Supplemental Figure Legends

Figure S1. NMDS results for the 16S (A) and 18S (B) rRNA gene communities. In each, circles and triangles represent the > 2.7 μm and 0.2-2.7 μm fractions, respectively.

Figure S2. Hclust results for the 16S (A) and 18S (B) rRNA gene communities.

Figure S3. Richness and Evenness indexes for the 16S > 2.7 μm (A) and 0.2-2.7 μm (B) and 18S > 2.7 (C) and 0.2-2.7 μm (D) communities. Non-linear regressions with 95% CI (gray shading) are provided for reference.

Figure S4. Separated upper and lower MSR core microbiome aggregate abundance for the 16S rRNA gene communities. For the upper and lower river, the core microbiome was defined separately requiring OTUs to have greater than one read in 90% of the samples. > 2.7 μm (A) and 0.2-2.7 μm (B) 16S rRNA gene communities in the upper and lower MSR.

Figure S5. Relative abundance, by environmental ontology group, according to transect distance for the 16S rRNA gene > 2.7 μm (A) and 0.2-2.7 μm (B) communities. Non-linear regressions with 95% CI (gray shading) are provided for reference.

Figure S6. WCGNA results for 0.2-2.7 μm 16S rRNA gene community submodules of interest based on Pearson correlations to nitrate and phosphate (A, B, D) and the resultant PLS regression of the predicted versus measured nutrient concentrations (C, E). Linear regressions with 95% CI (gray shading) are provided for reference.

Figure S7. WCGNA results for > 2.7 μm 16S rRNA gene community submodules of interest based on Pearson correlations to nitrate and phosphate (A, B, D) and the resultant PLS regression of the predicted versus measured nutrient concentrations (C, E). Linear regressions with 95% CI (gray shading) are provided for reference.

Figure S8. WCGNA results for 0.2-2.7 μm 18S rRNA gene community submodules of interest based on Pearson correlations to nitrate and phosphate (A, B, D) and the resultant PLS regression of the predicted versus measured nutrient concentrations (C, E). Linear regressions with 95% CI (gray shading) are provided for reference.

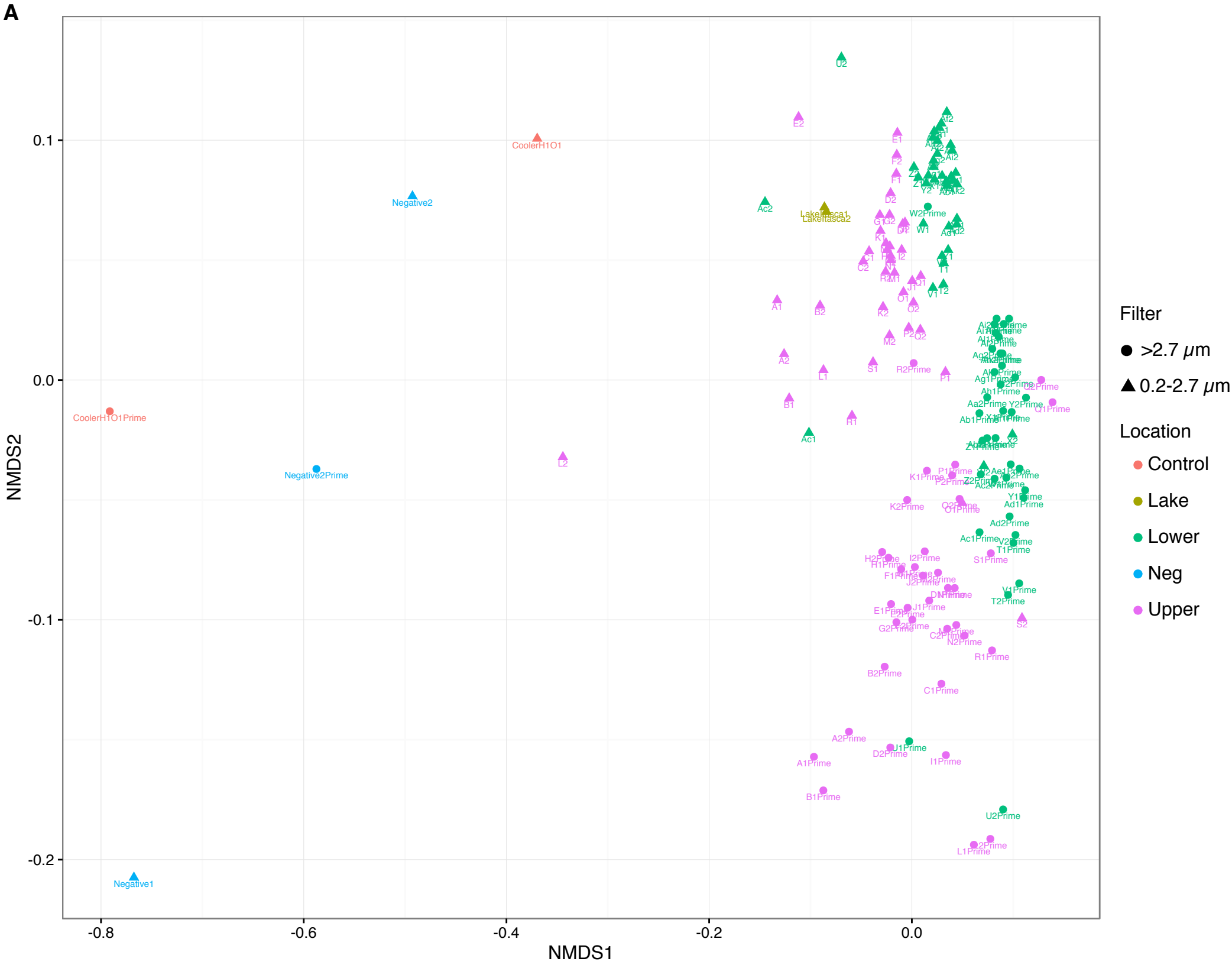
Figure S9. WCGNA results for > 2.7 μm 18S rRNA gene community submodules of interest based on Pearson correlations to nitrate and phosphate (A, B, D) and the resultant PLS regression of the predicted versus measured nutrient concentrations (C, E). Linear regressions with 95% CI (gray shading) are provided for reference.

Supplemental Tables

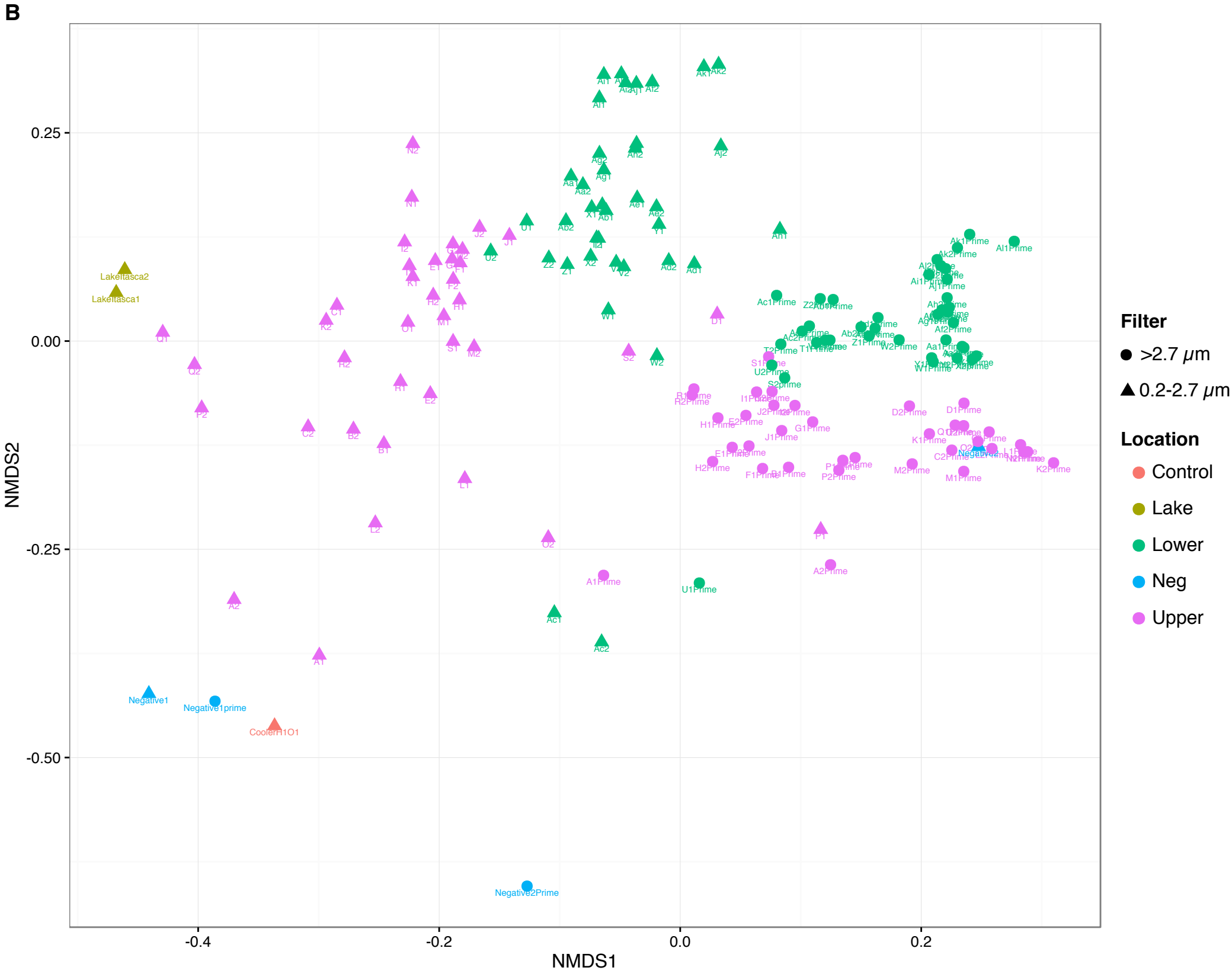
Supplemental Table S1 is a spreadsheet, TableS1.xlsx. This includes site data, NMDS correlations for environmental data, Relative abundances of the Core taxa, SeqENV data, 16S and 18S rRNA OTU tables, and VIP scores for all

samples and datum.

A


NMDS2
NMDS1
0.1
0.0
-0.1
-0.2
-0.8
-0.6
-0.4
-0.2
0.0
CoolerH1O1
Negative2
CoolerH1O1Prime
Negative2Prime
Negative1
Lakeltasca1
Lakeltasca2
Filter
>2.7 μm
0.2-2.7 μm
Location
Control
Lake
Lower
Neg
Upper

B


NMDS2
NMDS1
0.25
0.00
-0.25
-0.50
-0.4
-0.2
0.0
0.2
Lakeltasca2
Lakeltasca1
Negative1
Negative1prime
CoolerH1O1
Negative2Prime
Filter
>2.7 μm
0.2-2.7 μm
Location
Control
Lake
Lower
Neg
Upper

B

Height

0.0 0.2 0.4 0.6 0.8 1.0

Negative2prime
A1
U1prime
Ac2
Ac1
CoolerH2O1
Negative1
Negative1prime
A1prime
A2
A2prime
B1prime
B2prime
K1prime
J1prime
J2prime
H2prime
I1prime
I2prime
H1prime
G1prime
G2prime
E1prime
F2prime
E2prime
F1prime
D1prime
D2prime
W1prime
W2prime
U2prime
V1prime
V2prime
T1prime
T2prime
Z1prime
Z2prime
Ae1prime
Ab1prime
Ad1prime
Ab2prime
Ad2prime
Ac1prime
Ac2prime
Ak1prime
Al1prime
Ae2prime
Af1prime
Af2prime
Ah1prime
Ah2prime
Ag1prime
Ag2prime
Y1prime
Aa1prime
Aa2prime
Y2prime
X1prime
X2prime
Ai1prime
Aj2prime
Ai2prime
Aj1prime
Ak2prime
Al2prime
Negative2
O2prime
K2prime
N1prime
N2prime
L1prime
L2prime
M1prime
M2prime
Q1prime
Q2prime
C1prime
C2prime
P1
P1prime
P2prime
S2
S1prime
S2prime
R1prime
R2prime
Aj1
Aj2
Ai1
Ai2
Ak1
Ak2
Al1
Al2
Ah1
Ae1
V1
V2
Af1
Af2
Ag1
Ag2
Ae2
Ah2
LakeUNE1
LakeUNE2
Q1
Q2
O2
P2
O1
R2
R1
S1
C1
K2
L1
L2
N1
N2
M1
M2
C2
E2
B1
B2
W2
Ad1
Ad2
W1
U1
U2
T1
T2
Y1
Aa1
Aa2
X2
Ab2
Z1
Z2
Ab1
X1
Y2
D1
D2
F2
E1
F1
K1
I1
I2
J1
J2
G1
G2
H1
H2

