

Occurrence and potential biological effects of amphetamine on stream communities.

Sylvia S. Lee, Alexis M. Paspalof, Daniel D. Snow, Erinn K. Richmond, Emma J. Rosi-Marshall, and John J. Kelly

Supporting Information Table of Contents

S1: Supporting Information 1 Pharmaceutical analysis

- Pages 2-5, Tables 1-2

S2: Supporting Information 2 Analysis of stream community responses to AMPH Page 6

A. SAS code for selection of expected response distributions (proc univariate).

- Pages 7-10

B. Selected proc univariate output and selected distributions.

- Pages 11-62, figures S2B.1.1 – S2B.11.2, tables S2B.1.1 - S2B.12.1

C. SAS code for generalized linear mixed models (proc glimmix).

- Pages 63-66

D. Selected proc glimmix output.

- Pages 67-99, figures S2D.1.1 – S2D.11.2, tables S2D.1.1 – S2D.11.2

S3. Supporting Information 3 Power analysis (post hoc)

Page 100

S4. Supporting Information 4 Bacterial and diatom community analysis

Pages 101-106, figure 1, tables 1-2

Supporting Information 1.

Pharmaceutical Analysis

All water samples were extracted and analyzed using the following procedures.

Methods and Materials

Standard compounds, purchased from Sigma Aldrich (St. Louis, MO) and Cerilliant, included D-amphetamine (AMPH), methamphetamine, MDMA (3,4-methylenedioxy-methamphetamine), acetaminophen, caffeine, 1,7-dimethylxanthine, diphenhydramine, cimetidine, sulfamethoxazole, sulfadimethoxine, cotinine, morphine, carbamazepine, and thiabendazole. Labeled internal standards ($^{13}\text{C}_3$ -caffeine, methamphetamine-d8, MDMA-d8, morphine-d3, and $^{13}\text{C}_6$ -sulfamethazine) were purchased from Cerilliant (Round Rock, TX) and Cambridge Isotopes (Tewksbury, MA).

Surface water samples were collected in pre-cleaned 250 mL amber glass jars from each site and chilled on ice until they could be frozen upon return to the laboratory. Thawed samples were filtered using a Whatman 25 mm GF/F glass fiber filter, and then a 100 mL portion weighed for polymeric solid phase extraction (SPE) with Oasis 200 mg HLB sorbent (Waters Corporation, Milford, MA). Cartridges were conditioned with 6 mL each of high purity acetone, methanol (OptimaTM grade, Fisher Scientific, St. Louis, MO, USA), followed by 6 mL of purified reagent water (Barnstead Nanopure, Dubuque, IA, USA). Cartridges were eluted with 6 mL acetone, followed by 6 mL of methanol, and the eluates were concentrated under vacuum and constant stream of nitrogen gas. Residues were dissolved in 200 μL methanol:water (50:50) and fortified with 100 ng of internal standards.

Extracts were analyzed using multiple reaction monitoring (MRM) using liquid chromatography tandem mass spectrometry (LC-MS/MS) on a Quattro Micro triple quadrupole mass spectrometer interfaced with a Waters 2695 HPLC. Gradient separation used a Thermo HyPURITY C18 column (250 mm \times 2.1 mm ID, 5 μm particle size) at a temperature of 50°C and a flow rate of 0.20 ml/min. Mobile phase solvents: A)

methanol with 8mM ammonium formate and B) 8mM ammonium formate in reagent water. Initial conditions at 0%A, hold until 3.0 min, then a stepwise increase to 60%A followed by linear gradient to reach 95%A at 12.0 min, hold 6 min, then immediately back to initial conditions (0%A), hold for 8 min. The Quattro-Micro mass spectrometer with an ESI (electrospray ionization) source was operated in positive ion mode under the following conditions: 1) collision gas: argon at 4.0×10^{-3} torr; 2) desolvation gas: nitrogen at 600 L hr^{-1} ; 3) cone gas: nitrogen at 30 L hr^{-1} ; 4) source temperature: 125°C . 5) capillary volatage: 4 kV. Cone voltages and collision energies used for each standard and analyte are given in SI Table 1. Method detection limits, determined from repeated analysis of a low-level ($0.005 \mu\text{g L}^{-1}$) fortified water sample, ranged from 0.001 to $0.017 \mu\text{g L}^{-1}$ (SI Table 2).

S1 Table 1. Cone voltages, collision energies, and other details pertaining to standards and analytes.

Compound	Formula	MW (g mol ⁻¹)	Parent Ion (m/z)	Product Ion (m/z)	Cone Volta ge (V)	Collis- ion Energ y (eV)	Reten- tion time (min)
1,7-Dimethylxanthine	C ₇ H ₈ N ₄ O ₂	180.16	181	123.9	32	20	10.20
Caffeine	C ₈ H ₁₀ N ₄ O ₂	194.19	195	137.95	32	18	10.74
Caffeine- ¹³ C ₃ *	¹³ C ₃ C ₅ H ₁₀ N ₄ O ₂	197.19	198	139.95	37	19	10.74
Cotinine	C ₁₀ H ₁₂ N ₂ O	176.22	177	79.8	36	22	10.61
Carbamazepine	C ₁₅ H ₁₂ N ₂ O	236.27	237.05	194	32	22	13.27
Diphenhydramine	C ₁₇ H ₂₁ NO	255.36	256.1	167.05	25	20	13.47
Thiabendazole	C ₁₀ H ₇ N ₃ S	201.25	201.9	174.9	35	24	12.35
Acetaminophen	C ₈ H ₉ NO ₂	151.16	151.9	109.9	30	14	9.60
d-Amphetamine	C ₉ H ₁₃ N	135.21	136	90.8	18	15	10.96
Methamphetamine	C ₁₀ H ₁₅ N	149.23	150	90.8	20	25	11.04
Methamphetamine-d ₈ *	² H ₈ C ₁₀ H ₇ N	157.23	158.05	92.8	20	19	11.01
MDMA	C ₁₁ H ₁₅ NO ₂	193.25	194.05	163	20	13	10.93
MDMA-d ₅ *	² H ₅ C ₁₀ H ₁₀ NO ₂	198.25	199.05	165	20	13	10.91
MDA	C ₁₀ H ₁₃ NO ₂	179.22	180.05	163	13	10	10.88
			180.05	105	13	22	10.88
Morphine	C ₁₇ H ₁₉ NO ₃	285.34	286	165	45	38	10.88
Morphine-d ₃ *	² H ₃ C ₁₇ H ₁₆ NO ₃	288.34	289	165	45	38	10.80
Sulfamethazine	C ₁₂ H ₁₄ N ₄ O ₂ S	278.33	279.1	155.95	30	18	10.77
Sulfamethazine- ¹³ C ₆ *	¹³ C ₆ C ₆ H ₁₄ N ₄ O ₂ S	284.33	285.1	123.95	30	25	10.77
Sulfadimethoxine	C ₁₂ H ₁₄ N ₄ O ₄ S	310.33	311.05	155.95	28	20	10.99
Sulfamethoxazole	C ₁₀ H ₁₁ N ₃ O ₃ S	253.28	254.1	155.95	23	15	9.84
Cimetidine	C ₁₀ H ₁₆ N ₆ S	252.34	253.2	159.1	25	15	10.82

S1 Table 2. Method detection limits determined from replicate extraction and analysis of low-level ($0.005 \mu\text{g L}^{-1}$) fortified water samples (USEPA 1986).

Compound	MDL ($\mu\text{g L}^{-1}$)	AVG % Recovery	REL % S
1,7-Dimethylxanthine	0.0045	111.5	27.0
Acetaminophen	0.0018	120.8	10.1
Caffeine	0.0084	118.8	47.5
Carbamazepine	0.0020	56.95	23.6
Cimetidine	0.0005	140.6	2.5
Cotinine	0.0040	148.9	17.9
d-Amphetamine	0.0037	79.0	31.3
Diphenhydramine	0.0043	114.4	25.0
MDMA	0.0014	68.1	13.8
Methamphetamine	0.0025	80.6	20.1
Morphine	0.0022	44.2	33.2
Sulfadimethoxine	0.0012	87.9	9.1
Sulfamethoxazole	0.0017	123.6	8.6
Thiabendazole	0.0008	25.0	21.3

References

USEPA. 1986. "Guidelines for establishing test procedures for the analysis of pollutants—Definition and Procedure for the Determination of the Method Detection Limit—Revision 1.11." Electronic Code of Federal Regulations Title 40: Protection of Environment (Part 136): Appendix B to Part 136—Definition and Procedure for the Determination of the Method Detection Limit—Revision 131.111.

Supporting Information 2

Analysis of stream community responses to AMPH

Stream community response data were analyzed using generalized linear mixed models in SAS.

S2 includes the following sections:

- A. SAS code for selection of expected response distributions (proc univariate).
 - 1. Chlorophyll *a* biofilm
 - 2. Chlorophyll *a* seston
 - 3. Chlorophyll *a* per ash-free dry mass biofilm
 - 4. Chlorophyll *a* per ash-free dry mass seston
 - 5. Ash-free dry mass biofilm
 - 6. Ash-free dry mass seston
 - 7. Gross primary production biofilm
 - 8. Gross primary production seston
 - 9. Community respiration biofilm
 - 10. Community respiration seston
 - 11. Invertebrate emergence
 - 12. Selected distributions
- C. SAS code for generalized linear mixed models (proc glimmix).
- D. Selected proc glimmix output.

