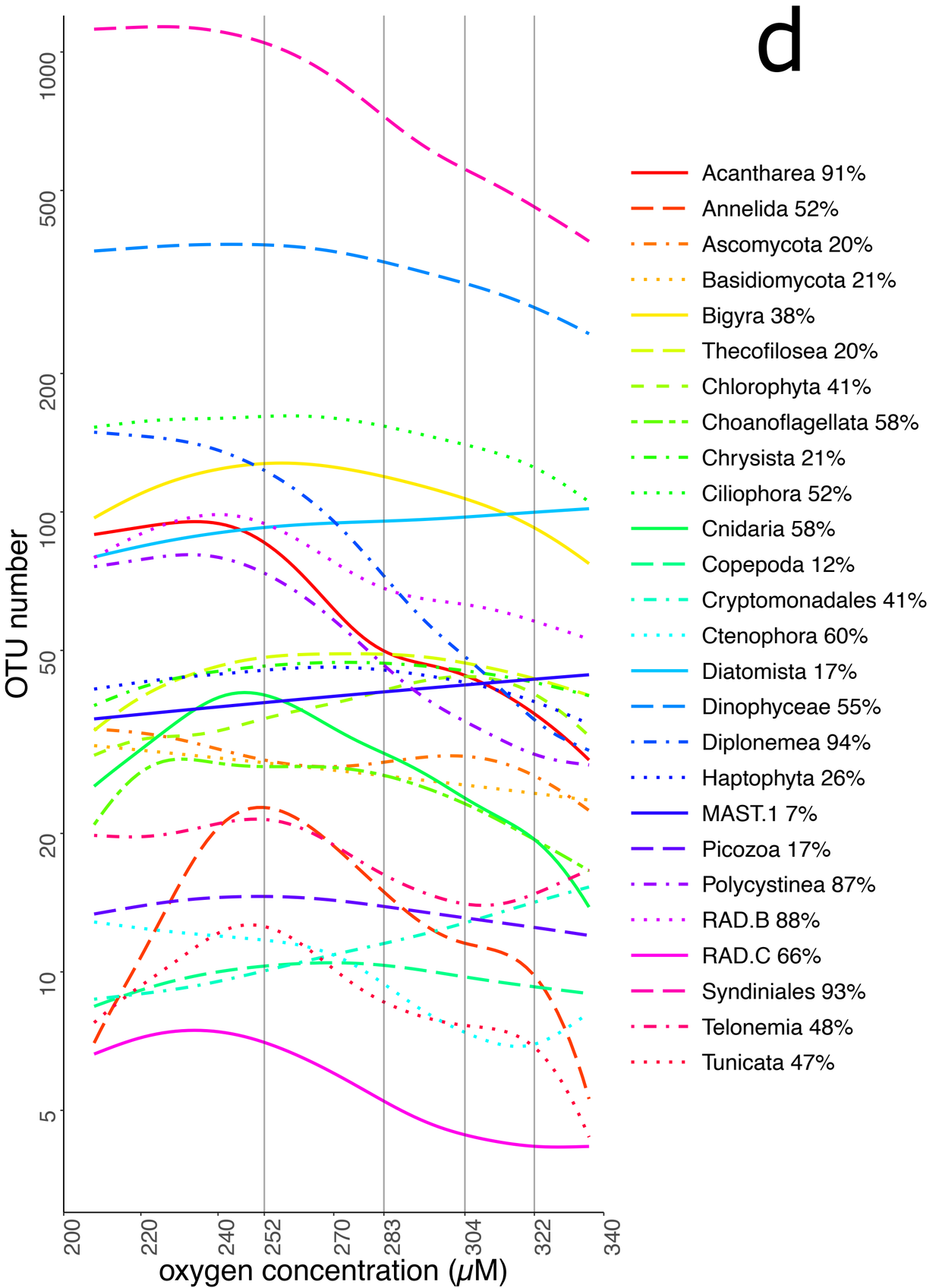
b


relative abundance
0.500
0.200
0.100
0.050
0.020
0.010
0.005
0.002
0.001
200
220
240
252
270
283
304
322
340
oxygen concentration (μM)
Acantharea 69%
Annelida 32%
Ascomycota n.–s.
Basidiomycota 7%
Bigyra 72%
Thecofilosea n.–s.
Chlorophyta 77%
Choanoflagellata 37%
Chrysista n.–s.
Ciliophora 41%
Cnidaria 37%
Copepoda n.–s.
Cryptomonadales 77%
Ctenophora 27%
Diatomista 52%
Dinophyceae 66%
Diplonemea 89%
Haptophyta 77%
MAST.1 47%
Picozoa 74%
Polycystinea 77%
RAD.B 82%
RAD.C 52%
Syndiniales 86%
Telonemia 21%
Tunicata 29%