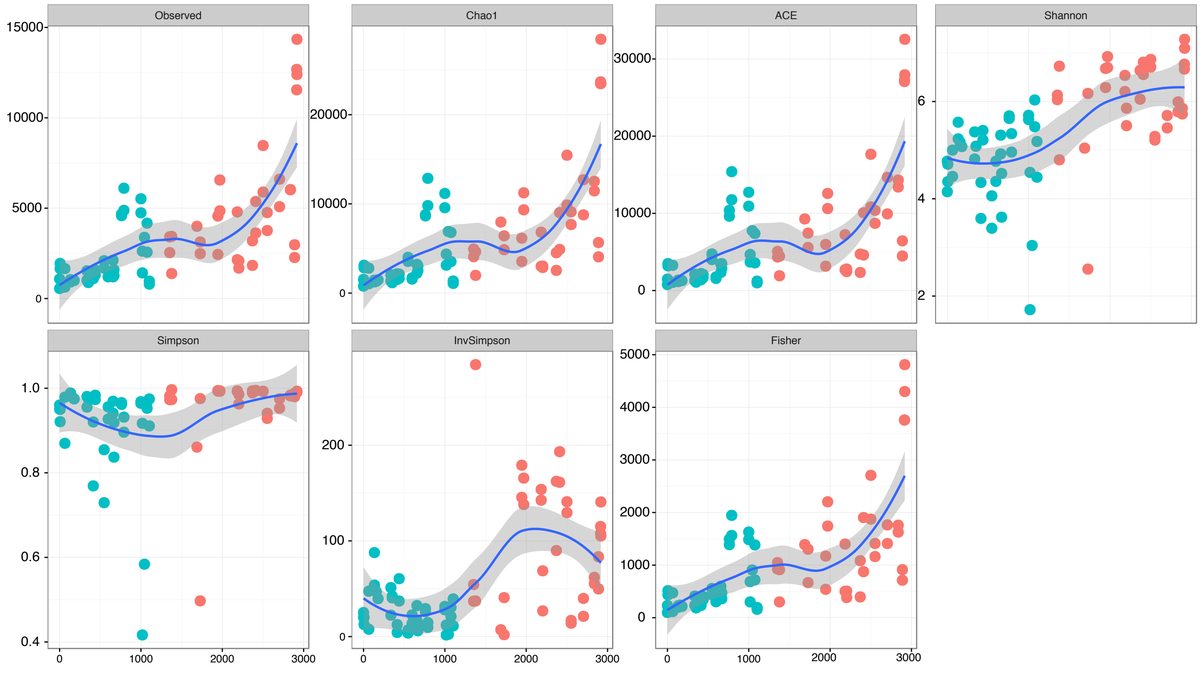
A

Height

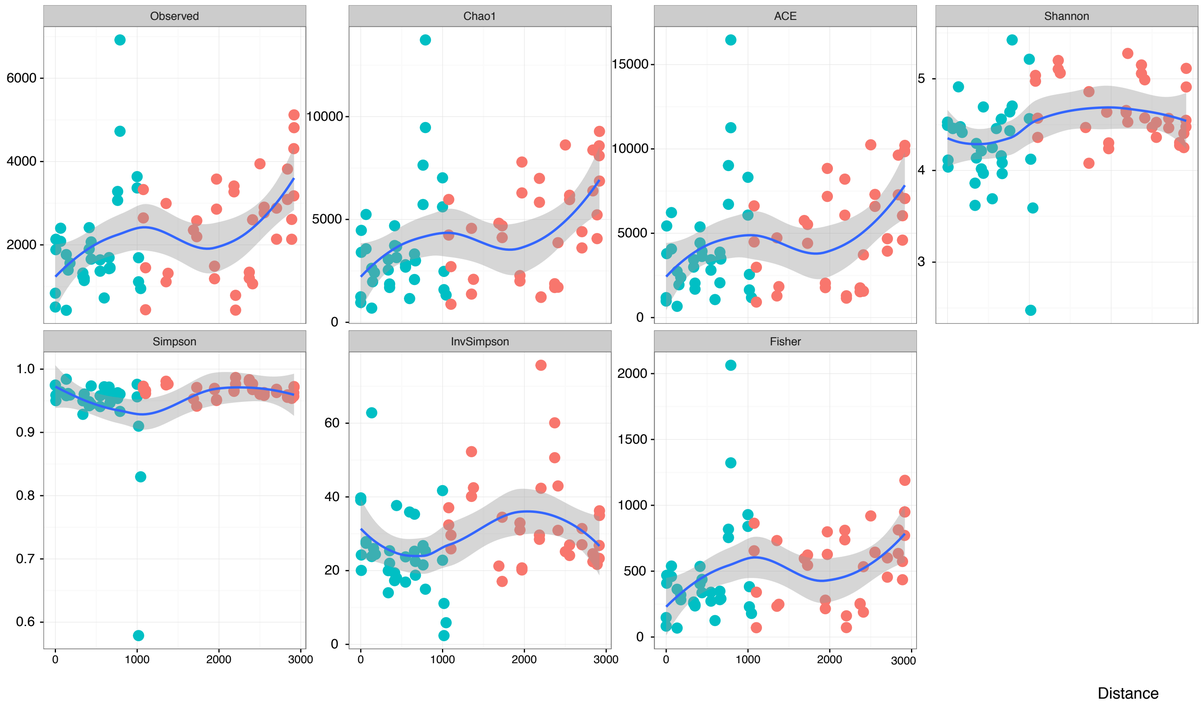
0.0 0.2 0.4 0.6 0.8

CoolerH1O1Prime
Negative1
CoolerH1O1
Negative2
Negative2Prime
L2
B1Prime
A1Prime
A2Prime
L1Prime
L2Prime
U1Prime
U2Prime
Ac1
Ac2
D2Prime
E1Prime
E2Prime
E2Prime
F1Prime
I1Prime
I2Prime
J2Prime
J2Prime
G2Prime
M2Prime
M1Prime
G1Prime
H1Prime
Y2Prime
Al1Prime
Al2Prime
Ak1Prime
Ak2Prime
Ai2Prime
Ai1Prime
Ai1Prime
Al2Prime
X1Prime
X2
Ag2Prime
Ag1Prime
Ah1Prime
Ah2Prime
Af1Prime
Af2Prime
Aa1Prime
Aa2Prime
R1Prime
V1Prime
V2Prime
T1Prime
T2Prime
Ac1Prime
Ac2Prime
Y1Prime
W1Prime
W2
Ad2Prime
Ab2Prime
Z2Prime
Ab1Prime
Z1Prime
Ae1Prime
Ad1Prime
Ae2Prime
S1Prime
S2
P1
B1Prime
B2Prime
Q1Prime
Q2Prime
Q1Prime
O2Prime
D1Prime
B2Prime
C1Prime
C2Prime
M1Prime
N1Prime
N2Prime
K1Prime
K2Prime
B1
E2
B2
A1
A2
L1
LakeItasca1
LakeItasca2
U2
R2Prime
Q1
Q2
P2
O1
O2
R1
B2
S1
D1
D2
E1
E2
F1
F2
M2
M1
N1
N2
H1
H2
J1
J2
G1
G2
K1
I1
I2
K2
C1
C2
Ad1
Ad2
Ae2
T1
T2
V2
V1
X1
Ab1
Ab2
Af2
Aa1
Aa2
Ak1
Ak2
Al1
Al2
Ai1
Ai2
Af1
Al2
Ah1
Ah2
Ag1
Ag2
U1
Y2
Ae1
W2Prime
Z1
Z2
V1
W1