S2A. SAS code for selection of expected response distributions (proc univariate).

```
libname amph1 '/folders/myfolders';
proc contents data=amph1.metdata;
run;

/*Testing the goodness of fit of probability distributions to data distributions of each variable*/
/*null hypothesis: values are a random sample from the specified distribution.*/
    /***if p<0.1, distribution NOT supported.*/
    /***if p>0.1, distribution supported.*/
    /***higher number is better*/
proc univariate normal data=amph1.metdata;
    var chlabio;
    histogram / normal (mu=est)
        lognormal (theta=est sigma=est zeta=est)
        gamma (theta=est alpha=est)
        weibull (c=est theta=est sigma=est);
    qqplot / normal (mu=est);
    qqplot / lognormal (theta=est sigma=est zeta=est);
    qqplot / gamma (theta=est alpha=est);
    qqplot / weibull (c=est theta=est sigma=est);
run;

proc univariate normal data=amph1.metdata;
    var chlasses;
    histogram / normal (mu=est)
        lognormal (theta=est sigma=est zeta=est)
        gamma (theta=est alpha=est)
        weibull (c=est theta=est sigma=est);
    qqplot / normal (mu=est);
    qqplot / lognormal (theta=est sigma=est zeta=est);
    qqplot / gamma (theta=est alpha=est);
    qqplot / weibull (c=est theta=est sigma=est);
run;

proc univariate normal data=amph1.metdata;
    var afdbio;
    histogram / normal (mu=est)
        lognormal (theta=est sigma=est zeta=est)
        gamma (theta=est alpha=est)
        weibull (c=est theta=est sigma=est);
    qqplot / normal (mu=est);
    qqplot / lognormal (theta=est sigma=est zeta=est);
    qqplot / gamma (theta=est alpha=est);
    qqplot / weibull (c=est theta=est sigma=est);
run;

proc univariate normal data=amph1.metdata;
```

```

var afdmses;
histogram / normal (mu=est)
    lognormal (theta=est sigma=est zeta=est)
    gamma (theta=est alpha=est)
    weibull (c=est theta=est sigma=est)
    exponential(theta=est sigma=est);

qqplot / normal (mu=est);
qqplot / lognormal (theta=est sigma=est zeta=est);
qqplot / gamma (theta=est alpha=est);
qqplot / weibull (c=est theta=est sigma=est);
qqplot / exponential(theta=est sigma=est);
run;

proc univariate normal data=amph1.metdata;
var gppafdmBio;
histogram / normal (mu=est)
    lognormal (theta=est sigma=est zeta=est)
    gamma (theta=est alpha=est)
    weibull (c=est theta=est sigma=est);

qqplot / normal (mu=est);
qqplot / lognormal (theta=est sigma=est zeta=est);
qqplot / gamma (theta=est alpha=est);
qqplot / weibull (c=est theta=est sigma=est);
run;

/*Subset data to remove zeros in gppafdmses data*/
/*zeros dropped by proc glimmix*/
/*If zeros included, exponential distrib selected*/
/*But exponential distrib does not converge in glimmix*/
data amph1.metdata2;
set amph1.metdata;
if (gppafdmses>0);

proc univariate data=amph1.metdata2;
var gppafdmses;
histogram / normal (mu=est)
    lognormal (theta=est sigma=est zeta=est)
    gamma (theta=est alpha=est)
    weibull (c=est theta=est sigma=est);

qqplot / normal (mu=est);
qqplot / lognormal (theta=est sigma=est zeta=est);
qqplot / gamma (theta=est alpha=est);
qqplot / weibull (c=est theta=est sigma=est);
run;

proc univariate normal data=amph1.metdata;
var crafmBio;

```

```

histogram / normal (mu=est)
    lognormal (theta=est sigma=est zeta=est)
    gamma (theta=est alpha=est)
    weibull (c=est theta=est sigma=est);
qqplot / normal (mu=est);
qqplot / lognormal (theta=est sigma=est zeta=est);
qqplot / gamma (theta=est alpha=est);
qqplot / weibull (c=est theta=est sigma=est);
run;

proc univariate normal data=amph1.metdata;
var crafmsses;
histogram / normal (mu=est)
    lognormal (theta=est sigma=est zeta=est)
    gamma (theta=est alpha=est)
    weibull (c=est theta=est sigma=est);
qqplot / normal (mu=est);
qqplot / lognormal (theta=est sigma=est zeta=est);
qqplot / gamma (theta=est alpha=est);
qqplot / weibull (c=est theta=est sigma=est);
run;

proc univariate normal data=amph1.metdata;
var cpabio;
histogram / normal (mu=est)
    lognormal (theta=est sigma=est zeta=est)
    gamma (theta=est alpha=est)
    weibull (c=est theta=est sigma=est);
qqplot / normal (mu=est);
qqplot / lognormal (theta=est sigma=est zeta=est);
qqplot / gamma (theta=est alpha=est);
qqplot / weibull (c=est theta=est sigma=est);
run;

proc univariate normal data=amph1.metdata;
var cpases;
histogram / normal (mu=est)
    lognormal (theta=est sigma=est zeta=est)
    gamma (theta=est alpha=est)
    weibull (c=est theta=est sigma=est);
qqplot / normal (mu=est);
qqplot / lognormal (theta=est sigma=est zeta=est);
qqplot / gamma (theta=est alpha=est);
qqplot / weibull (c=est theta=est sigma=est);
run;

libname amph1 '/folders/myfolders';

```

```

/**Datalines for Emergence*/
data amph1.emerg;
input trt stream day emerg;
/*NOTE: trt are control=1, amph=0*/
datalines;
0 4 7 165
0 5 7 150
0 6 7 44
1 1 7 31
1 2 7 147
1 3 7 39
0 4 14 56
0 5 14 39
0 6 14 103
1 1 14 22
1 2 14 85
1 3 14 118
0 4 21 224
0 5 21 61
0 6 21 66
1 1 21 15
1 2 21 58
1 3 21 113
;

proc contents data=amph1.emerg;
run;
proc univariate normal data=amph1.emerg;
  var emerg;
  histogram / normal (mu=est);
  qqplot / normal (mu=est);
run;

/**discrete data cannot be analyzed with proc univariate. Use proc genmod to do poisson and negative binomial
regression.*/
proc genmod data=amph1.emerg;
  model emerg= / dist=poisson;
run;

proc genmod data=amph1.emerg;
  model emerg= / dist=negbin;
run;

proc genmod data=amph1.emerg;
  model emerg= / dist=normal;
run;

```

S2B. Selected proc univariate output and selected distributions.

S2B.1 Chlorophyll a – Biofilm (ug/m2).

Table S2B.1.1. Moments of response variable Chlorophyll a – Biofilm (ug/m2).

Moments			
N	40	Sum Weights	40
Mean	0.00009572	Sum Observations	0.00382863
Std Deviation	0.00008336	Variance	6.94901E-9
Skewness	3.1102096	Kurtosis	10.6141902
Uncorrected SS	6.37471E-7	Corrected SS	2.71011E-7
Coeff Variation	87.0919572	Std Error Mean	0.00001318

Figure S2B.1.1. Histogram of Chlorophyll a – Biofilm (ug/m2) with fitted distribution curves.

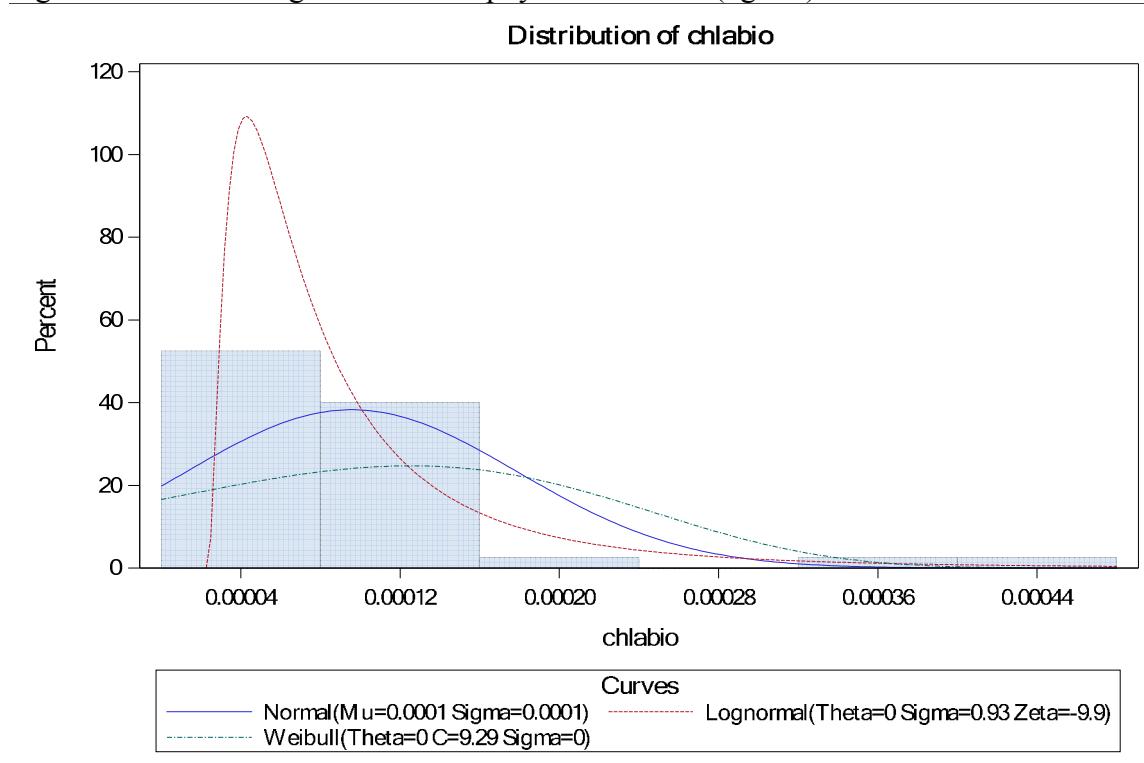


Figure S2B.1.2. Q-Q plot for normal distribution fit for response variable Chlorophyll a – Biofilm (ug/m²).