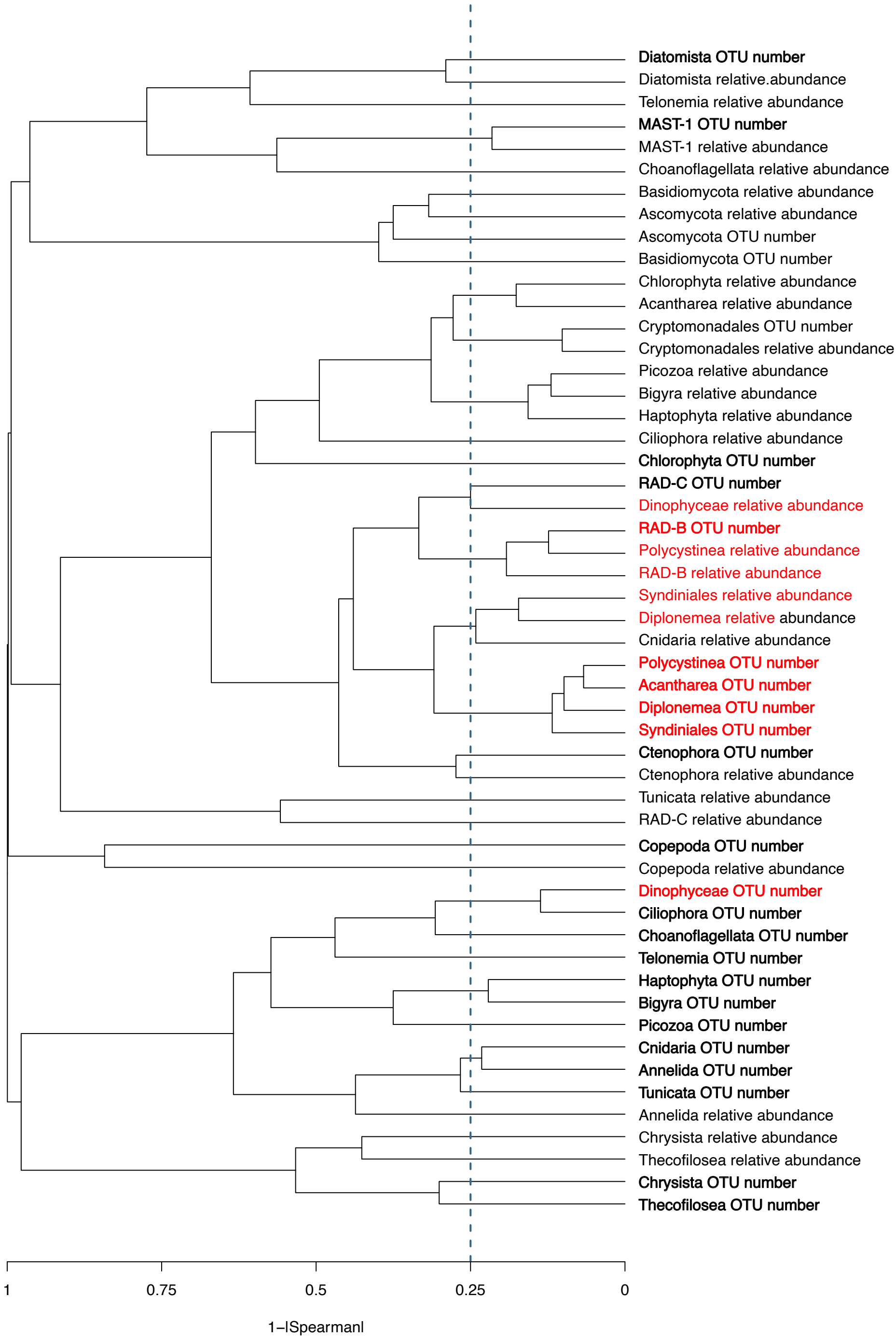
c


OTU number
1000
500
200
100
50
20
10
5
80
201
401
600
800
1000
1200
1400
1600
1800
2000
2200
2400
2600
2800
3000
3200
depth (m)
Acantharea 79%
Annelida 31%
Ascomycota 17%
Basidiomycota 29%
Bigyra 31%
Thecofilosea n.–s.
Chlorophyta 23%
Choanoflagellata 40%
Chrysista n.–s.
Ciliophora 46%
Cnidaria 49%
Copepoda n.–s.
Cryptomonadales 54%
Ctenophora 43%
Diatomista 14%
Dinophyceae 49%
Diplonemea 77%
Haptophyta 28%
MAST.1 48%
Picozoa 22%
Polycystinea 73%
RAD.B 83%
RAD.C 71%
Syndiniales 70%
Telonemia 20%
Tunicata 46%