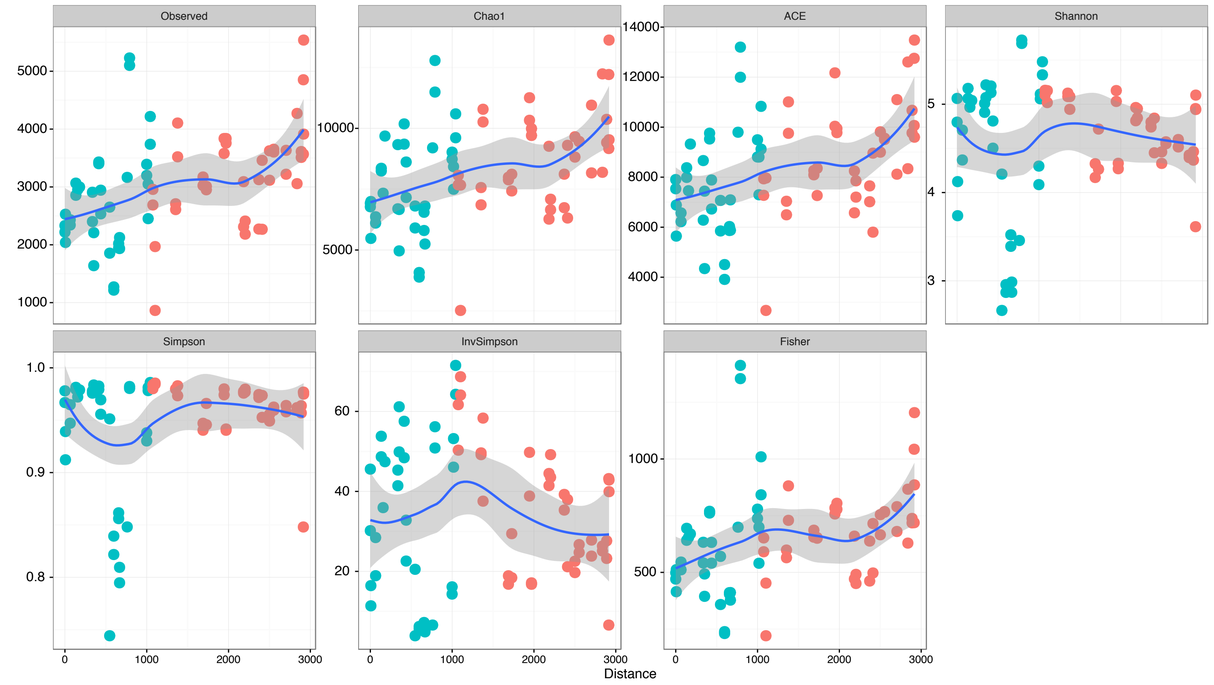
A


Observed
Chao1
ACE
Shannon
Simpson
InvSimpson
Fisher
Count
Distance

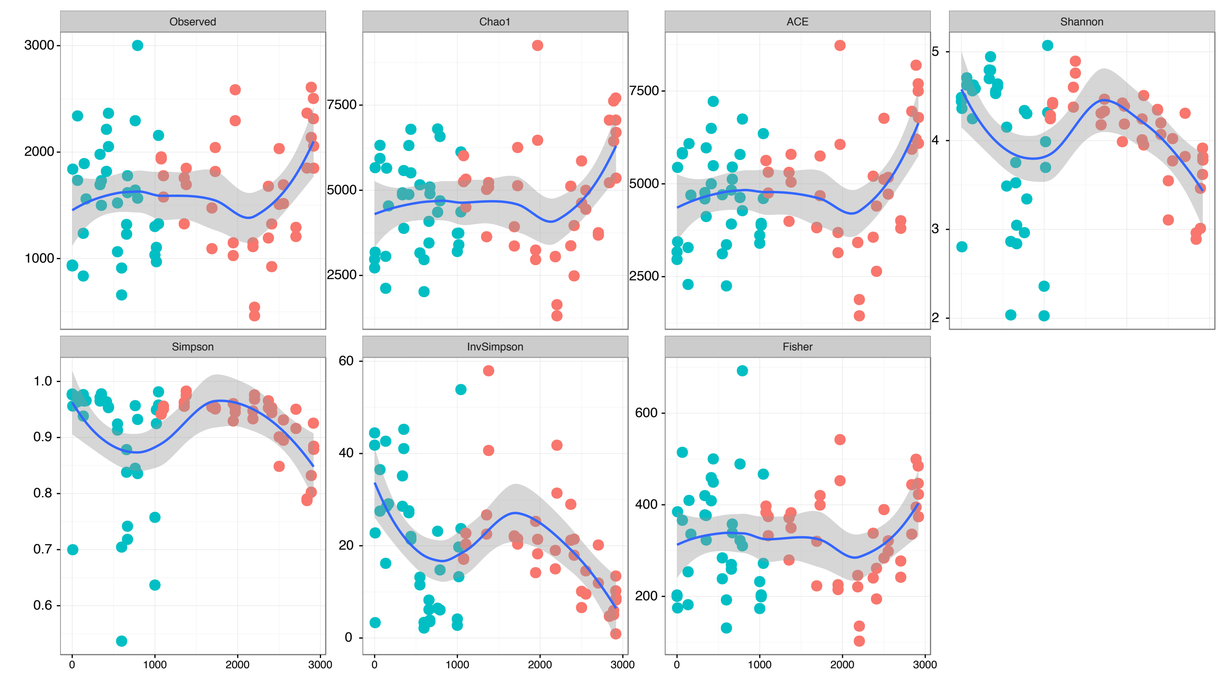
B

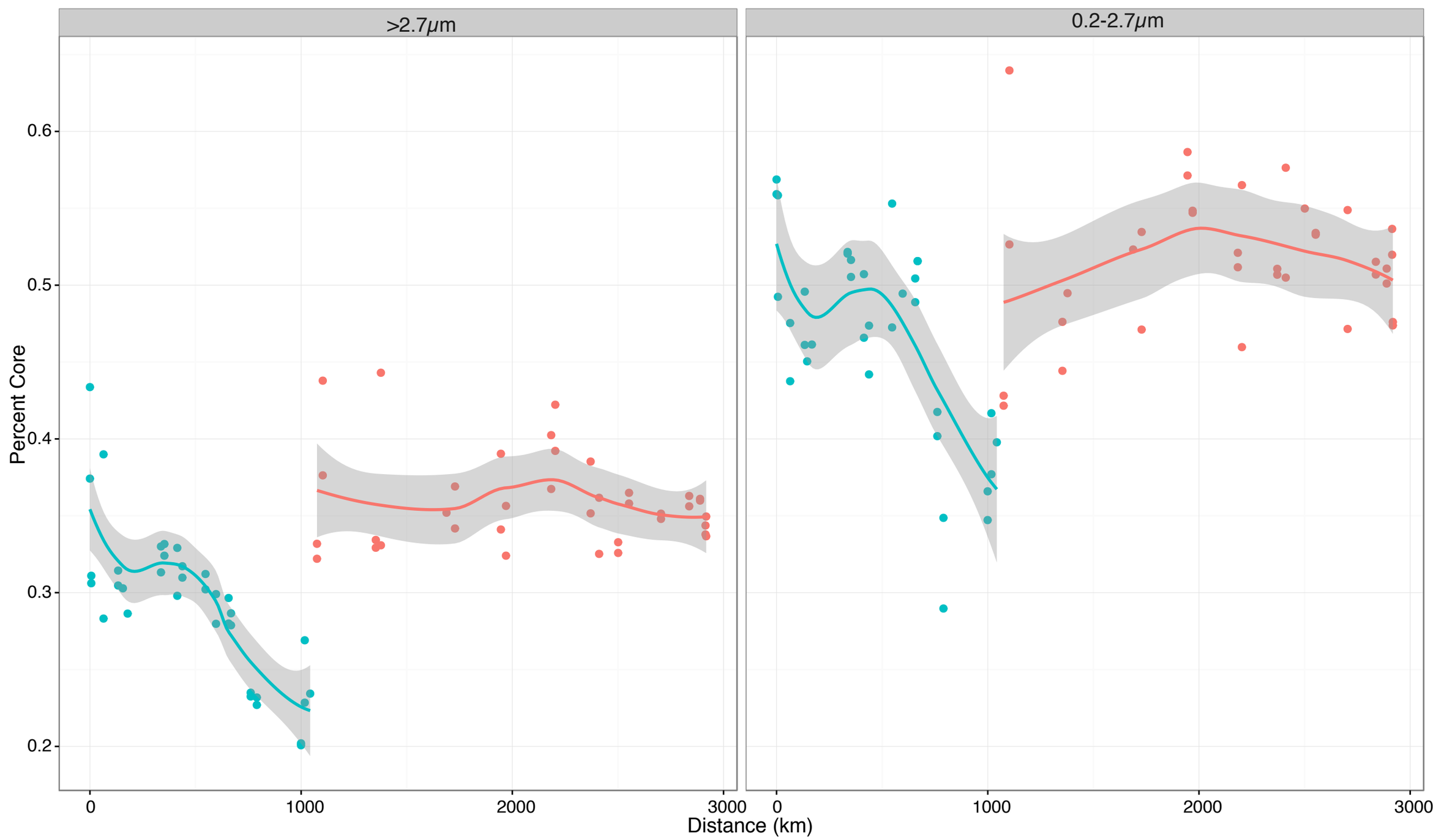

Observed
Chao1
ACE
Shannon
Simpson
InvSimpson
Fisher
Distance

C

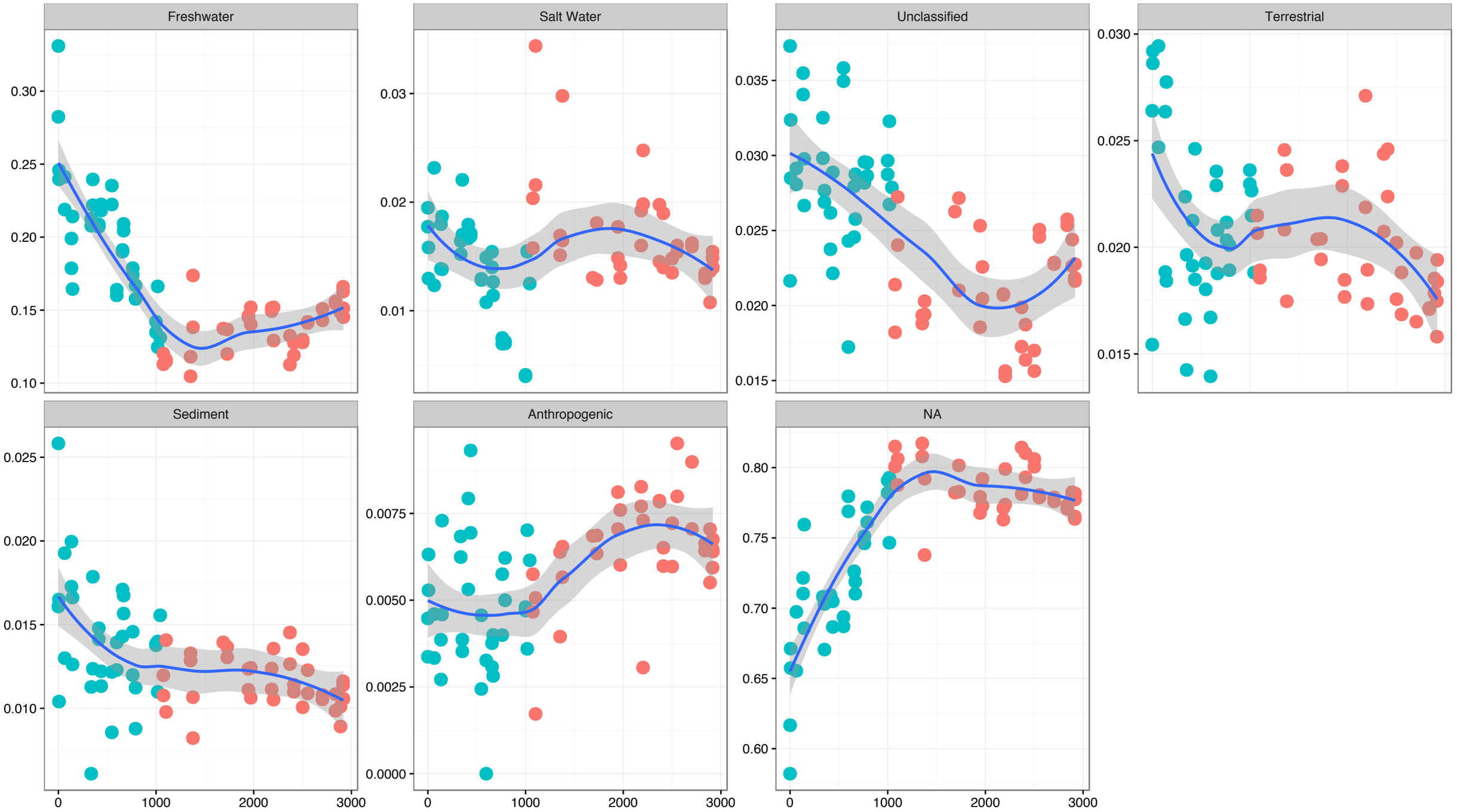

Observed
Chao1
ACE
Shannon
Simpson
InvSimpson
Fisher
Distance

D

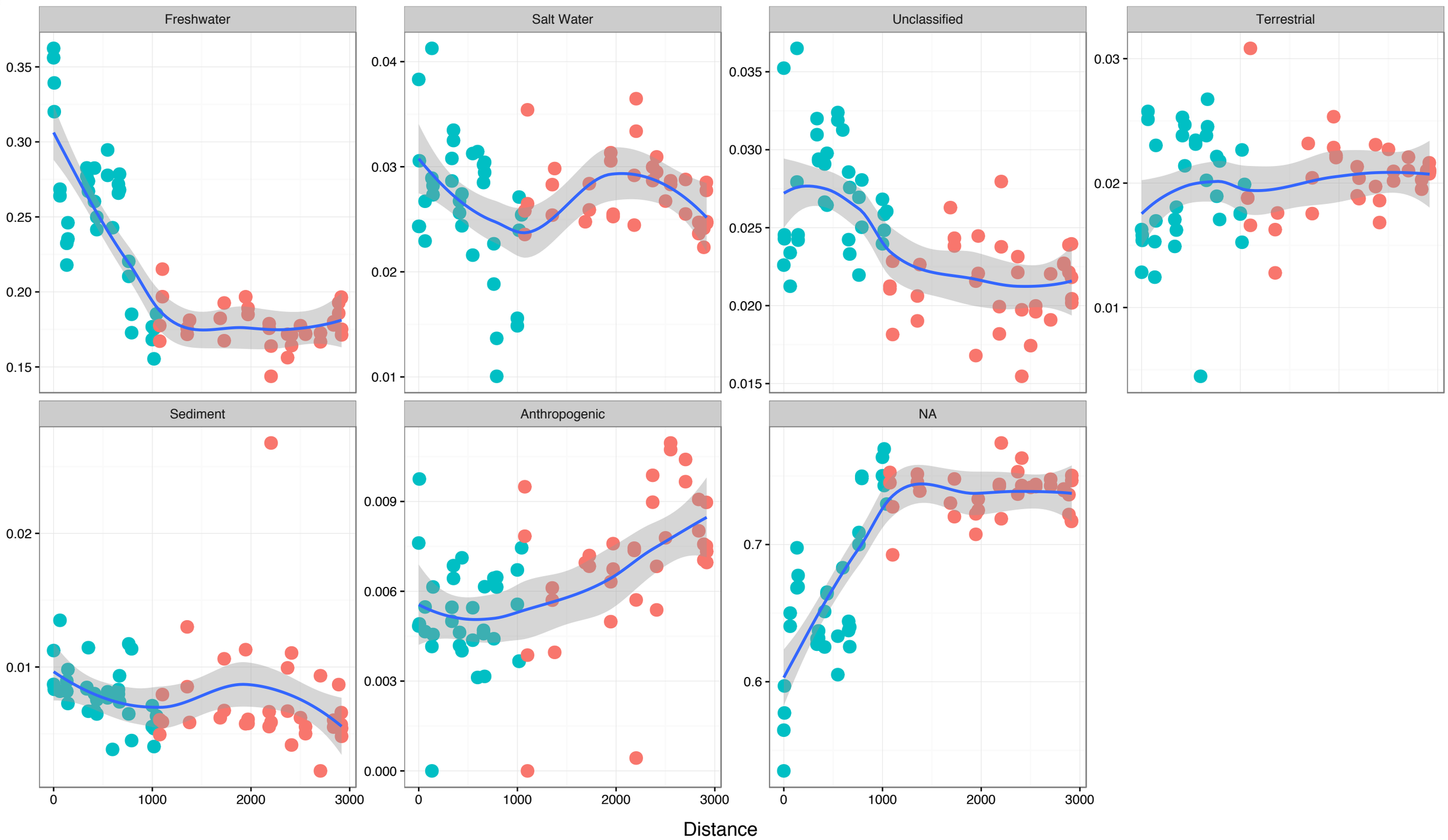

Observed
Chao1
ACE
Shannon
Simpson
InvSimpson
Fisher
Distance


>2.7μm
0.2-2.7μm
Percent Core
0.6
0.5
0.4
0.3
0.2
0
1000
2000
3000
Distance (km)

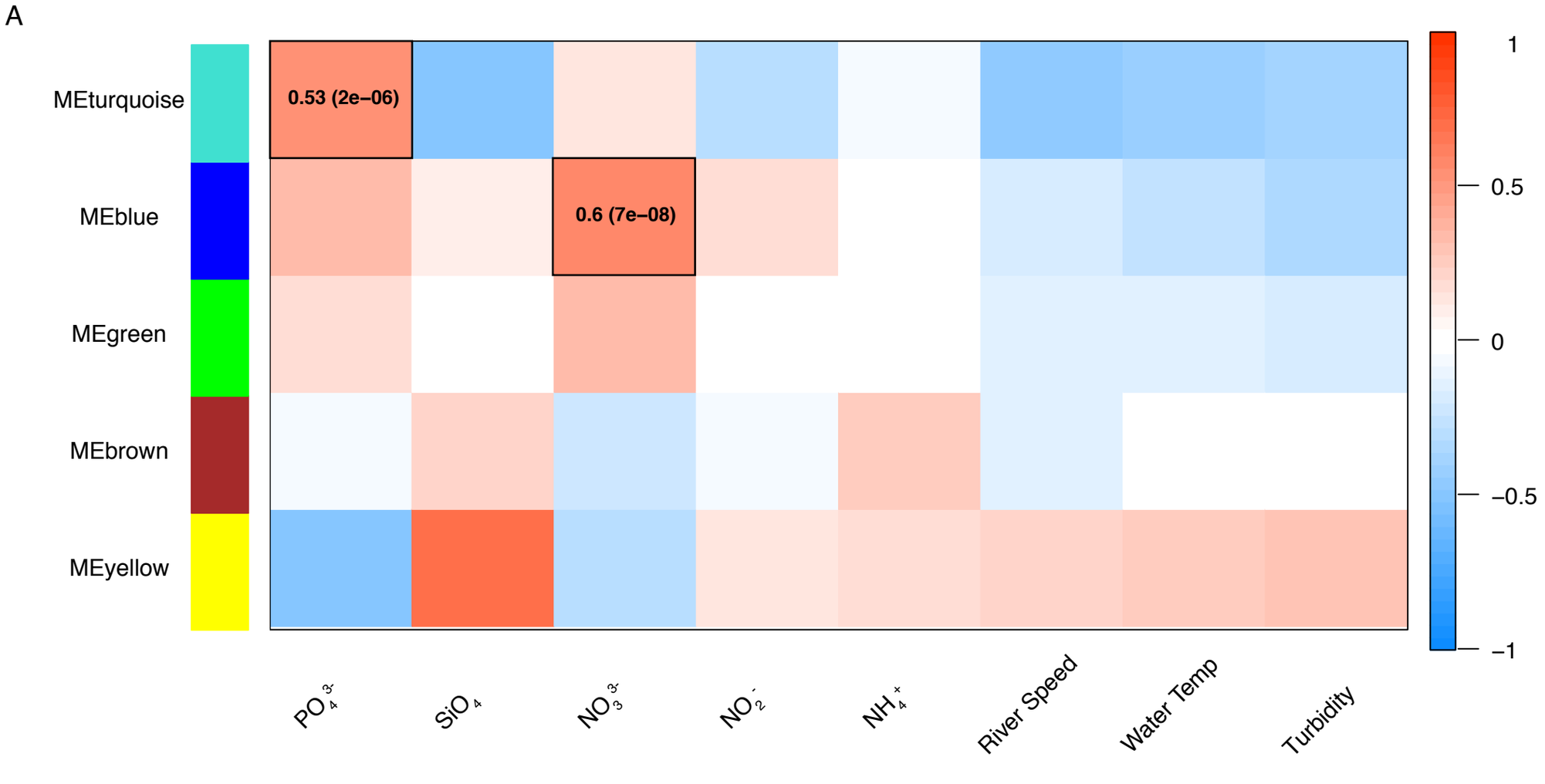
A


Freshwater
Salt Water
Unclassified
Terrestrial
Sediment
Anthropogenic
NA
Relative abundance
0
1000
2000
3000

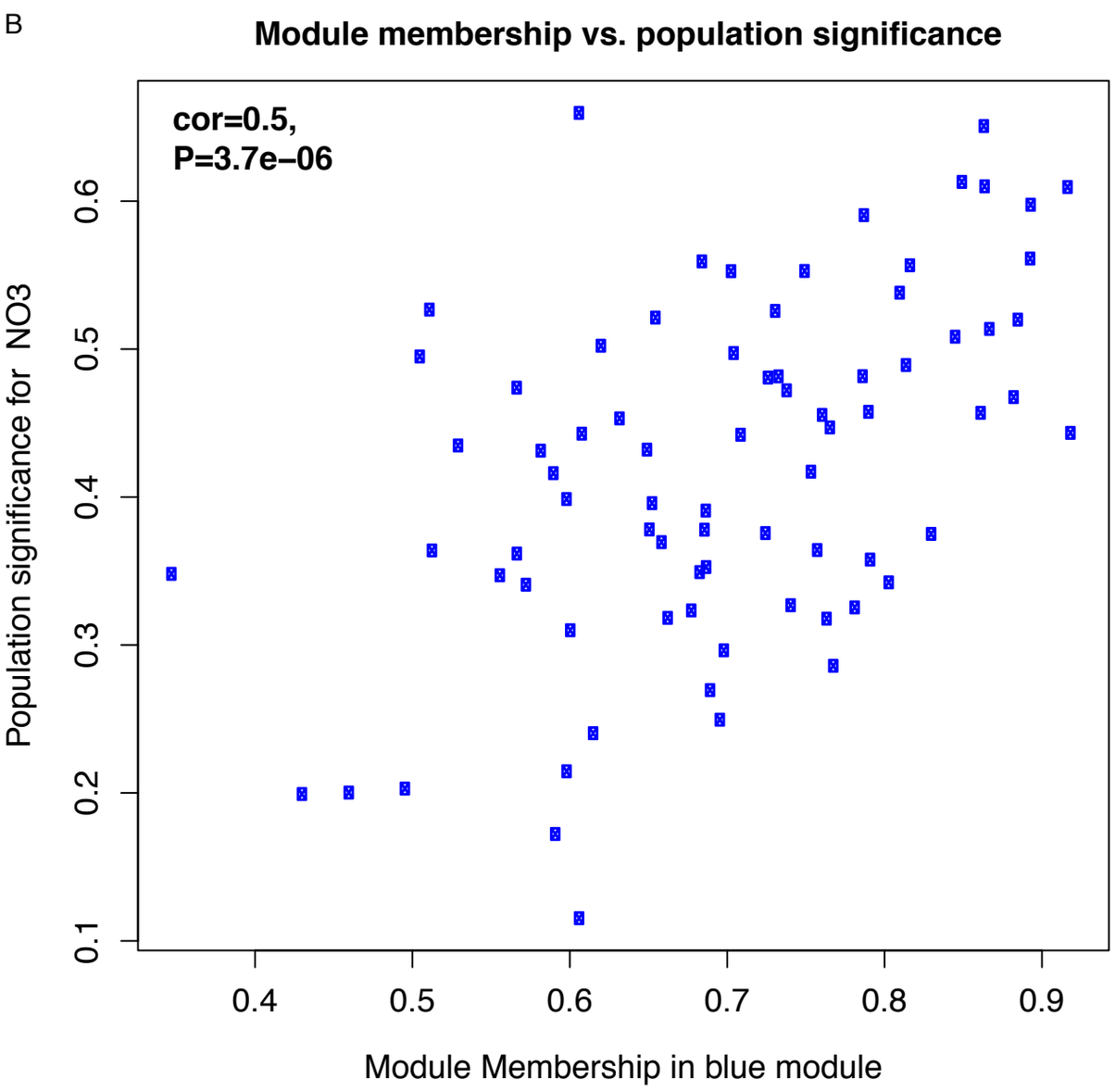
B


Freshwater
Salt Water
Unclassified
Terrestrial
Sediment
Anthropogenic
NA
Distance
0
1000
2000
3000