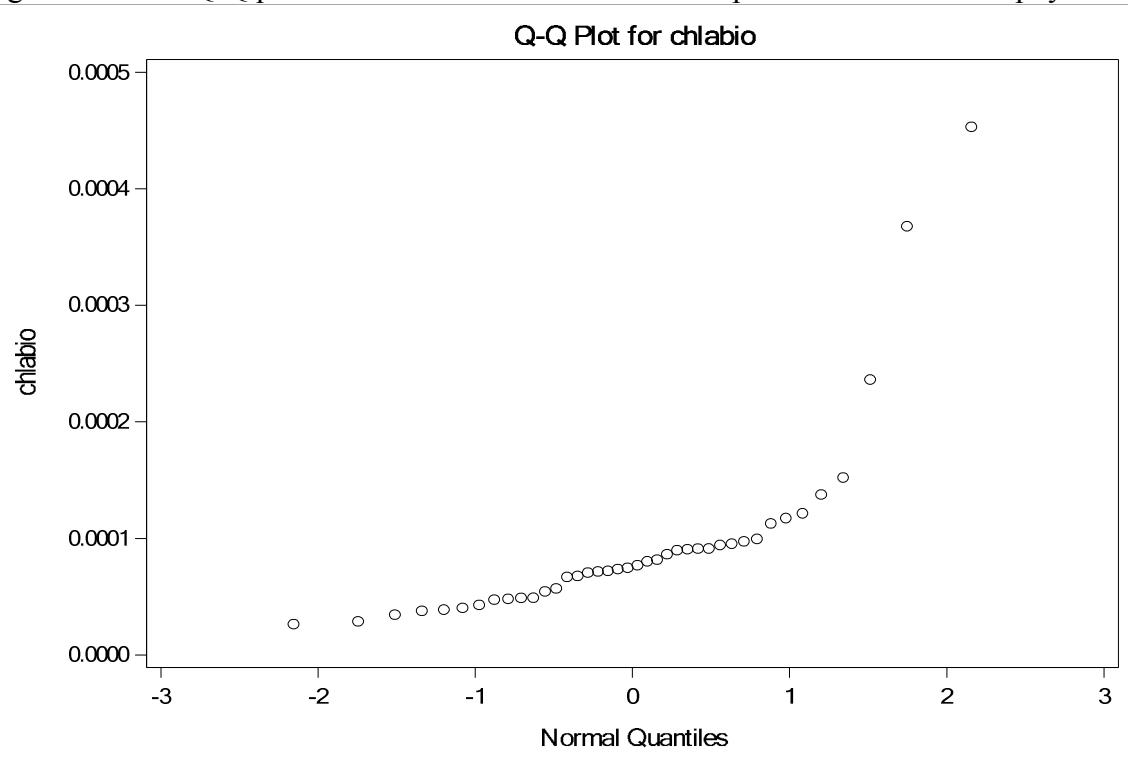


Figure S2B.1.3. Q-Q plot for lognormal distribution fit for response variable Chlorophyll a – Biofilm (ug/m²).

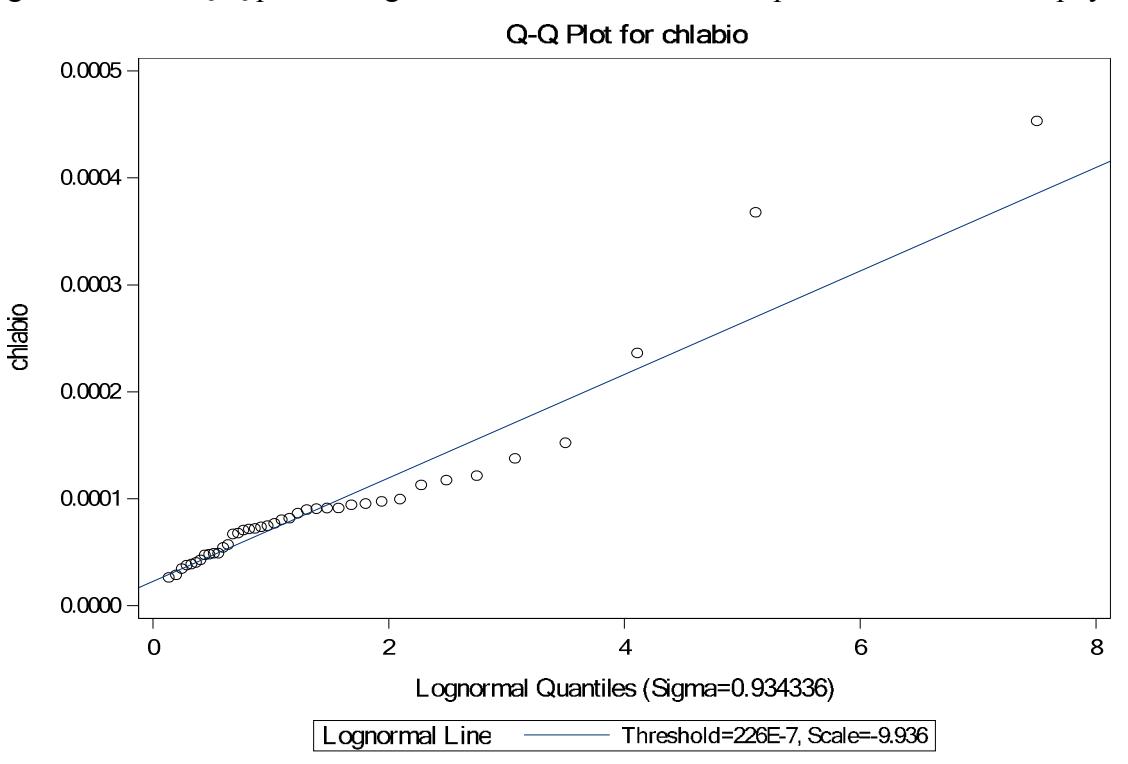


Figure S2B.1.4. Q-Q plot for Weibull distribution fit for response variable Chlorophyll a – Biofilm (ug/m²).

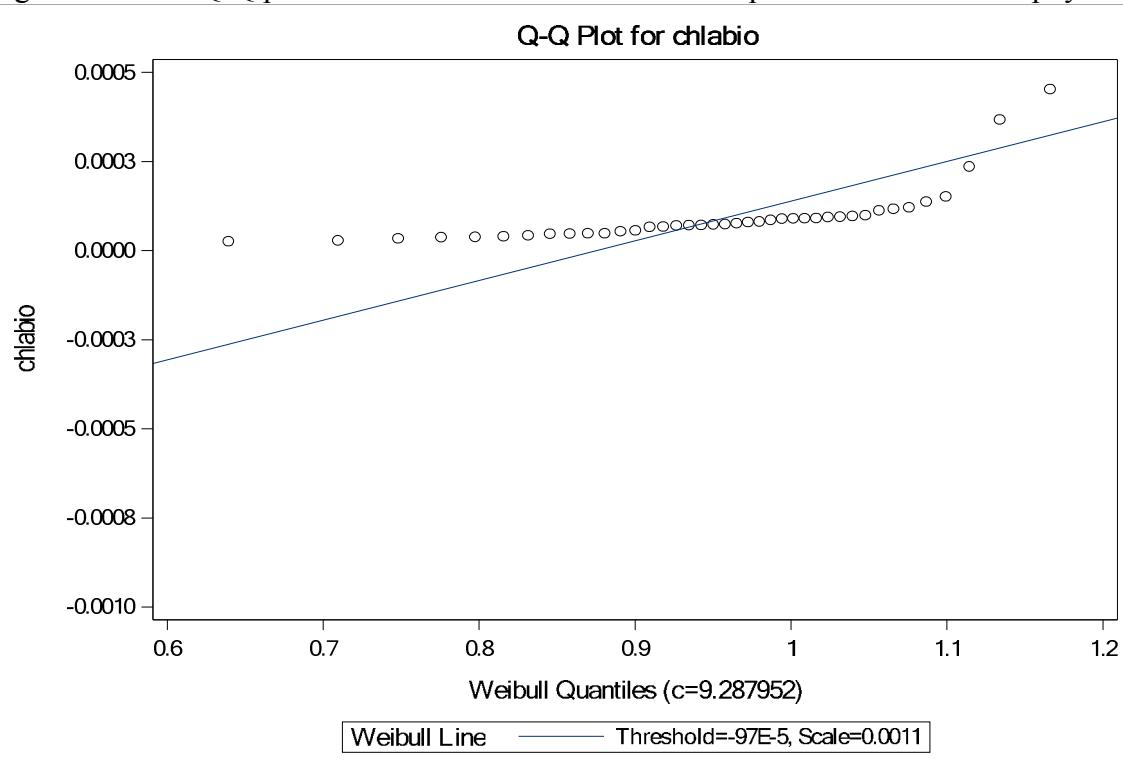


Table S2B.1.2. Parameter estimates for normal distribution fit for response variable Chlorophyll a – Biofilm (ug/m²).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	0.000096
Std Dev	Sigma	0.000083

Table S2B.1.3. Results of tests for normality for response variable Chlorophyll a – Biofilm (ug/m²).

Tests for Normality				
Test		Statistic	p Value	
Shapiro-Wilk		W	0.623615	Pr < W
Kolmogorov-Smirnov		D	0.281418	Pr > D
Cramer-von Mises		W-Sq	0.8497	Pr > W-Sq
Anderson-Darling		A-Sq	4.740459	Pr > A-Sq

Table S2B.1.4. Parameter estimates for lognormal distribution fit for response variable Chlorophyll a – Biofilm (ug/m²).

Parameters for Lognormal Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	0.000023
Scale	Zeta	-9.93585
Shape	Sigma	0.934336
Mean		0.000097
Std Dev		0.000088

Table S2B.1.5. Results of goodness-of-fit tests for lognormal distribution fit for response variable Chlorophyll a – Biofilm (ug/m²).

Goodness-of-Fit Tests for Lognormal Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.13829269	Pr > D	0.023
Cramer-von Mises	W-Sq	0.12572160	Pr > W-Sq	0.021
Anderson-Darling	A-Sq	0.68340131	Pr > A-Sq	0.028

Table S2B.1.6. Parameter estimates for Weibull distribution fit for response variable Chlorophyll a – Biofilm (ug/m²).

Parameters for Weibull Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.00097
Scale	Sigma	0.001113
Shape	C	9.287952
Mean		0.000081
Std Dev		0.000136

Table S2B.1.7. Results of goodness-of-fit tests for Weibull distribution fit for response variable Chlorophyll a – Biofilm (ug/m²).

Goodness-of-Fit Tests for Weibull Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.31028631	Pr > D	<0.001
Cramer-von Mises	W-Sq	1.28901175	Pr > W-Sq	<0.001
Anderson-Darling	A-Sq	6.69137578	Pr > A-Sq	<0.001

Gamma distribution could not be fit.

S2B.2 Chlorophyll a – Seston (ug/L).

Table S2B.2.1. Moments of response variable Chlorophyll a – Seston (ug/L).

Moments			
N	40	Sum Weights	40
Mean	9.10353439	Sum Observations	364.141375
Std Deviation	9.34651207	Variance	87.3572878
Skewness	1.45594556	Kurtosis	1.44205064
Uncorrected SS	6721.90776	Corrected SS	3406.93422
Coeff Variation	102.669048	Std Error Mean	1.47781332

Figure S2B.2.1. Histogram of Chlorophyll a – Seston (ug/L) with fitted distribution curves.