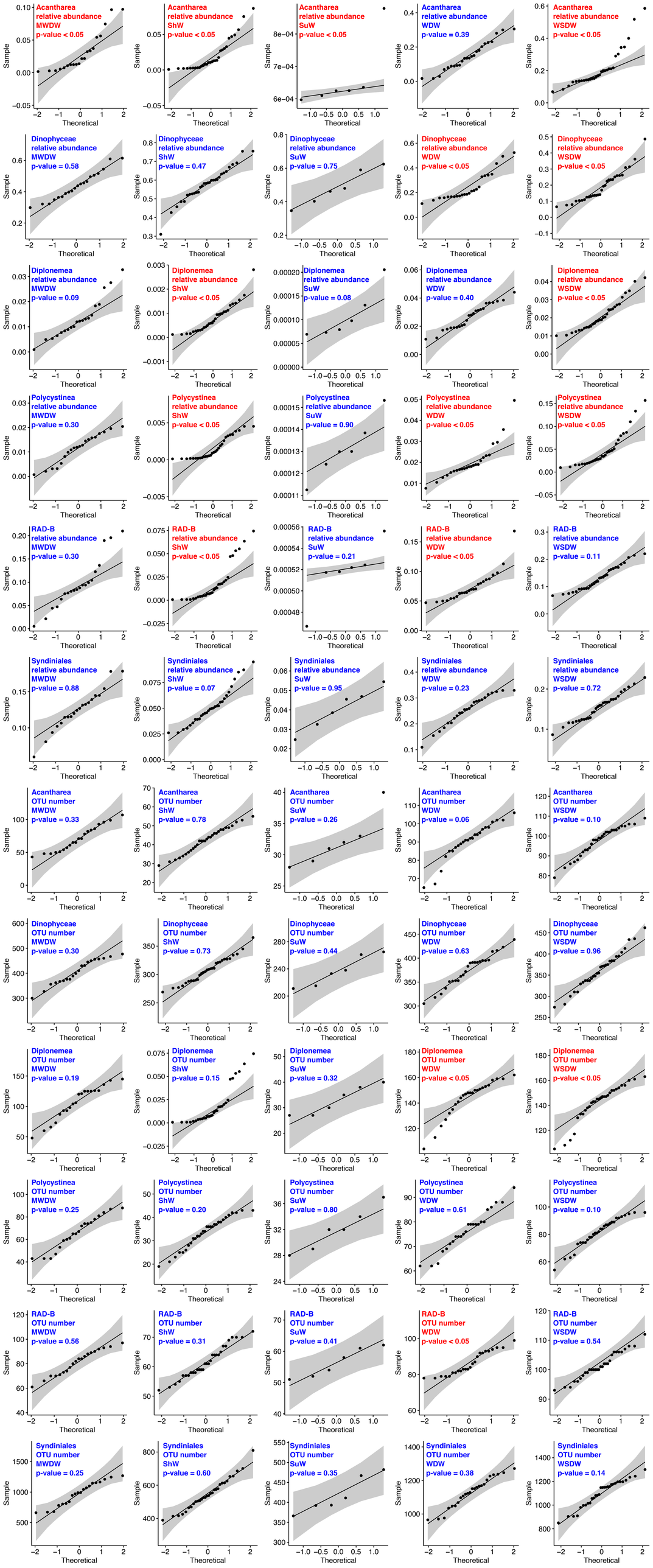
d


OTU number
1000
500
200
100
50
20
10
5
200
220
240
252
270
283
304
322
340
oxygen concentration (μM)
Acantharea 91%
Annelida 52%
Ascomycota 20%
Basidiomycota 21%
Bigyra 38%
Thecofilosea 20%
Chlorophyta 41%
Choanoflagellata 58%
Chrysista 21%
Ciliophora 52%
Cnidaria 58%
Copepoda 12%
Cryptomonadales 41%
Ctenophora 60%
Diatomista 17%
Dinophyceae 55%
Diplonemea 94%
Haptophyta 26%
MAST.1 7%
Picozoa 17%
Polycystinea 87%
RAD.B 88%
RAD.C 66%
Syndiniales 93%
Telonemia 48%
Tunicata 47%

Suppl. Fig. 6. Plots illustrating relative abundance (**a** , **b**) or OTU richness (**c** , **d**) of 26 eukaryotic taxonomic groups changing with depth (**a** , **c**) or oxygen concentration (**b** , **d**) in the Western Weddell Sea. Only trend lines calculated using the GAM approach are shown along with percentage of variance explained. Confidence intervals for GAMs and individual data points are not shown for simplicity. The y-axes scales are logarithmic. Oxygen concentration or depth values identified as ecological boundary points are marked with vertical grey lines.


Diatomista OTU number
Diatomista relative.abundance
Telonemia relative abundance
MAST-1 OTU number
MAST-1 relative abundance
Choanoflagellata relative abundance
Basidiomycota relative abundance
Ascomycota relative abundance
Ascomycota OTU number
Basidiomycota OTU number