A


MEturquoise
MEblue
MEgreen
MEbrown
MEyellow
0.53 (2e−06)
0.6 (7e−08)
1
0.5
0
−0.5
−1
PO4 3-
SiO4
NO3 3-
NO2 -
NH4 +
River Speed
Water Temp
Turbidity

B


Module membership vs. population significance
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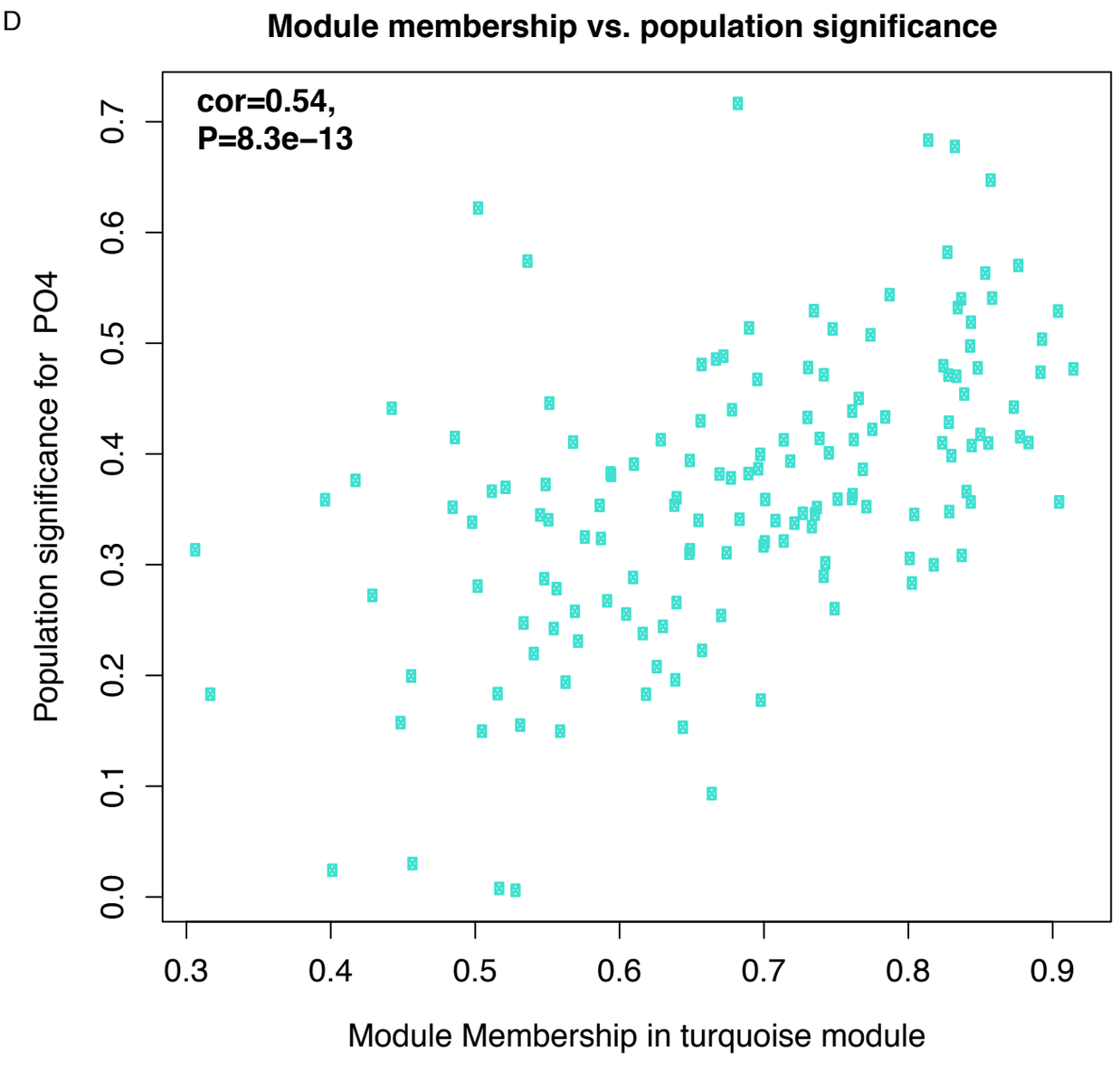
P=3.7e−06
Population significance for NO3
0.1
0.2
0.3
0.4
0.5
0.6
0.4
0.5
0.6
0.7
0.8
0.9
Module Membership in blue module

D


Module membership vs. population significance
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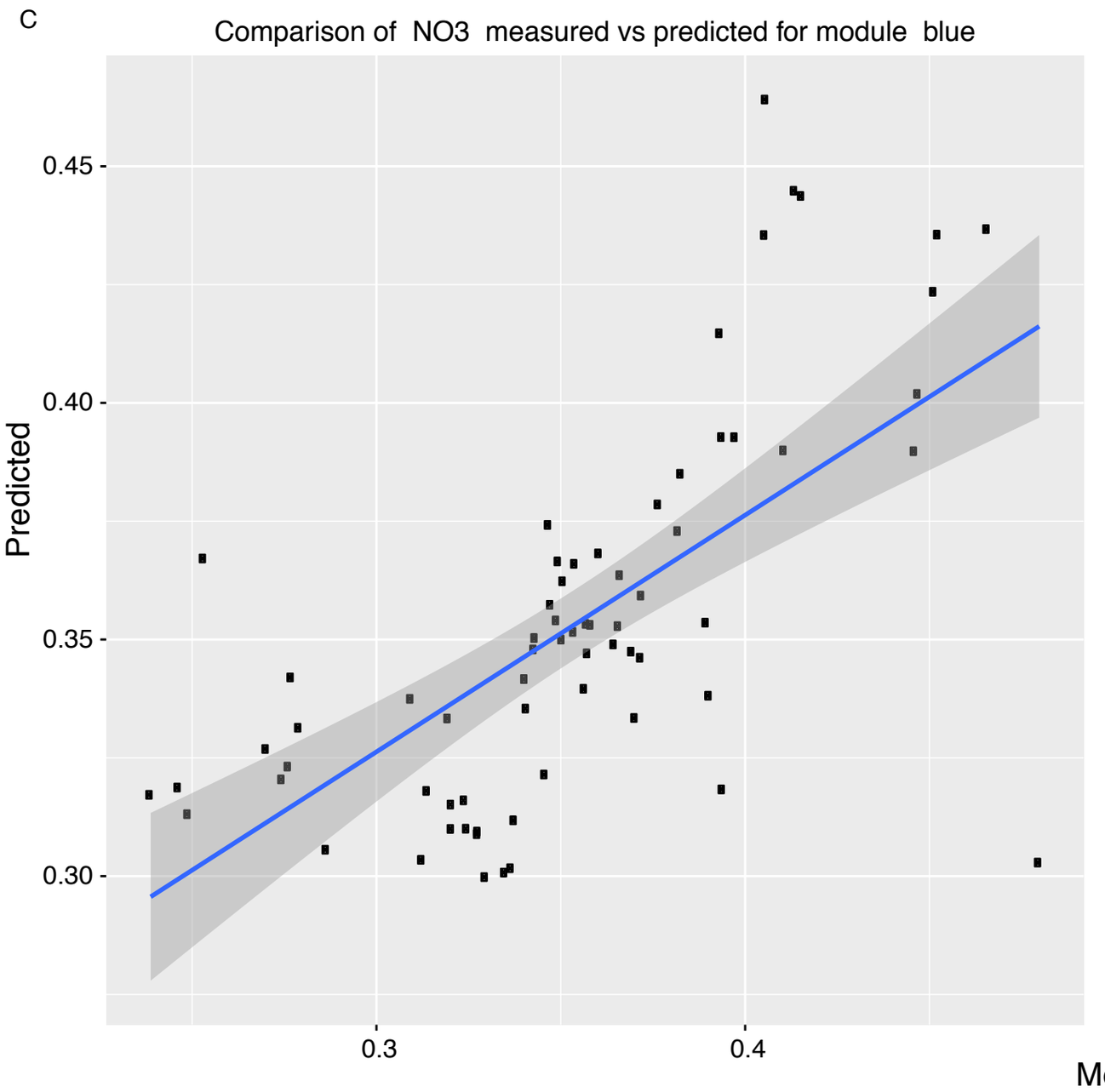
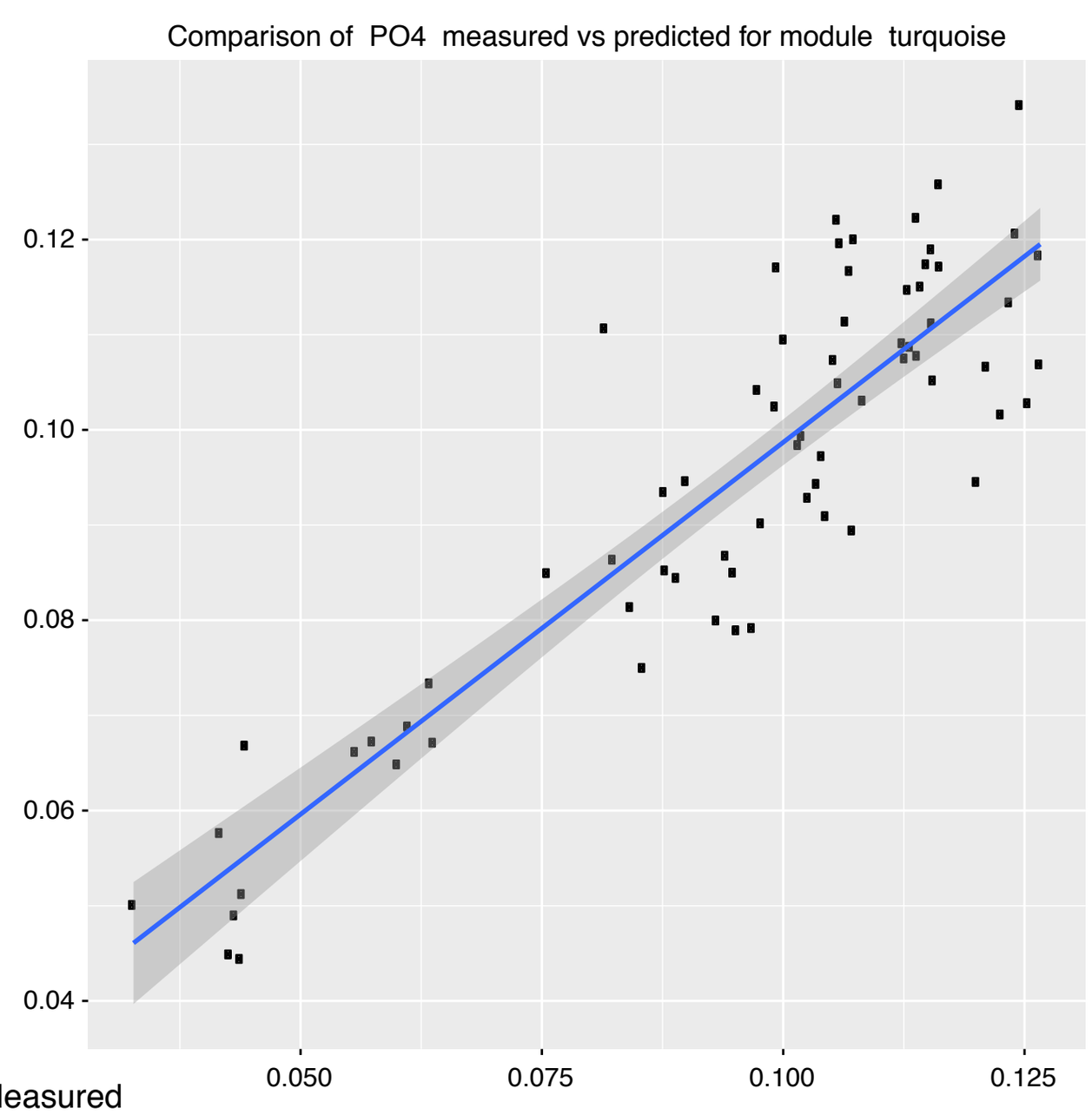
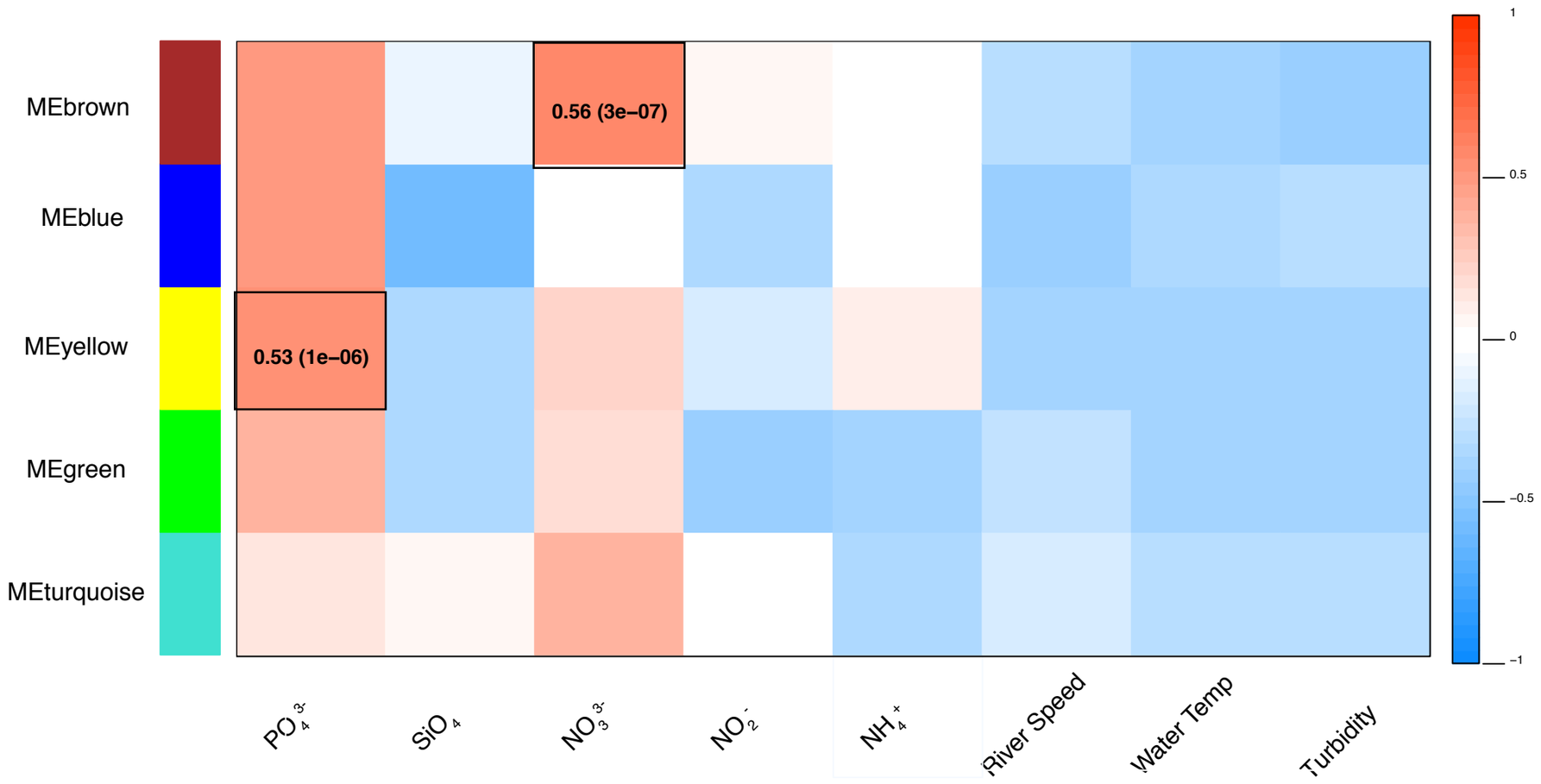
P=8.3e−13
Population significance for PO4
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Module Membership in turquoise module