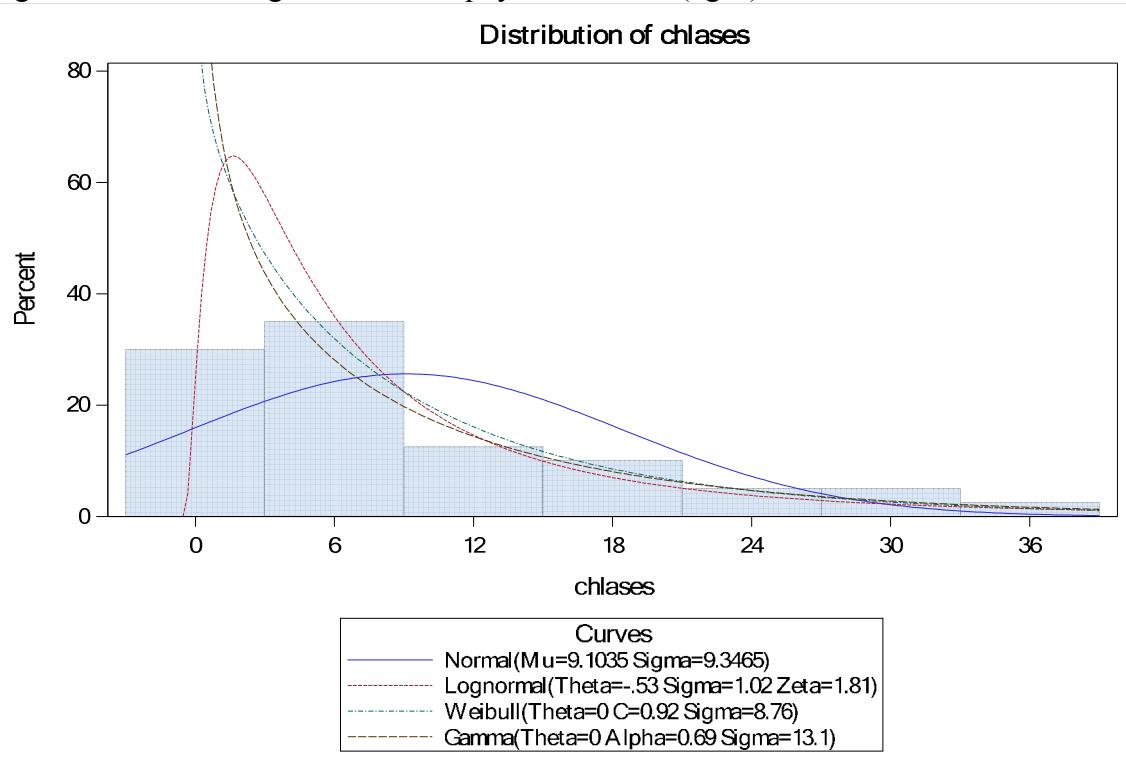


Figure S2B.2.2. Q-Q plot for normal distribution fit for response variable Chlorophyll a – Seston (ug/L).

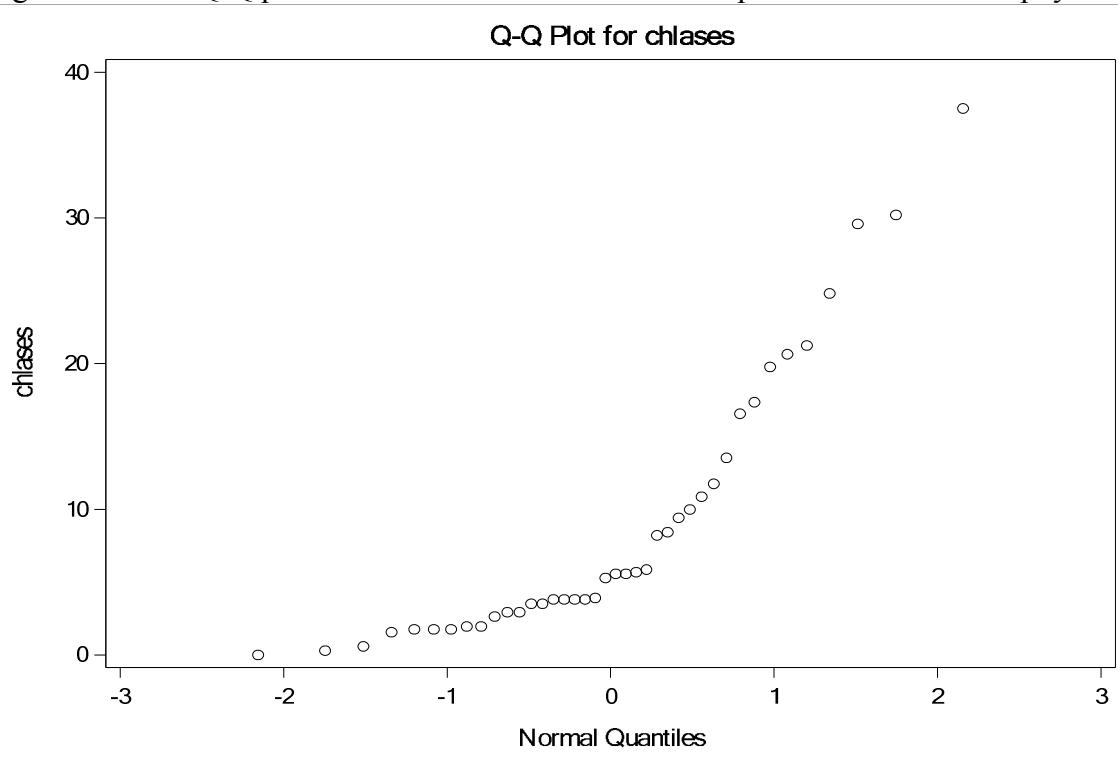


Figure S2B.2.3. Q-Q plot for lognormal distribution fit for response variable Chlorophyll a – Seston (ug/L).

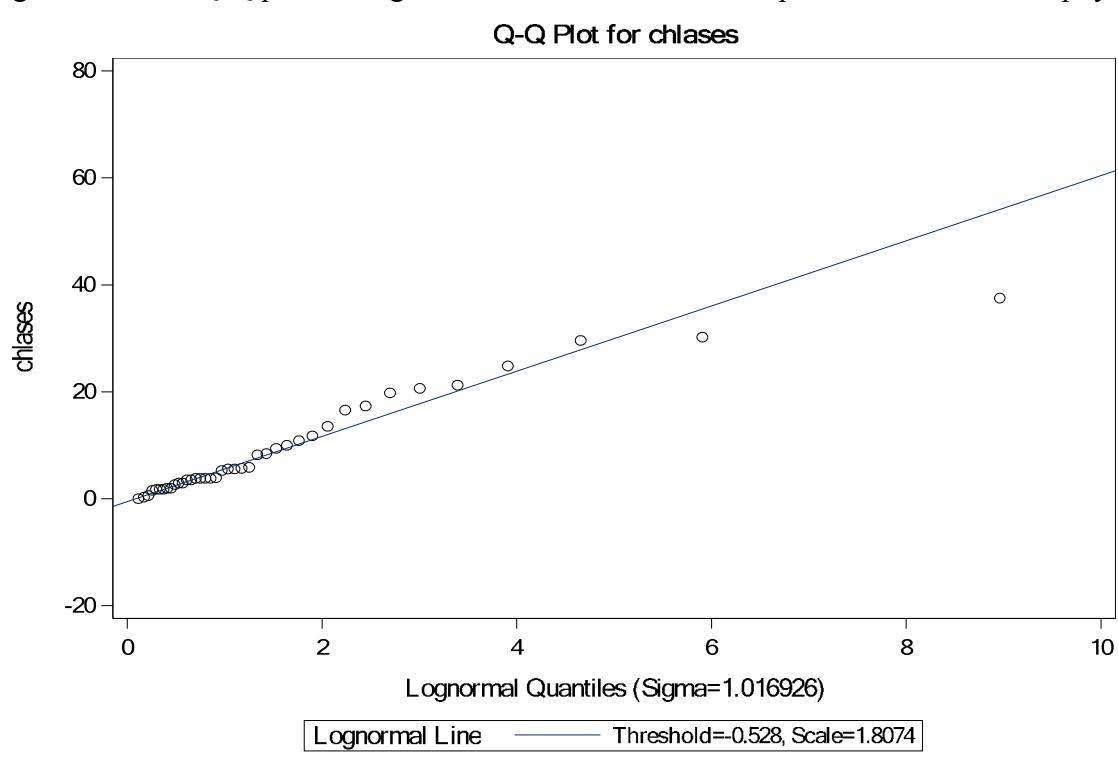


Figure S2B.2.4. Q-Q plot for gamma distribution fit for response variable Chlorophyll a – Seston (ug/L).

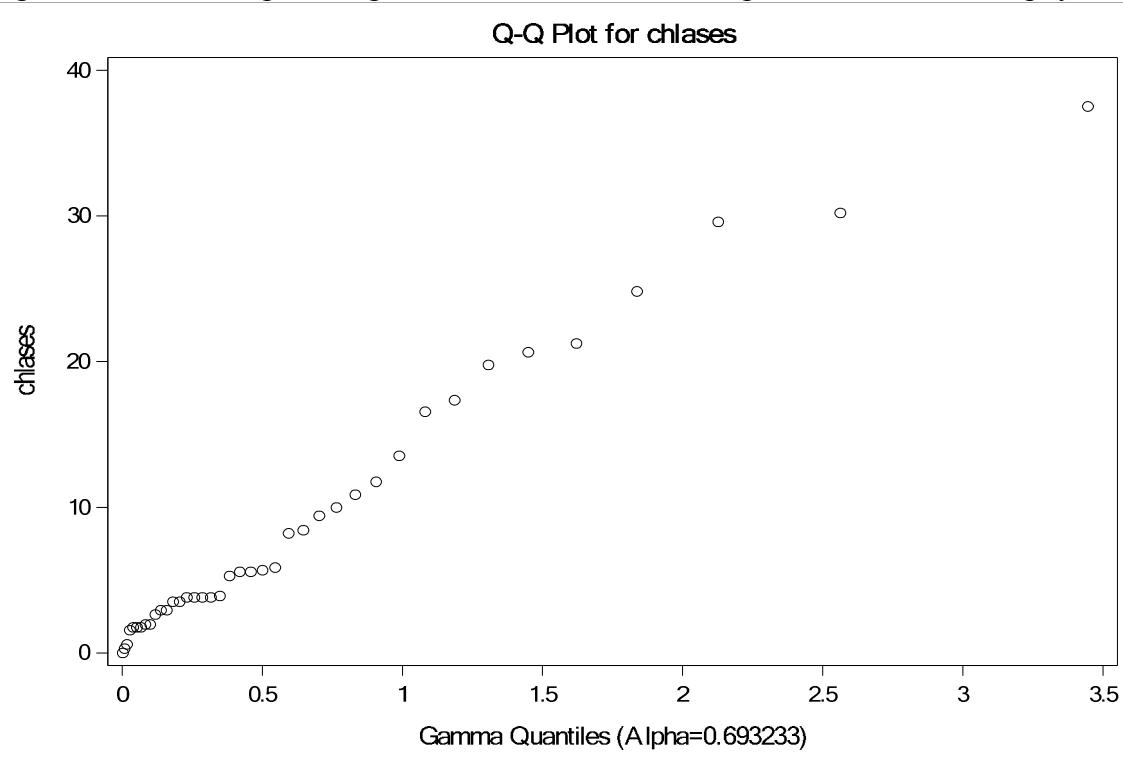


Figure S2B.2.5. Q-Q plot for Weibull distribution fit for response variable Chlorophyll a – Seston (ug/L).