Chlorophyta relative abundance
Acantharea relative abundance
Cryptomonadales OTU number
Cryptomonadales relative abundance
Picozoa relative abundance
Bigyra relative abundance
Haptophyta relative abundance
Ciliophora relative abundance
Chlorophyta OTU number
RAD-C OTU number
Dinophyceae relative abundance
RAD-B OTU number
Polycystinea relative abundance
RAD-B relative abundance
Syndiniales relative abundance
Diplonemea relative abundance
Cnidaria relative abundance
Polycystinea OTU number
Acantharea OTU number
Diplonemea OTU number
Syndiniales OTU number
Ctenophora OTU number
Ctenophora relative abundance
Tunicata relative abundance
RAD-C relative abundance
Copepoda OTU number
Copepoda relative abundance
Dinophyceae OTU number
Ciliophora OTU number
Choanoflagellata OTU number
Telonemia OTU number
Haptophyta OTU number
Bigyra OTU number
Picozoa OTU number
Cnidaria OTU number
Annelida OTU number
Tunicata OTU number
Annelida relative abundance
Chrysista relative abundance
Thecofilosea relative abundance
Chrysista OTU number
Thecofilosea OTU number
1
0.75
0.5
0.25
0
1−|Spearman|

Suppl. Fig. 7. A dendrogram visualizing a matrix of pairwise Spearman correlation coefficients (1 – |Spearman coefficient|) for relative abundance and OTU richness of 26 eukaryotic clades. Most important members of the deep-sea community are highlighted in red.