C

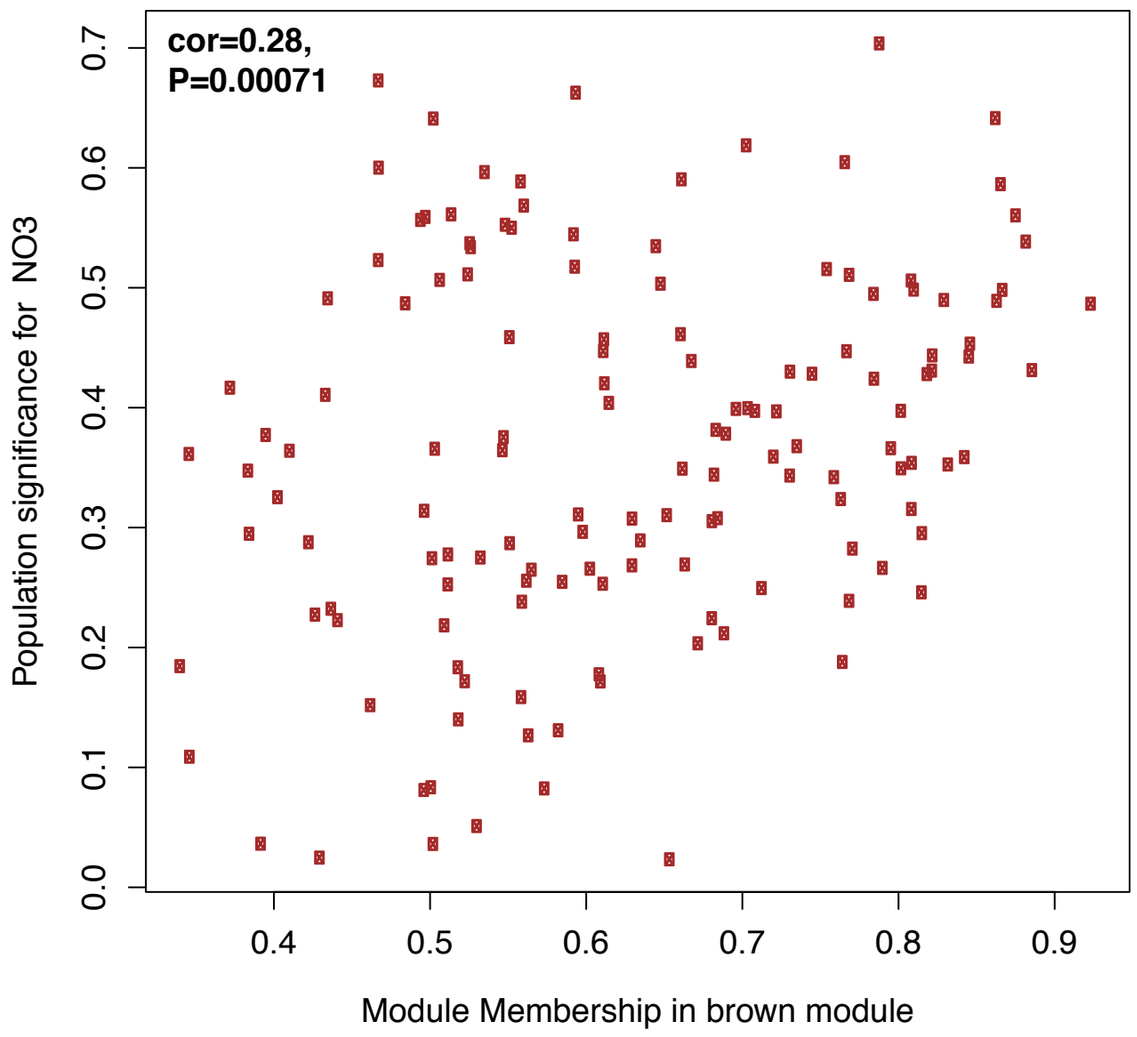

Comparison of NO3 measured vs predicted for module blue
Predicted
0.30
0.35
0.40
0.45
0.3
0.4


Comparison of PO4 measured vs predicted for module turquoise
0.04
0.06
0.08
0.10
0.12
0.050
0.075
0.100
0.125
Measured

A


MEbrown
MEblue
MEyellow
MEgreen
MEturquoise
0.56 (3e−07)
0.53 (1e−06)
1
0.5
0
−0.5
−1
PO_4^{3-}
SiO_4
NO_3^{3-}
NO_2^-
NH_4^+
River Speed
Water Temp
Turbidity

B


Module membership vs. population significance
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P=0.00071
Population significance for NO3
Module Membership in brown module
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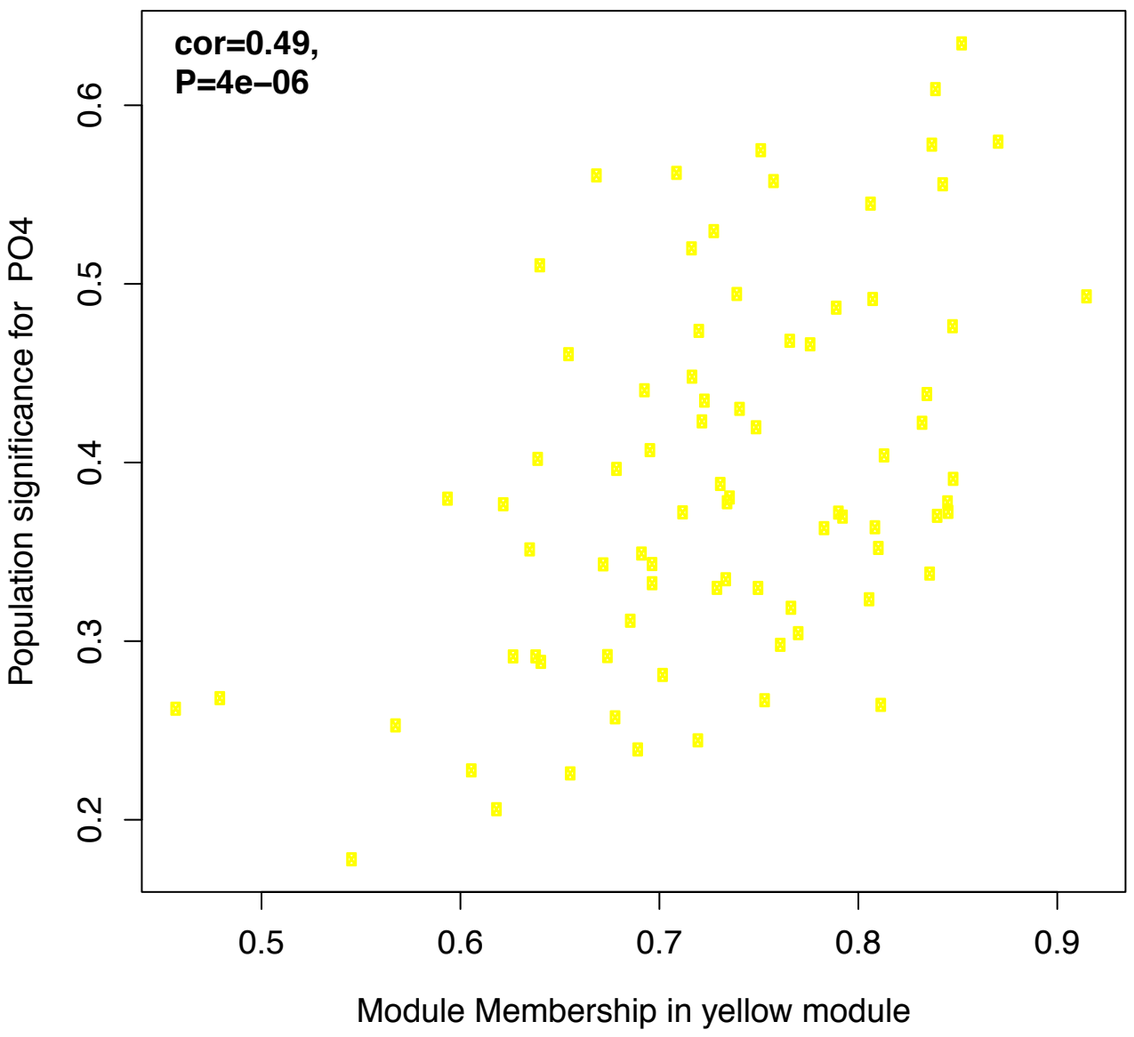
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.4
0.5
0.6
0.7
0.8
0.9

D


Module membership vs. population significance
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P=4e−06
Population significance for PO4
Module Membership in yellow module
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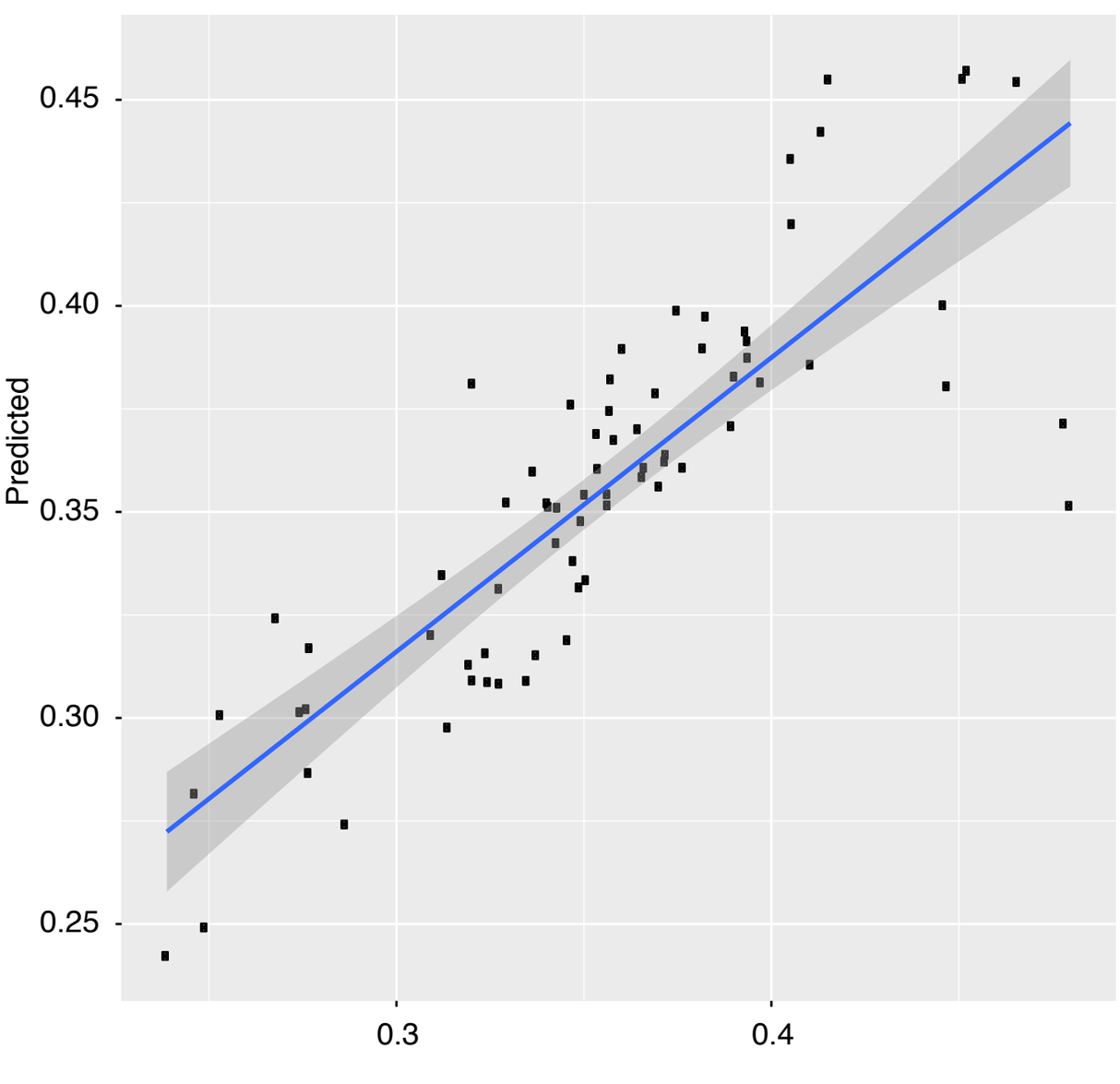
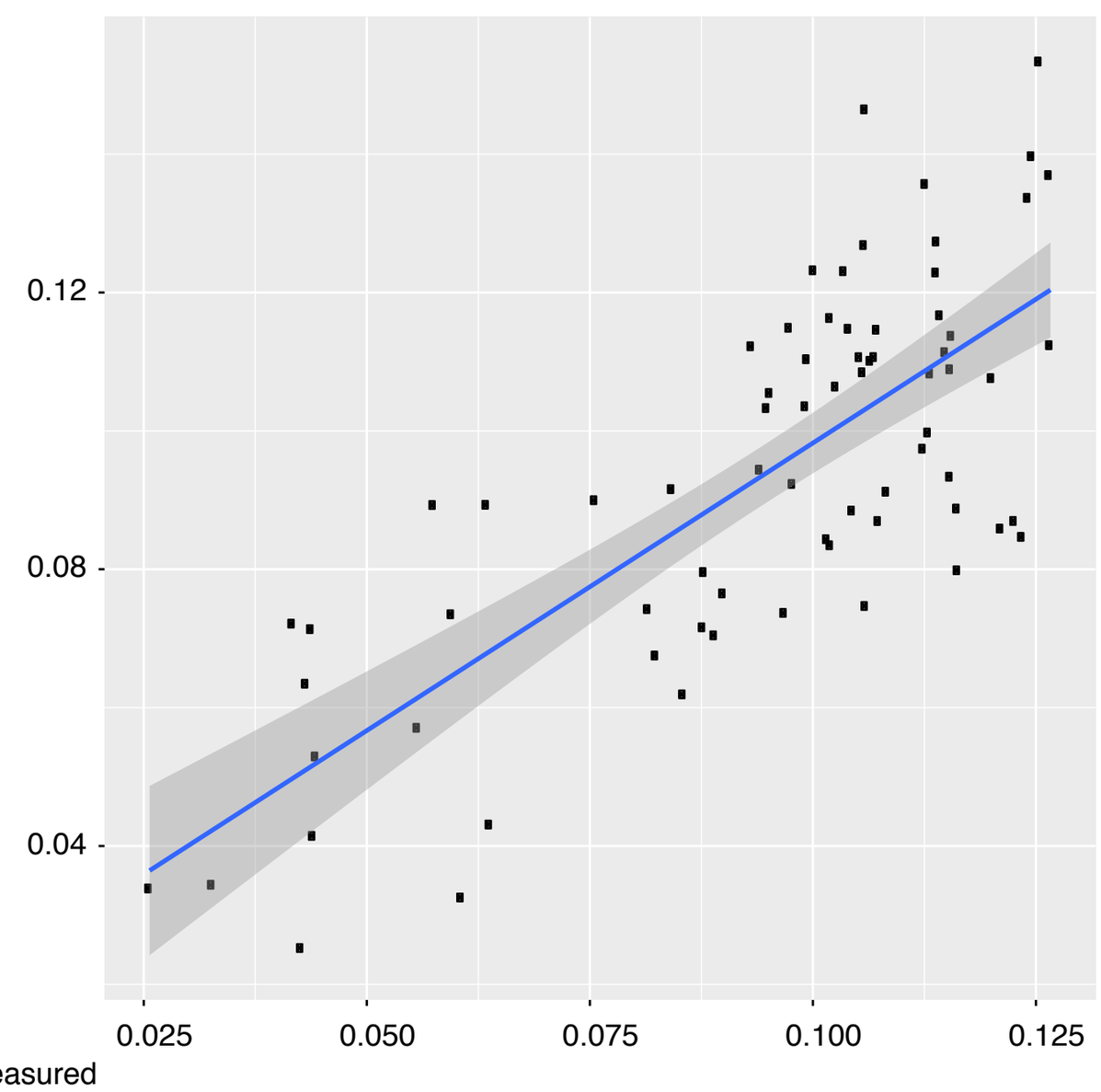
0.3
0.4
0.5
0.6
0.5
0.6
0.7
0.8
0.9