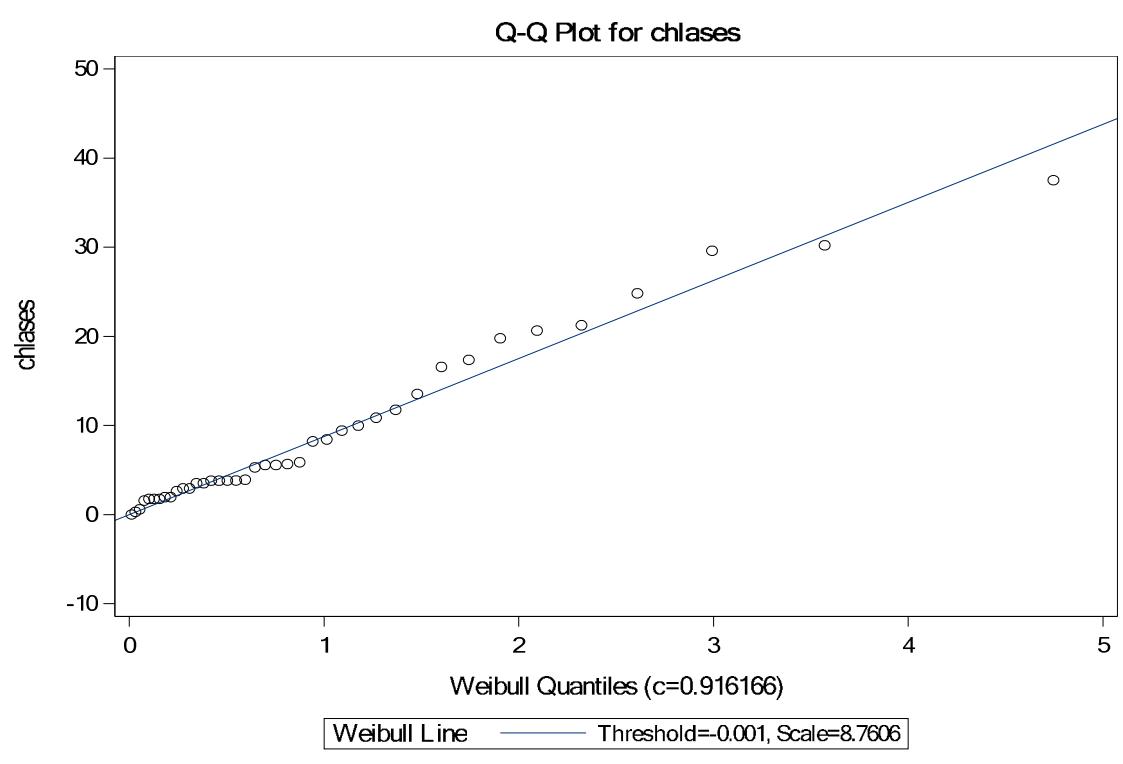


Table S2B.2.2. Parameter estimates for normal distribution fit for response variable Chlorophyll a – Seston (ug/L).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	9.103534
Std Dev	Sigma	9.346512

Table S2B.2.3. Results of tests for normality for response variable Chlorophyll a – Seston (ug/L).

Tests for Normality				
Test	Statistic	p Value		
Shapiro-Wilk	W	0.8139	Pr < W	<0.0001
Kolmogorov-Smirnov	D	0.235742	Pr > D	<0.0100
Cramer-von Mises	W-Sq	0.502792	Pr > W-Sq	<0.0050
Anderson-Darling	A-Sq	2.763291	Pr > A-Sq	<0.0050

Table S2B.2.4. Parameter estimates for lognormal distribution fit for response variable Chlorophyll a – Seston (ug/L).

Parameters for Lognormal Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.52796
Scale	Zeta	1.807435
Shape	Sigma	1.016926
Mean		9.693654
Std Dev		13.76197

Table S2B.2.5. Results of goodness-of-fit tests for lognormal distribution fit for response variable Chlorophyll a – Seston (ug/L).

Goodness-of-Fit Tests for Lognormal Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.09722316	Pr > D	>0.250
Cramer-von Mises	W-Sq	0.04816470	Pr > W-Sq	>0.250
Anderson-Darling	A-Sq	0.31765577	Pr > A-Sq	>0.250

Table S2B.2.6. Parameter estimates for Weibull distribution fit for response variable Chlorophyll a – Seston (ug/L).

Parameters for Weibull Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.001
Scale	Sigma	8.7606
Shape	C	0.916166
Mean		9.129324
Std Dev		9.977537

Goodness of fit test not available for Weibull distribution.

Table S2B.2.7. Parameter estimates for gamma distribution fit for response variable Chlorophyll a – Seston (ug/L).

Parameters for Gamma Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-1E-6
Scale	Sigma	13.13201
Shape	Alpha	0.693233
Mean		9.103534
Std Dev		10.93379

Goodness of fit test not available for Gamma distribution.

S2B.3 Ash-free dry mass – Biofilm (mg/m²)

Table S2B.3.1. Moments of response variable Ash-free dry mass – Biofilm (mg/m²).

Moments			
N	40	Sum Weights	40
Mean	0.00015251	Sum Observations	0.00610054
Std Deviation	0.00007609	Variance	5.7894E-9
Skewness	1.44756938	Kurtosis	2.48618807
Uncorrected SS	1.1562E-6	Corrected SS	2.25786E-7
Coeff Variation	49.8893752	Std Error Mean	0.00001203

Figure S2B.3.1. Histogram of Ash-free dry mass – Biofilm (mg/m²) with fitted distribution curves.

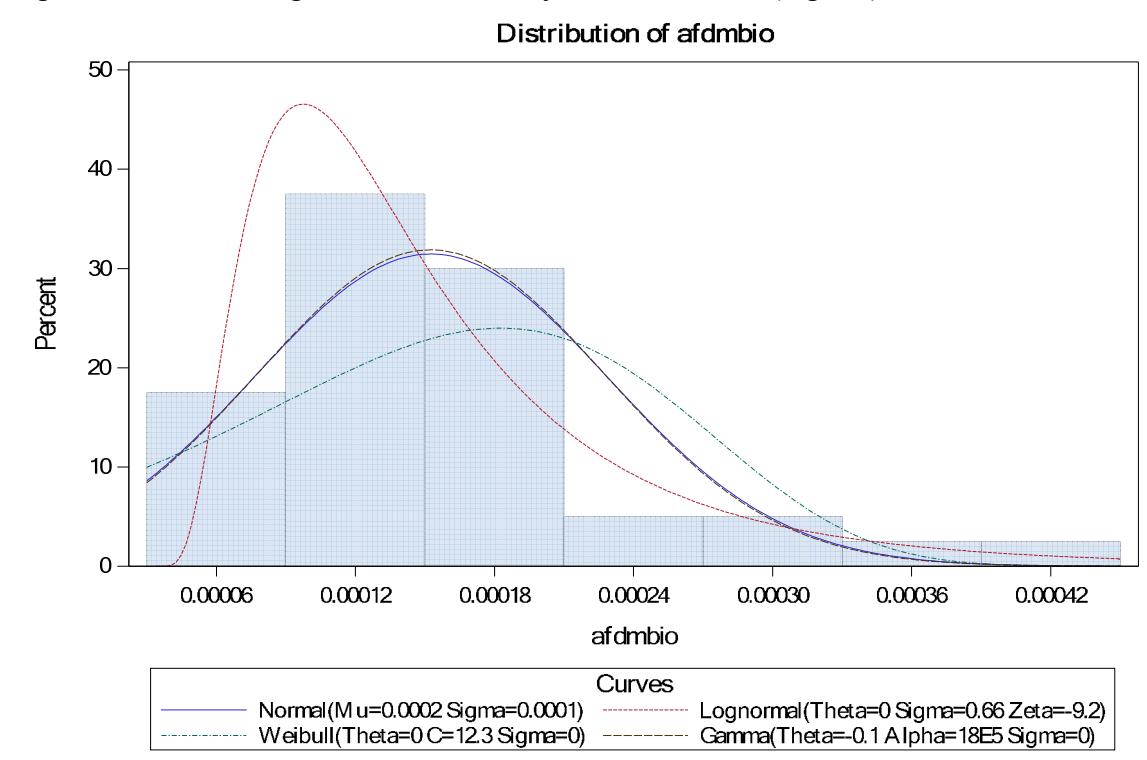


Figure S2B.3.2. Q-Q plot for normal distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