Acantharea
relative abundance
MWDW
p-value < 0.05
Acantharea
relative abundance
ShW
p-value < 0.05
Acantharea
relative abundance
SuW
p-value < 0.05
Acantharea
relative abundance
WDW
p-value = 0.39
Acantharea
relative abundance
WSDW
p-value < 0.05
Dinophyceae
relative abundance
MWDW
p-value = 0.58
Dinophyceae
relative abundance
ShW
p-value = 0.47
Dinophyceae
relative abundance
SuW
p-value = 0.75
Dinophyceae
relative abundance
WDW
p-value < 0.05
Dinophyceae
relative abundance
WSDW
p-value < 0.05
Diplonemea
relative abundance
MWDW
p-value = 0.09
Diplonemea
relative abundance
ShW
p-value < 0.05
Diplonemea
relative abundance
SuW
p-value = 0.08
Diplonemea
relative abundance
WDW
p-value = 0.40
Diplonemea
relative abundance
WSDW
p-value < 0.05
Polycystinea
relative abundance
MWDW
p-value = 0.30
Polycystinea
relative abundance
ShW
p-value < 0.05
Polycystinea
relative abundance
SuW
p-value = 0.90
Polycystinea
relative abundance
WDW
p-value < 0.05
Polycystinea
relative abundance
WSDW
p-value < 0.05
RAD-B
relative abundance
MWDW
p-value = 0.30
RAD-B
relative abundance
ShW
p-value < 0.05
RAD-B
relative abundance
SuW
p-value = 0.21
RAD-B
relative abundance
WDW
p-value < 0.05
RAD-B
relative abundance
WSDW
p-value = 0.11
Syndiniales
relative abundance
MWDW
p-value = 0.88
Syndiniales
relative abundance
ShW
p-value = 0.07
Syndiniales
relative abundance
SuW
p-value = 0.95
Syndiniales
relative abundance
WDW
p-value = 0.23
Syndiniales
relative abundance
WSDW
p-value = 0.72
Acantharea
OTU number
MWDW
p-value = 0.33
Acantharea
OTU number
ShW
p-value = 0.78
Acantharea
OTU number
SuW
p-value = 0.26
Acantharea
OTU number
WDW
p-value = 0.06
Acantharea
OTU number
WSDW
p-value = 0.10
Dinophyceae
OTU number
MWDW
p-value = 0.30
Dinophyceae
OTU number
ShW
p-value = 0.73
Dinophyceae
OTU number
SuW
p-value = 0.44
Dinophyceae
OTU number
WDW
p-value = 0.63
Dinophyceae
OTU number
WSDW
p-value = 0.96
Diplonemea
OTU number
MWDW
p-value = 0.19
Diplonemea
OTU number
ShW
p-value = 0.15
Diplonemea
OTU number
SuW
p-value = 0.32
Diplonemea
OTU number
WDW
p-value < 0.05
Diplonemea
OTU number
WSDW
p-value < 0.05
Polycystinea
OTU number
MWDW
p-value = 0.25
Polycystinea
OTU number
ShW
p-value = 0.20
Polycystinea
OTU number
SuW
p-value = 0.80
Polycystinea
OTU number
WDW
p-value = 0.61
Polycystinea
OTU number
WSDW
p-value = 0.10
RAD-B
OTU number
MWDW
p-value = 0.56
RAD-B
OTU number
ShW
p-value = 0.31
RAD-B
OTU number
SuW
p-value = 0.41
RAD-B
OTU number
WDW
p-value < 0.05
RAD-B
OTU number
WSDW
p-value = 0.54
Syndiniales
OTU number
MWDW
p-value = 0.25
Syndiniales
OTU number
ShW
p-value = 0.60
Syndiniales
OTU number
SuW
p-value = 0.35
Syndiniales
OTU number
WDW
p-value = 0.38
Syndiniales
OTU number
WSDW
p-value = 0.14
Sample
Theoretical

Suppl. Fig. 8. Normality test results for relative abundance values and OTU counts of six key players in the deep-sea eukaryotic community distributed across five water masses. Quantile-Quantile plots, confidence intervals and p-values of the Shapiro-Wilk test are shown.