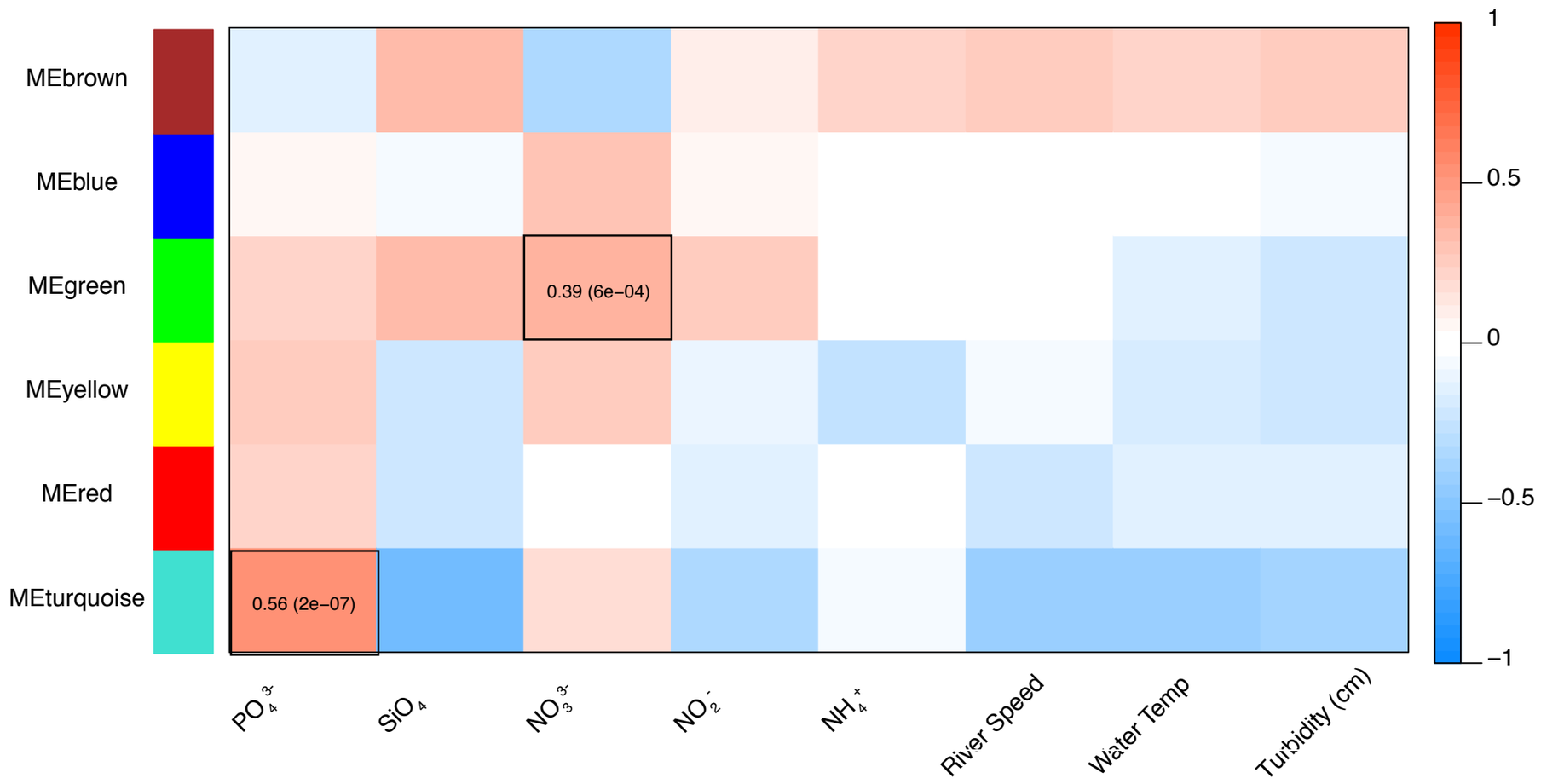
C


Comparison of NO3 measured vs predicted for module brown
Predicted
0.25
0.30
0.35
0.40
0.45
0.3
0.4

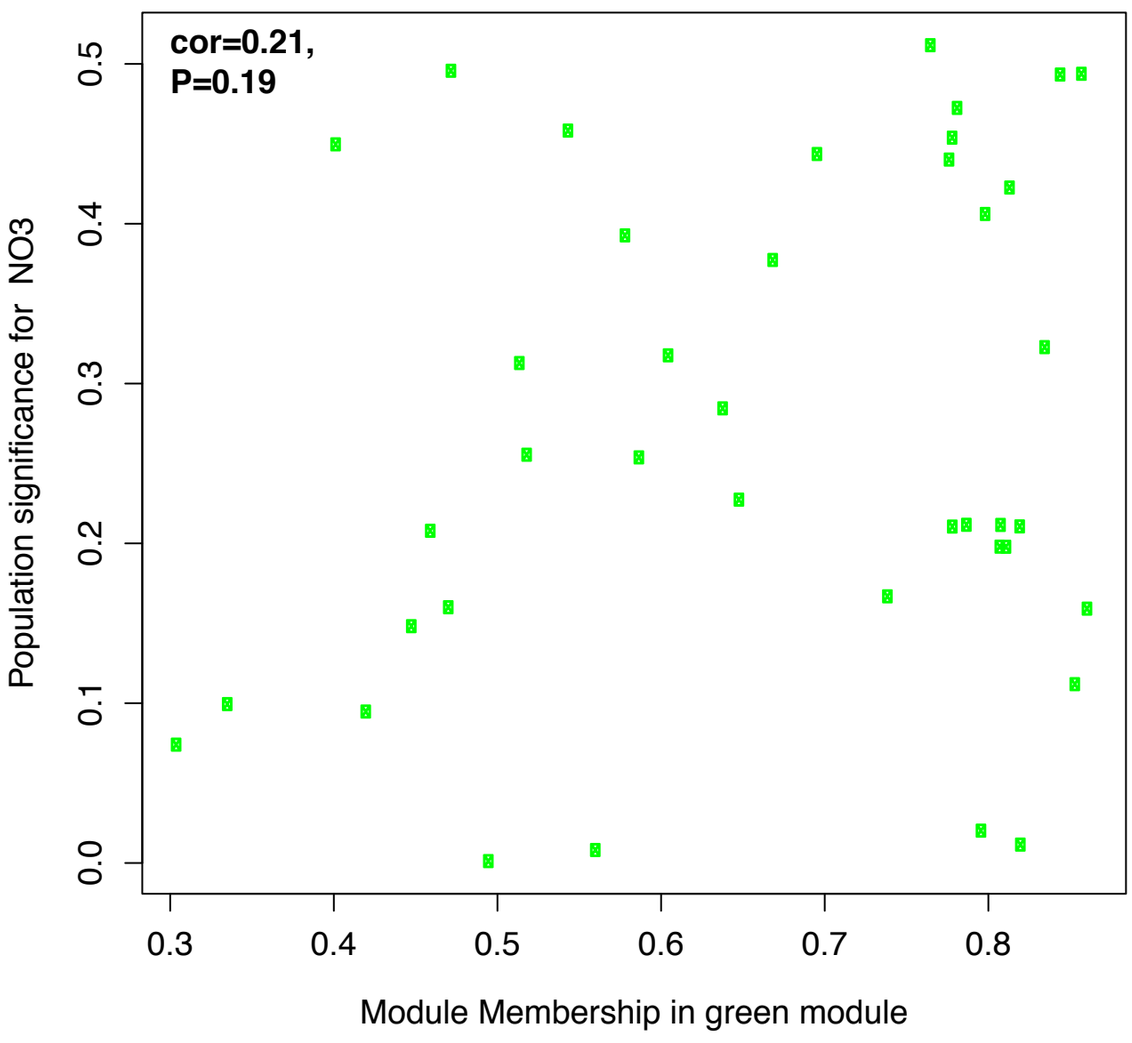
E


Comparison of PO4 measured vs. predicted for module yellow
Measured
0.04
0.08
0.12
0.025
0.050
0.075
0.100
0.125

A


MEbrown
MEblue
MEgreen
MEyellow
MEred
MEturquoise
0.39 (6e−04)
0.56 (2e−07)
1
0.5
0
−0.5
−1
PO_4^{3-}
SiO_4
NO_3^{3-}
NO_2^-
NH_4^+
River Speed
Water Temp
Turbidity (cm)