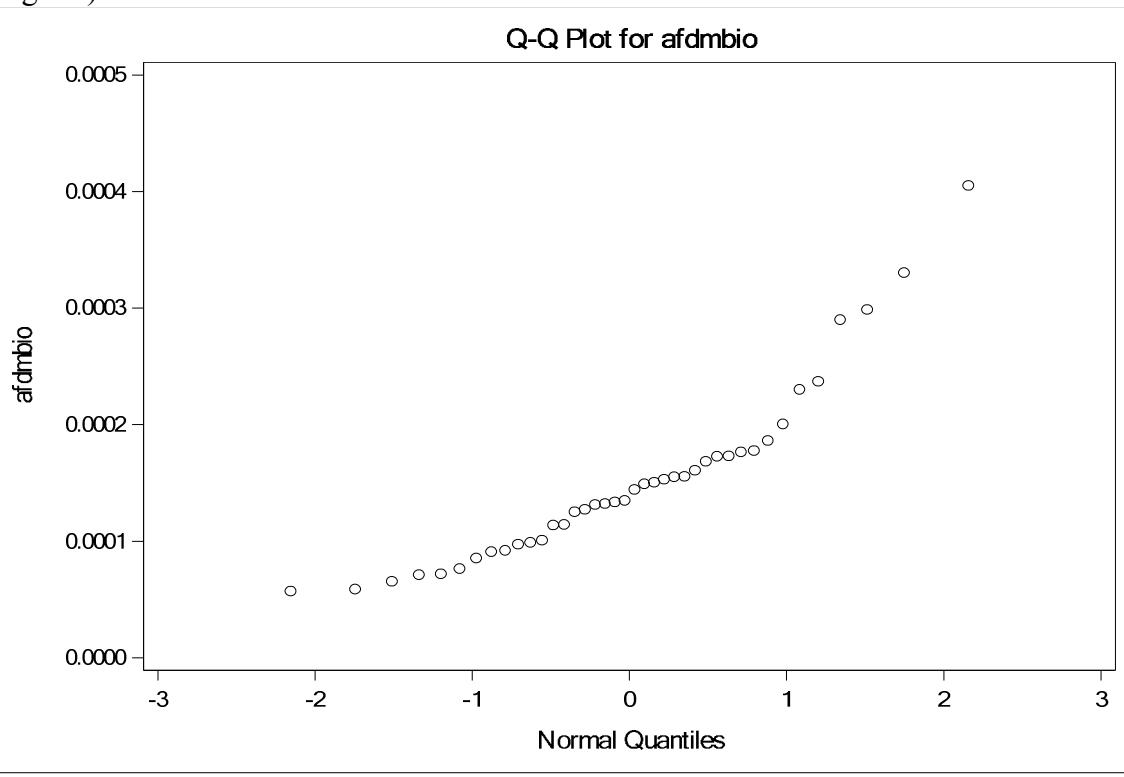


Figure S2B.3.3. Q-Q plot for lognormal distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

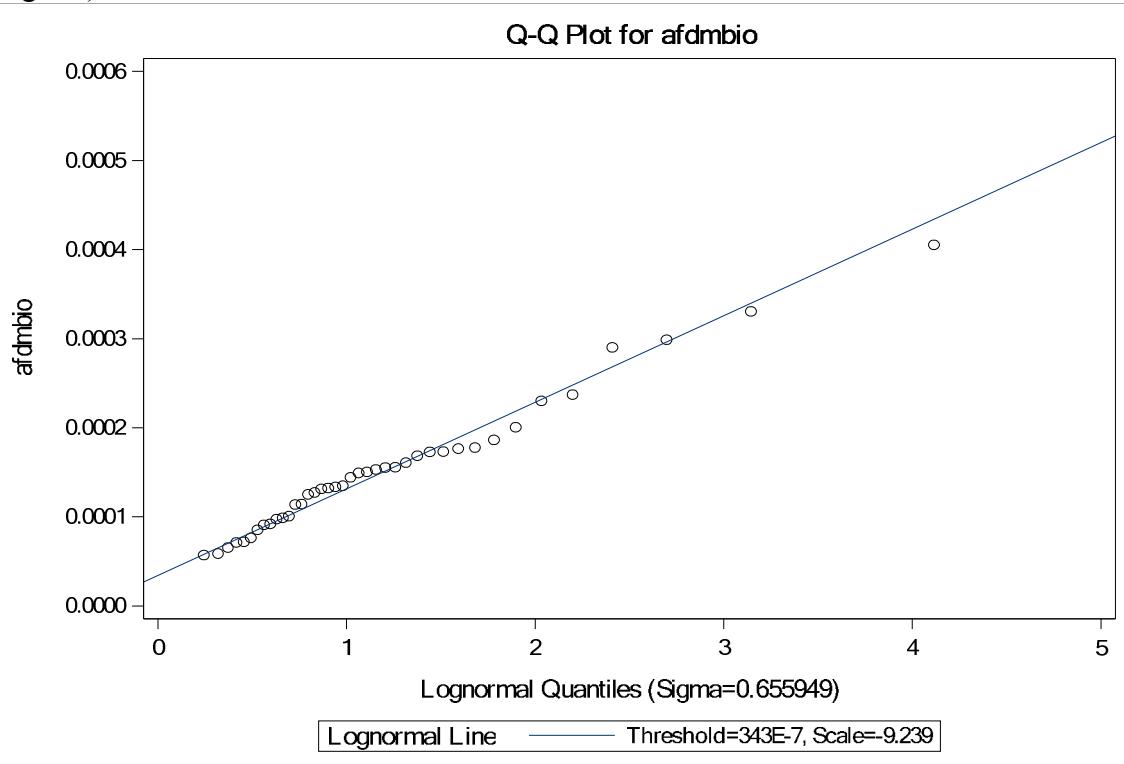


Figure S2B.3.4. Q-Q plot for Weibull distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

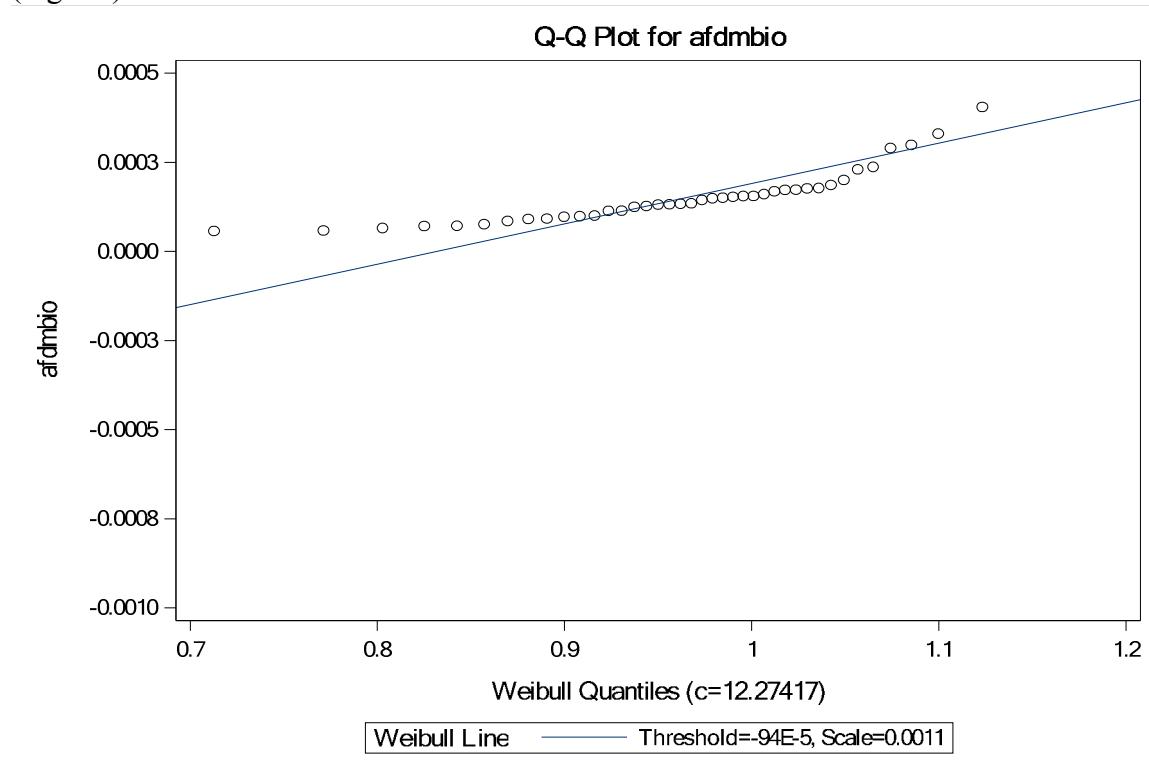


Table S2B.3.2. Parameter estimates for normal distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	0.000153
Std Dev	Sigma	0.000076

Table S2B.3.3. Results of tests for normality for response variable Ash-free dry mass – Biofilm (mg/m²).

Tests for Normality				
Test		Statistic	p Value	
Shapiro-Wilk		W	Pr < W	0.0005
Kolmogorov-Smirnov		D	Pr > D	<0.0100
Cramer-von Mises		W-Sq	Pr > W-Sq	<0.0050
Anderson-Darling		A-Sq	Pr > A-Sq	<0.0050

Table S2B.3.4. Parameter estimates for lognormal distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

Parameters for Lognormal Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	0.000034
Scale	Zeta	-9.23905
Shape	Sigma	0.655949
Mean		0.000155
Std Dev		0.000088

Table S2B.3.5. Results of goodness-of-fit tests for lognormal distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

Goodness-of-Fit Tests for Lognormal Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.11027574	Pr > D	0.151
Cramer-von Mises	W-Sq	0.07152210	Pr > W-Sq	0.159
Anderson-Darling	A-Sq	0.38319156	Pr > A-Sq	0.244

Table S2B.3.6. Parameter estimates for Weibull distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

Parameters for Weibull Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.00094
Scale	Sigma	0.001133
Shape	C	12.27417
Mean		0.000144
Std Dev		0.000108

Table S2B.3.7. Results of goodness-of-fit tests for Weibull distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

Goodness-of-Fit Tests for Weibull Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.21815873	Pr > D	<0.001
Cramer-von Mises	W-Sq	0.47515765	Pr > W-Sq	<0.001
Anderson-Darling	A-Sq	2.74025761	Pr > A-Sq	<0.001

Table S2B.3.8. Parameter estimates for gamma distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

Parameters for Gamma Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.09993
Scale	Sigma	5.634E-8
Shape	Alpha	1776200
Mean		0.000153
Std Dev		0.000075

Table S2B.3.9. Results of goodness-of-fit tests for gamma distribution fit for response variable Ash-free dry mass – Biofilm (mg/m²).

Goodness-of-Fit Tests for Gamma Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.00000000	Pr > D	>0.500
Cramer-von Mises	W-Sq	0.00208333	Pr > W-Sq	>0.500
Anderson-Darling	A-Sq		Pr > A-Sq	>0.500

S2B.4 Ash-free dry mass – Seston (mg/L)

Table S2B.4.1. Moments of response variable Ash-free dry mass – Seston (mg/L).