B


Module membership vs. population significance
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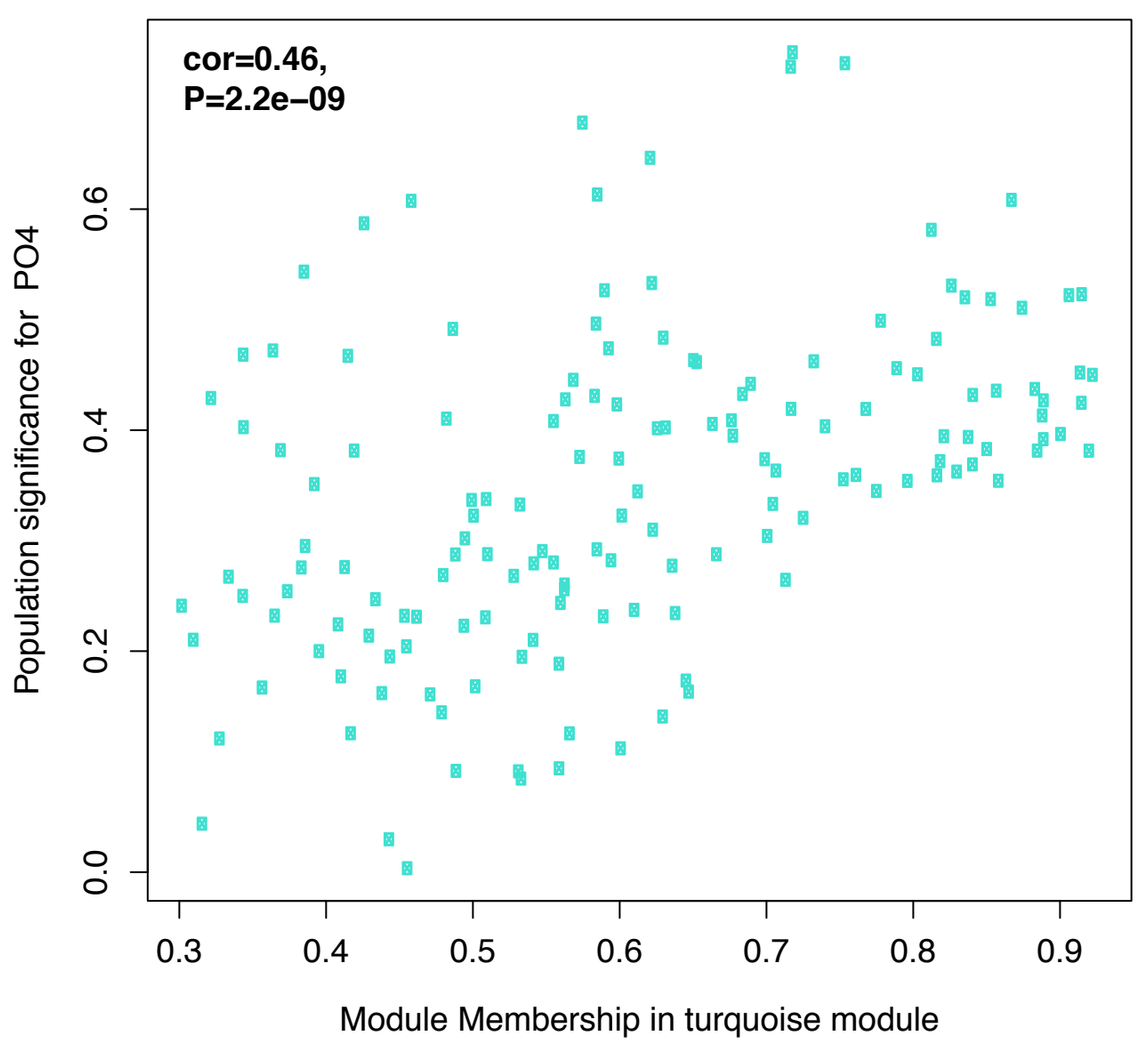
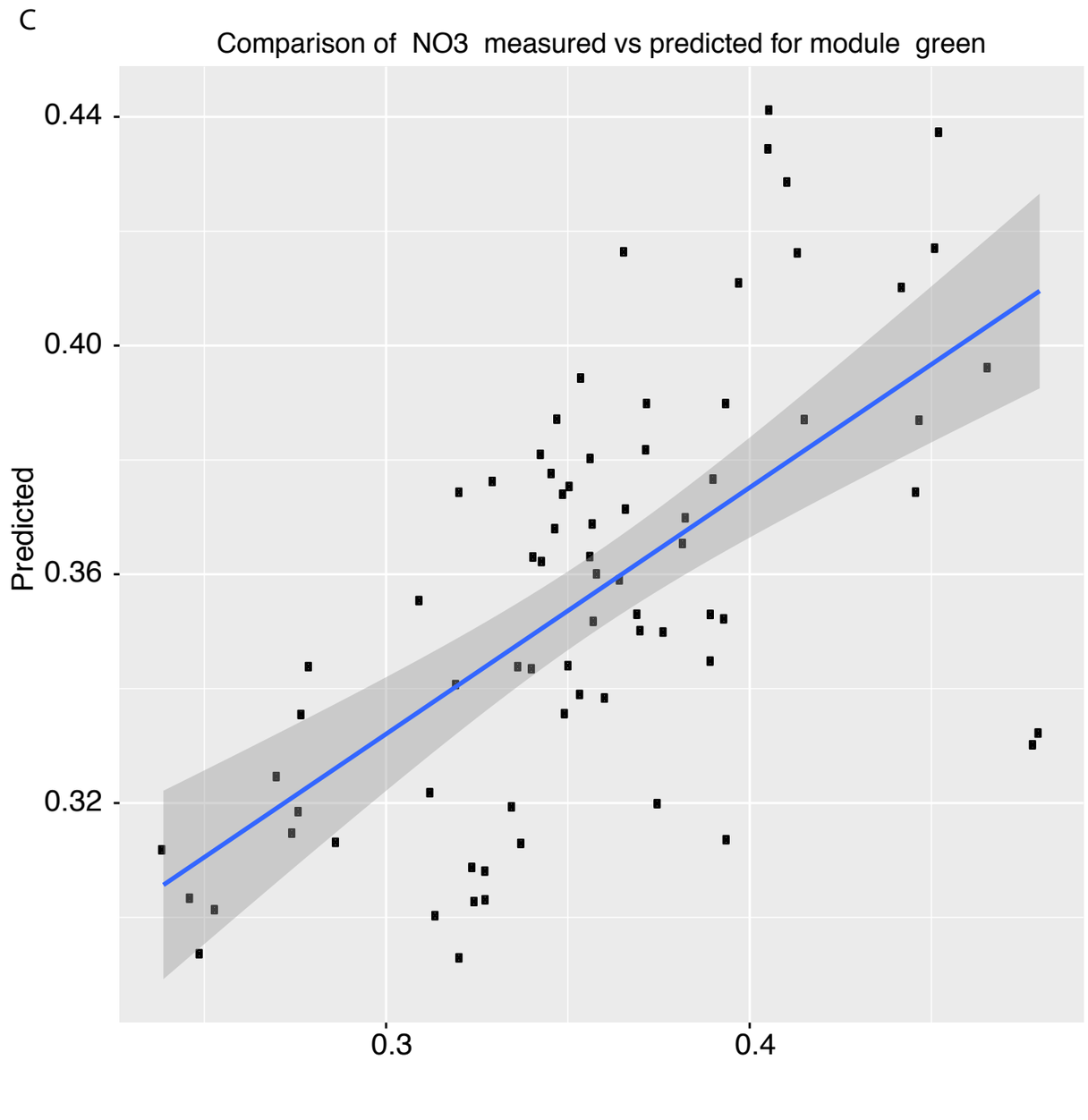
P=0.19
Population significance for NO3
0.0
0.1
0.2
0.3
0.4
0.5
0.3
0.4
0.5
0.6
0.7
0.8
Module Membership in green module

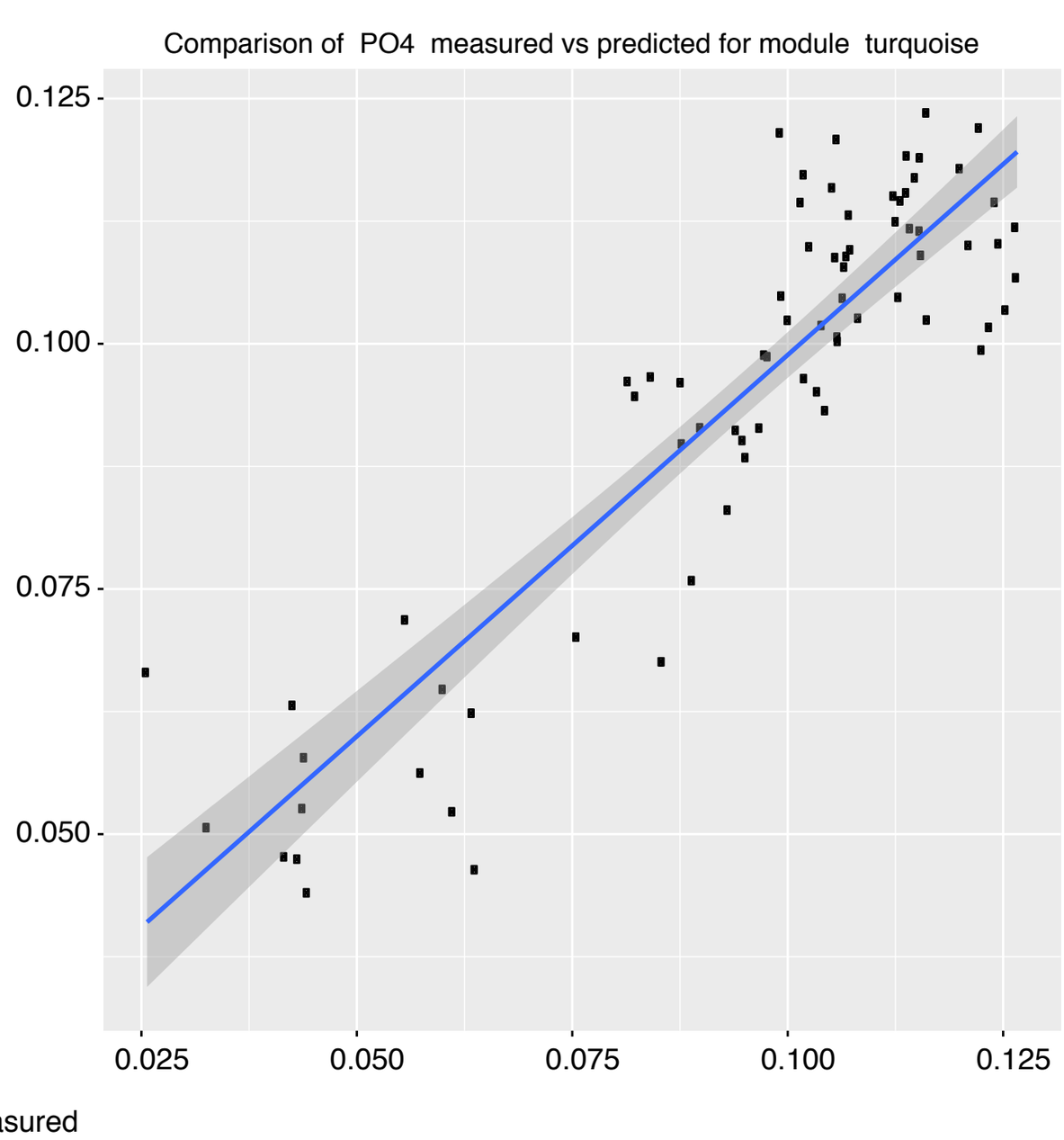
D


Module membership vs. population significance
cor=0.46,
P=2.2e−09
Population significance for PO4
0.0
0.2
0.4
0.6
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Module Membership in turquoise module

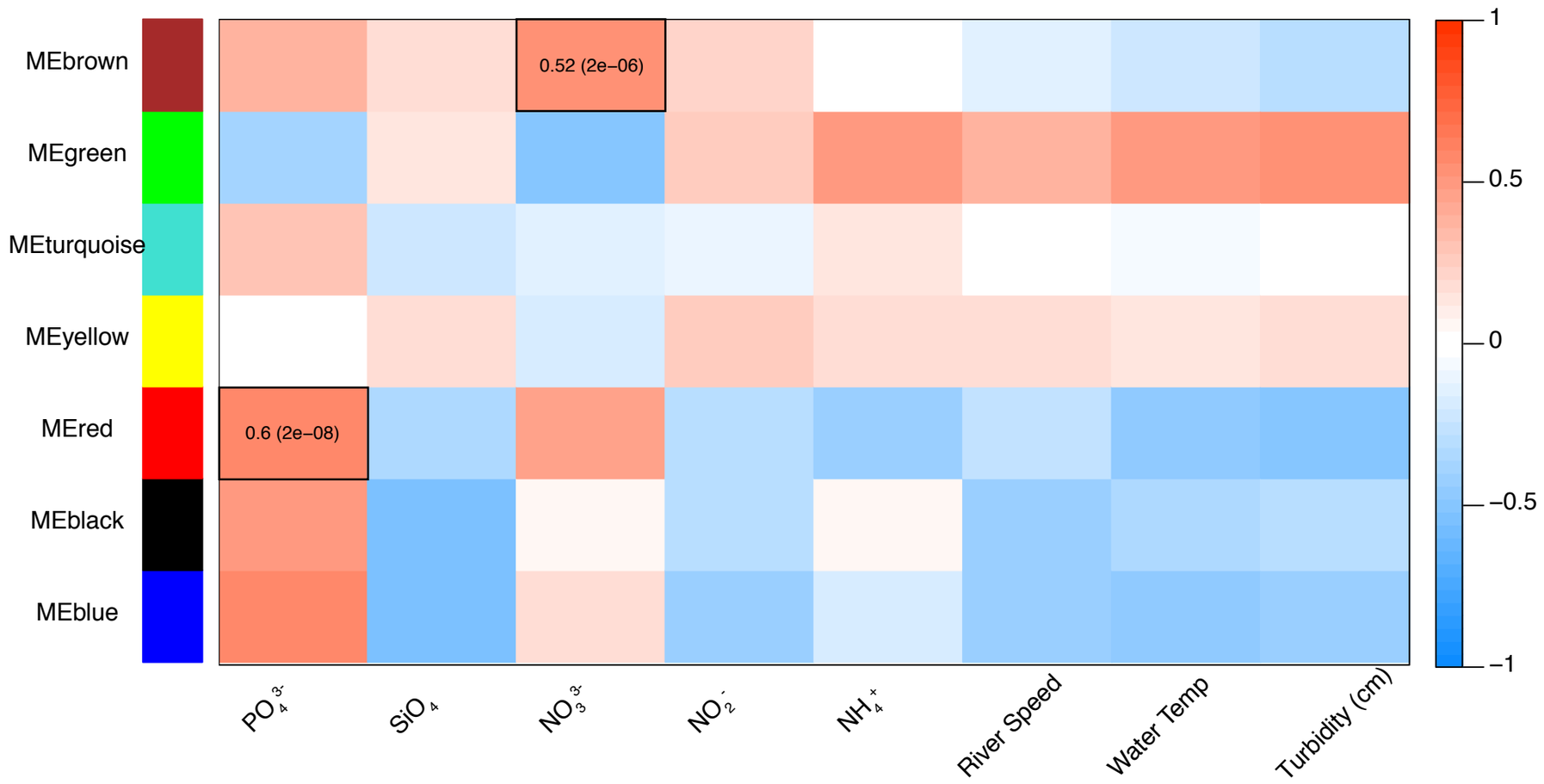
C


Comparison of NO3 measured vs predicted for module green
Predicted
0.32
0.36
0.40
0.44
0.3
0.4

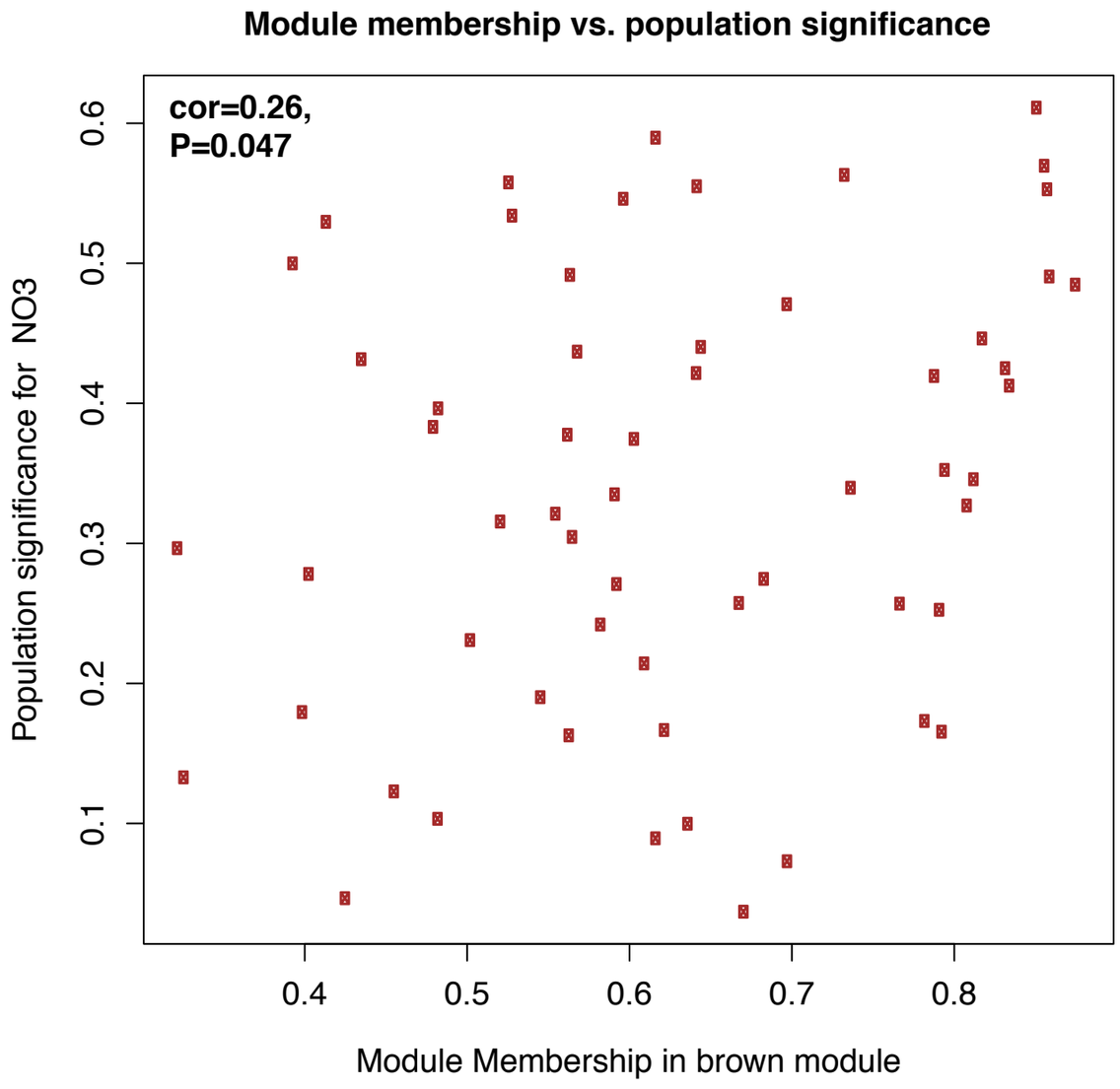
E


Comparison of PO4 measured vs predicted for module turquoise
0.050
0.075
0.100
0.125
0.025
0.050
0.075
0.100
0.125
Measured

A


MEbrown
MEgreen
MEturquoise
MEyellow
MEred
MEblack
MEblue
0.52 (2e−06)
0.6 (2e−08)
1
0.5
0
−0.5
−1
PO4 3-
SiO4
NO3 3-
NO2 -
NH4 +
River Speed
Water Temp
Turbidity (cm)

B


Module membership vs. population significance
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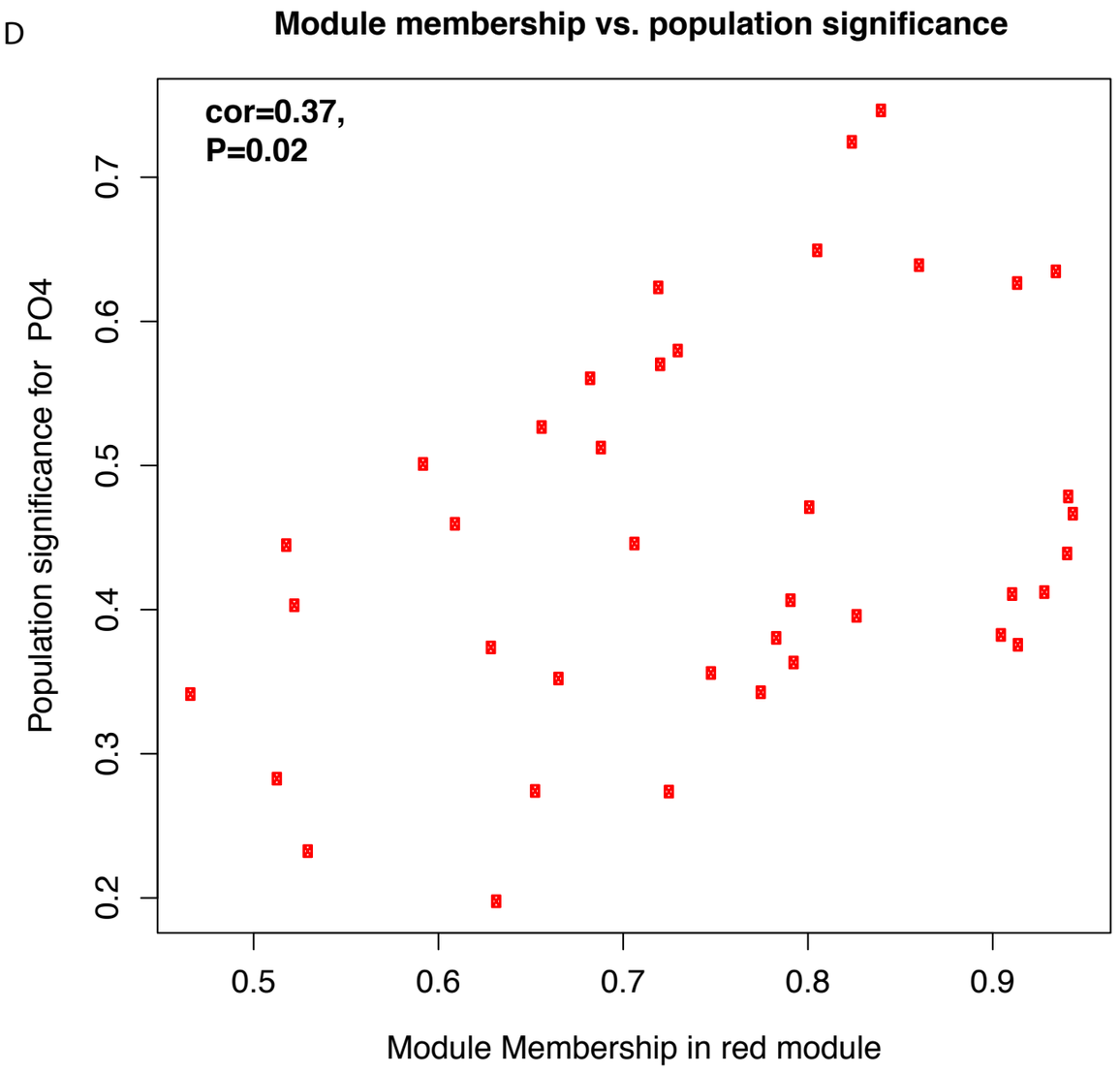
P=0.047
Population significance for NO3
0.1
0.2
0.3
0.4
0.5
0.6
0.4
0.5
0.6
0.7
0.8
Module Membership in brown module

D


Module membership vs. population significance
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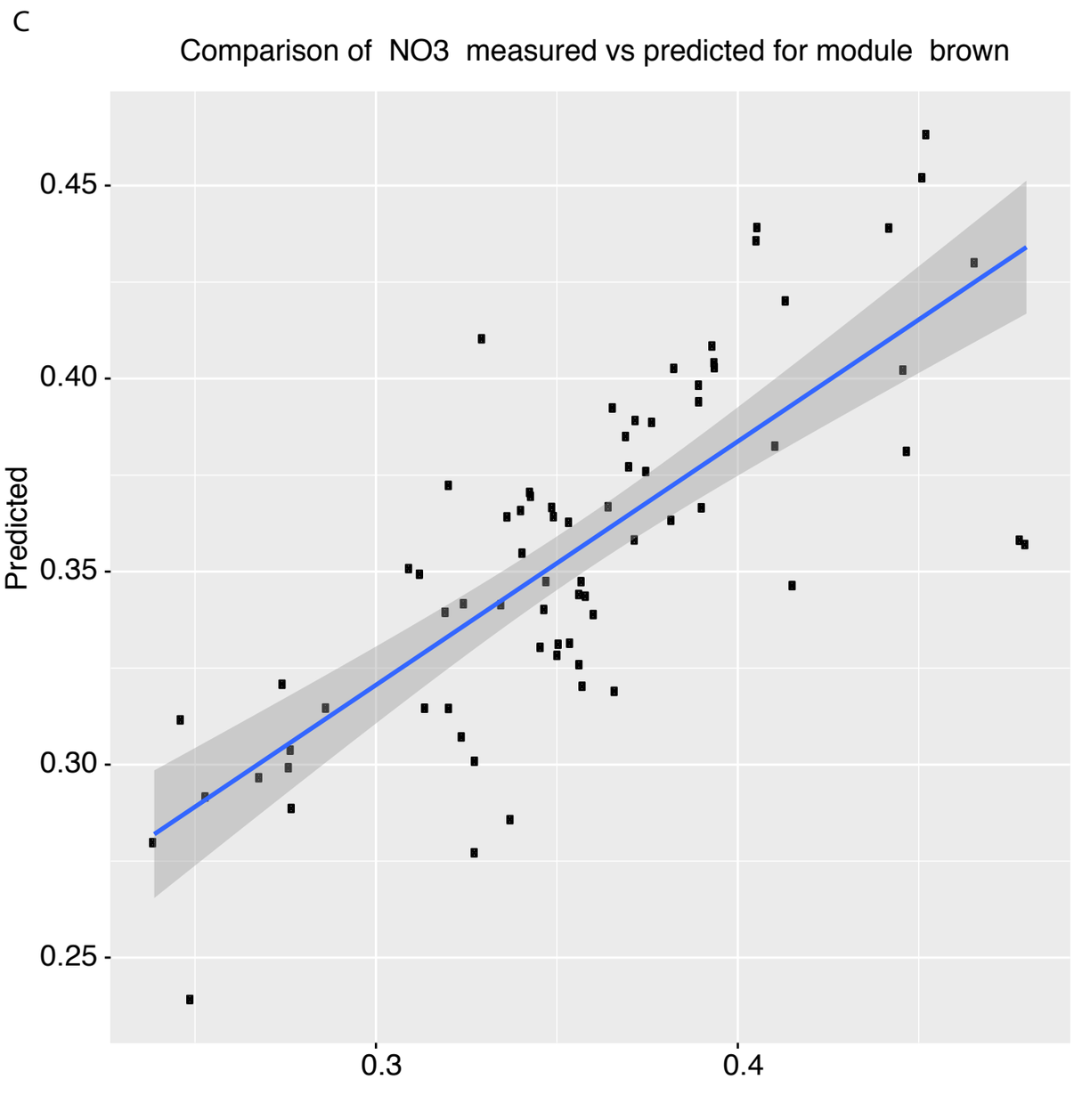
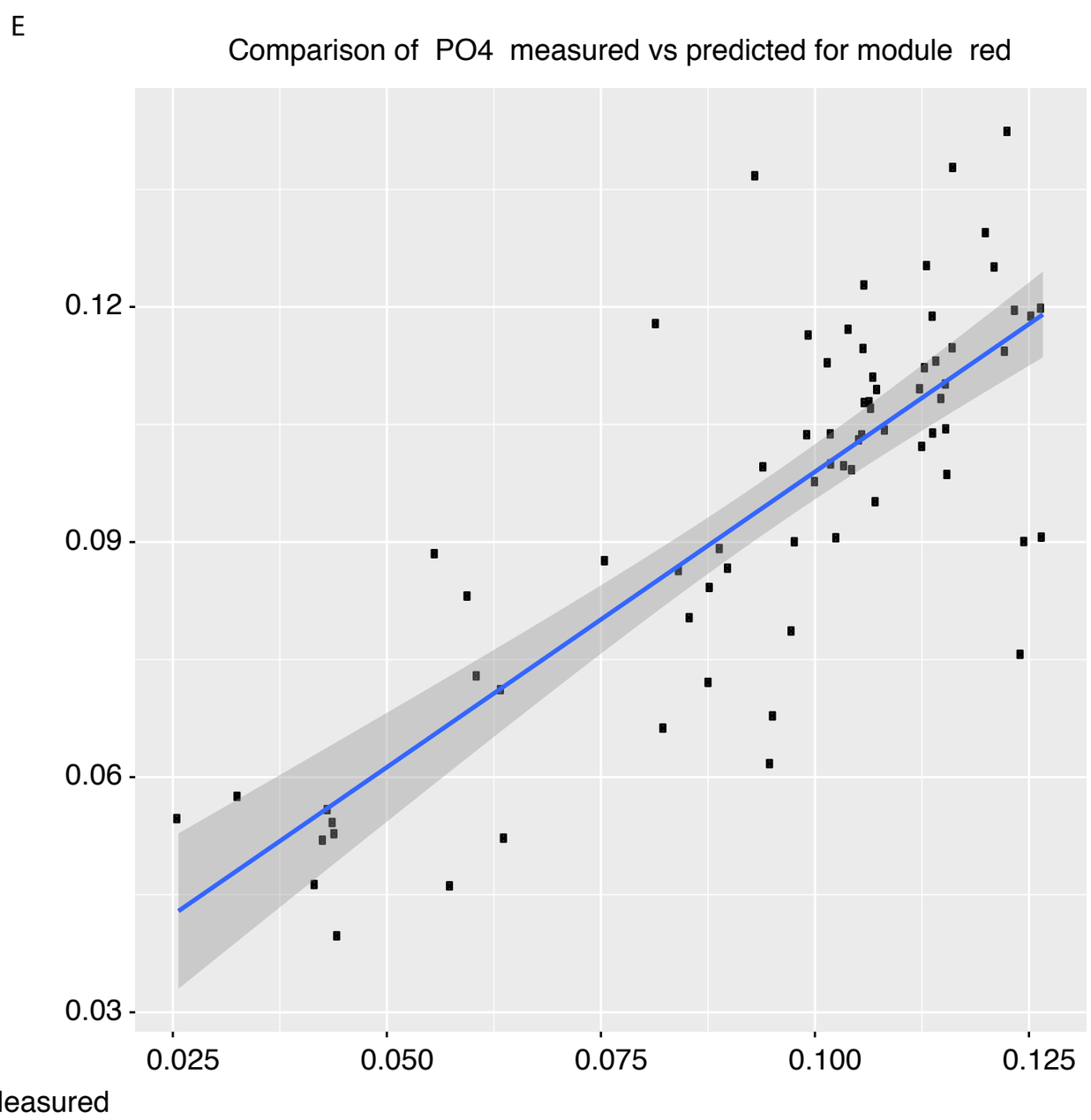
P=0.02
Population significance for PO4
0.2
0.3
0.4
0.5
0.6
0.7
0.5
0.6
0.7
0.8
0.9
Module Membership in red module

C


Comparison of NO3 measured vs predicted for module brown
Predicted
0.25
0.30
0.35
0.40
0.45
0.3
0.4

E


Comparison of PO4 measured vs predicted for module red
0.03
0.06
0.09
0.12
0.025
0.050
0.075
0.100
0.125
Measured