Moments			
N	40	Sum Weights	40
Mean	72.6166667	Sum Observations	2904.66667
Std Deviation	19.8509474	Variance	394.060114
Skewness	-0.4657155	Kurtosis	-1.0491776
Uncorrected SS	226295.556	Corrected SS	15368.3444
Coeff Variation	27.3366272	Std Error Mean	3.13871038

Figure S2B.4.1. Histogram of Ash-free dry mass – Seston (mg/L) with fitted distribution curves.

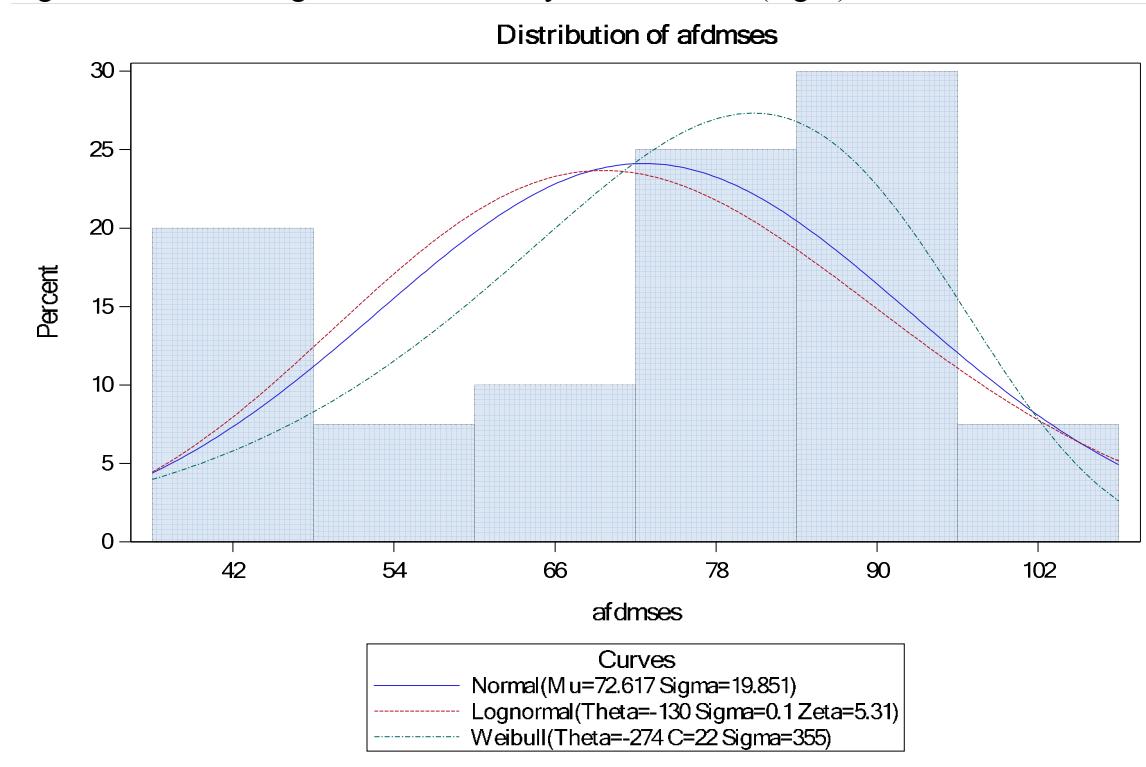


Figure S2B.4.2. Q-Q plot for normal distribution fit for response variable Ash-free dry mass – Seston (mg/L).

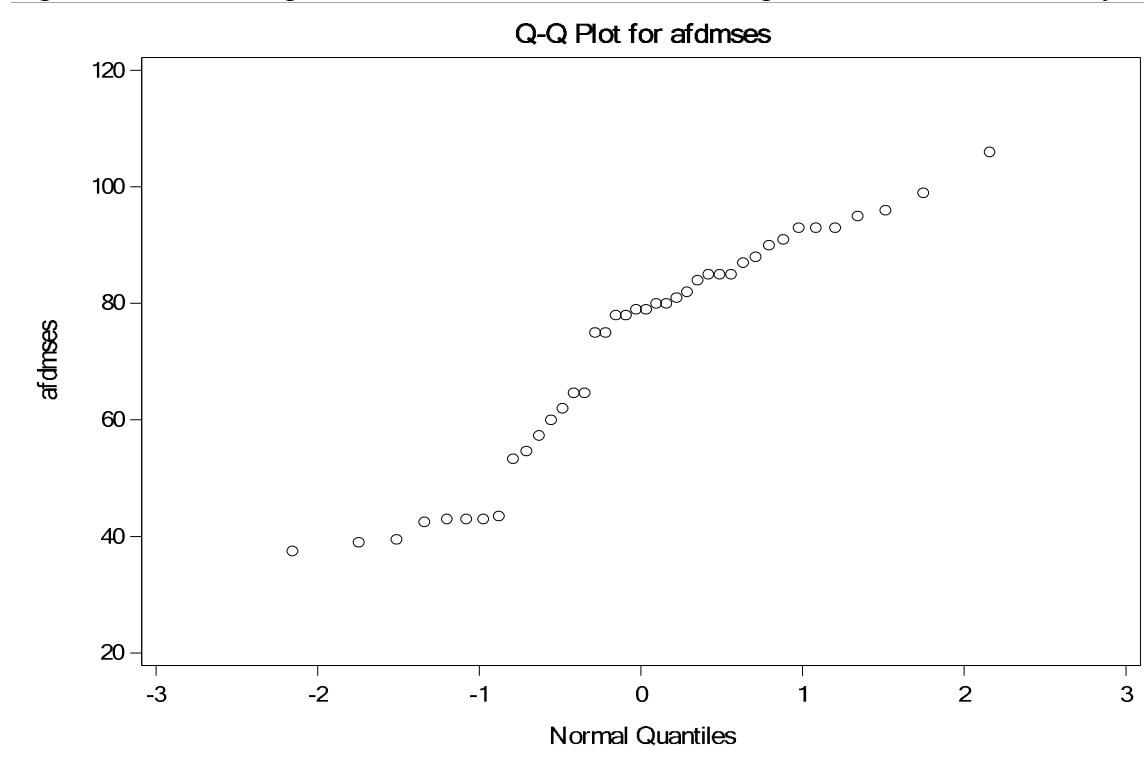


Figure S2B.4.3. Q-Q plot for lognormal distribution fit for response variable Ash-free dry mass – Seston (mg/L).

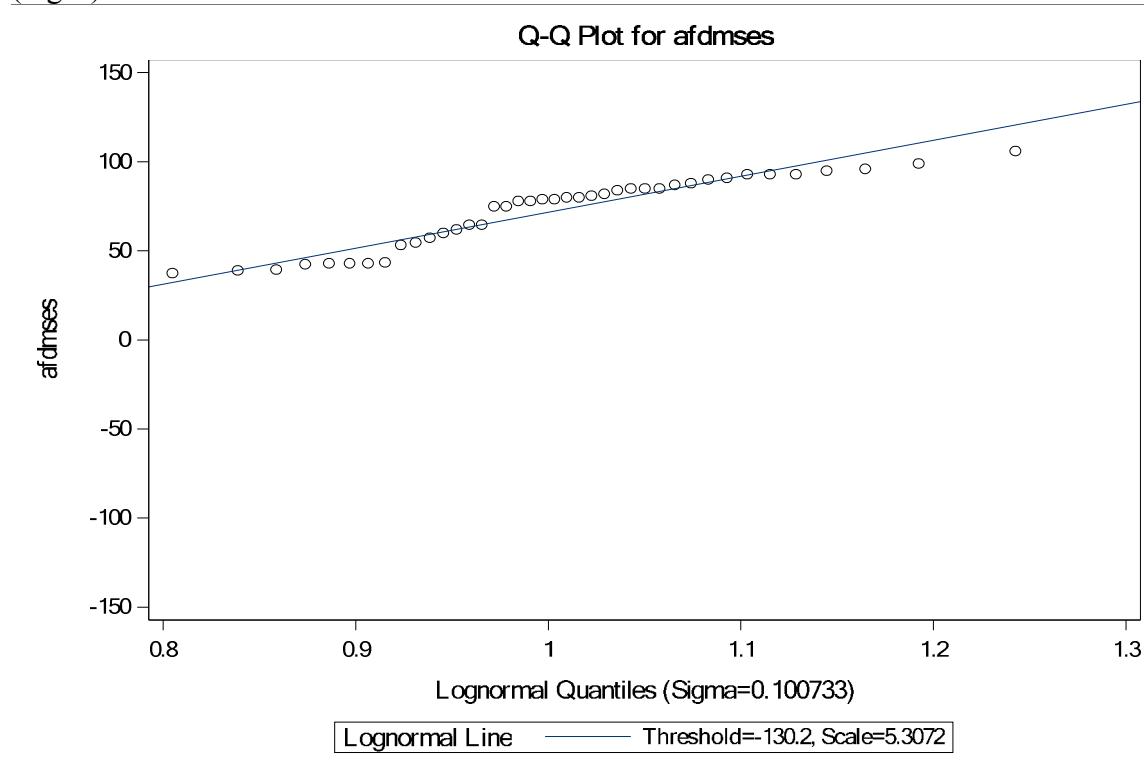


Figure S2B.4.4. Q-Q plot for Weibull distribution fit for response variable Ash-free dry mass – Seston (mg/L).

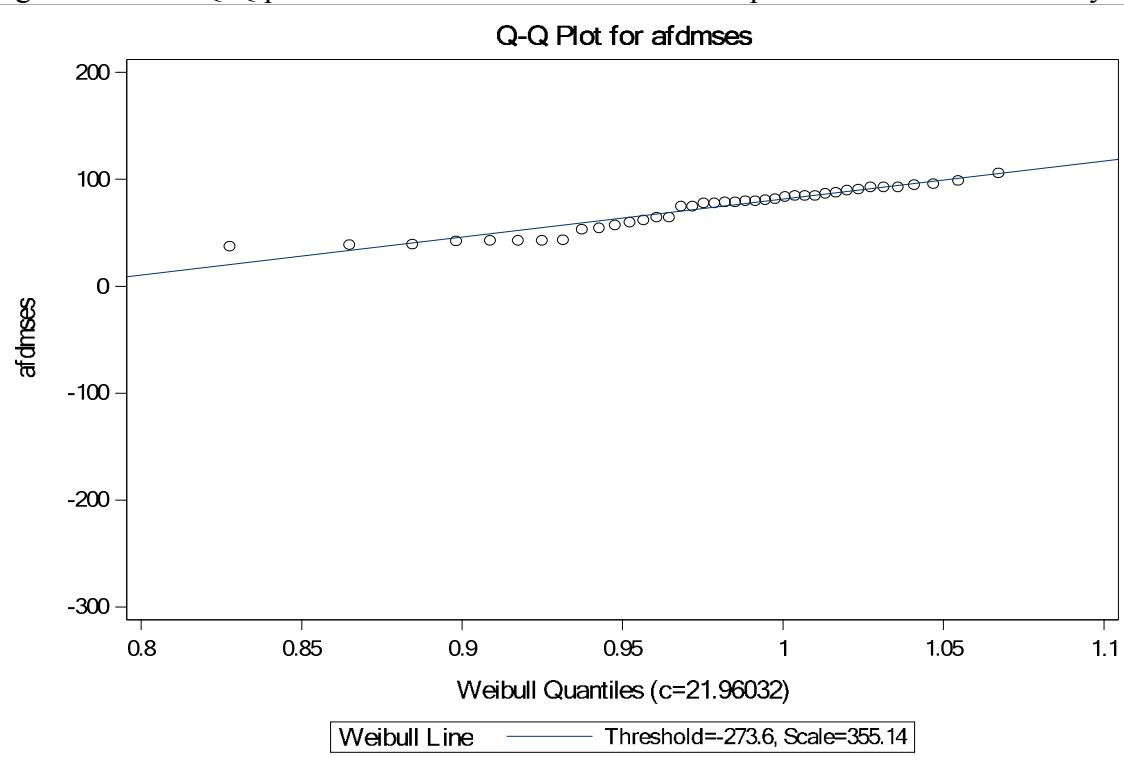


Table S2B.4.2. Parameter estimates for normal distribution fit for response variable Ash-free dry mass – Seston (mg/L).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	72.61667
Std Dev	Sigma	19.85095

Table S2B.4.3. Results of tests for normality for response variable Ash-free dry mass – Seston (mg/L).

Tests for Normality				
Test	Statistic	p Value		
Shapiro-Wilk	W	0.914877	Pr < W	0.0053
Kolmogorov-Smirnov	D	0.181877	Pr > D	<0.0100
Cramer-von Mises	W-Sq	0.222339	Pr > W-Sq	<0.0050
Anderson-Darling	A-Sq	1.312394	Pr > A-Sq	<0.0050

Table S2B.4.4. Parameter estimates for lognormal distribution fit for response variable Ash-free dry mass – Seston (mg/L).

Parameters for Lognormal Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-130.158
Scale	Zeta	5.307244
Shape	Sigma	0.100733
Mean		72.66154
Std Dev		20.48262

Table S2B.4.5. Results of goodness-of-fit tests for lognormal distribution fit for response variable Ash-free dry mass – Seston (mg/L).

Goodness-of-Fit Tests for Lognormal Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.19606661	Pr > D	<0.001
Cramer-von Mises	W-Sq	0.26362269	Pr > W-Sq	<0.001
Anderson-Darling	A-Sq	1.54584930	Pr > A-Sq	<0.001

Table S2B.4.6. Parameter estimates for Weibull distribution fit for response variable Ash-free dry mass – Seston (mg/L).

Parameters for Weibull Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-273.605
Scale	Sigma	355.1363
Shape	C	21.96032
Mean		72.89565
Std Dev		19.61389

Table S2B.4.7. Results of goodness-of-fit tests for Weibull distribution fit for response variable Ash-free dry mass – Seston (mg/L).

Goodness-of-Fit Tests for Weibull Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.12700680	Pr > D	0.046
Cramer-von Mises	W-Sq	0.12168199	Pr > W-Sq	0.023
Anderson-Darling	A-Sq	0.79485576	Pr > A-Sq	0.014

Gamma distribution could not be fit.

S2B.5 Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM)

Table S2B.5.1. Moments of response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Moments			
N	40	Sum Weights	40
Mean	0.60883298	Sum Observations	24.3533192
Std Deviation	0.26142998	Variance	0.06834563
Skewness	1.88826542	Kurtosis	4.67177342
Uncorrected SS	17.4925836	Corrected SS	2.66547968
Coeff Variation	42.9395229	Std Error Mean	0.04133571

Figure S2B.5.1. Histogram of Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM) with fitted distribution curves.

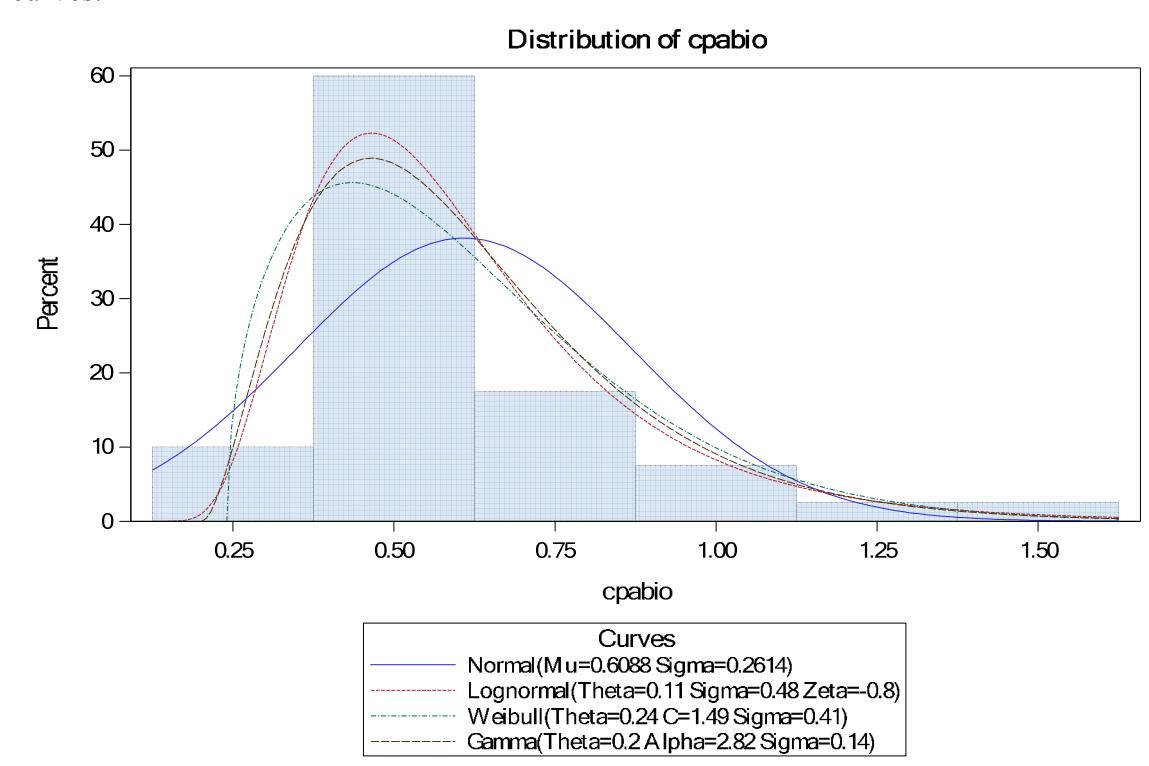


Figure S2B.5.2. Q-Q plot for normal distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

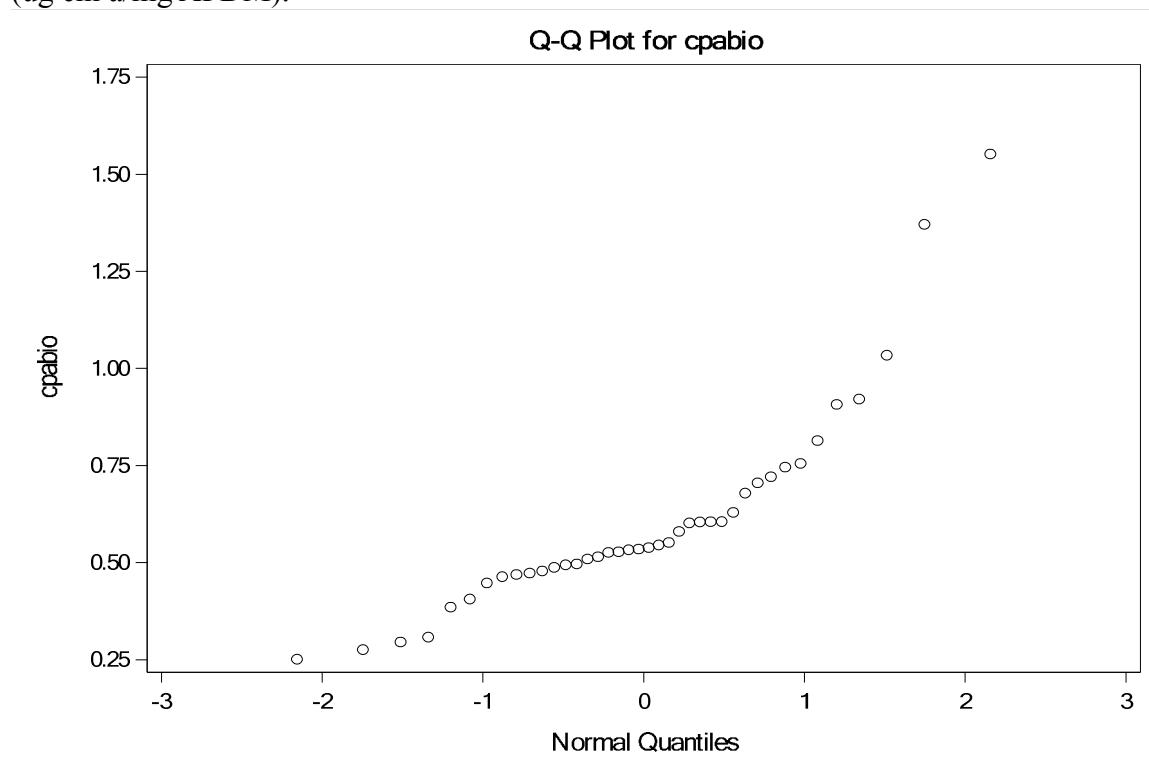


Figure S2B.5.3. Q-Q plot for lognormal distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

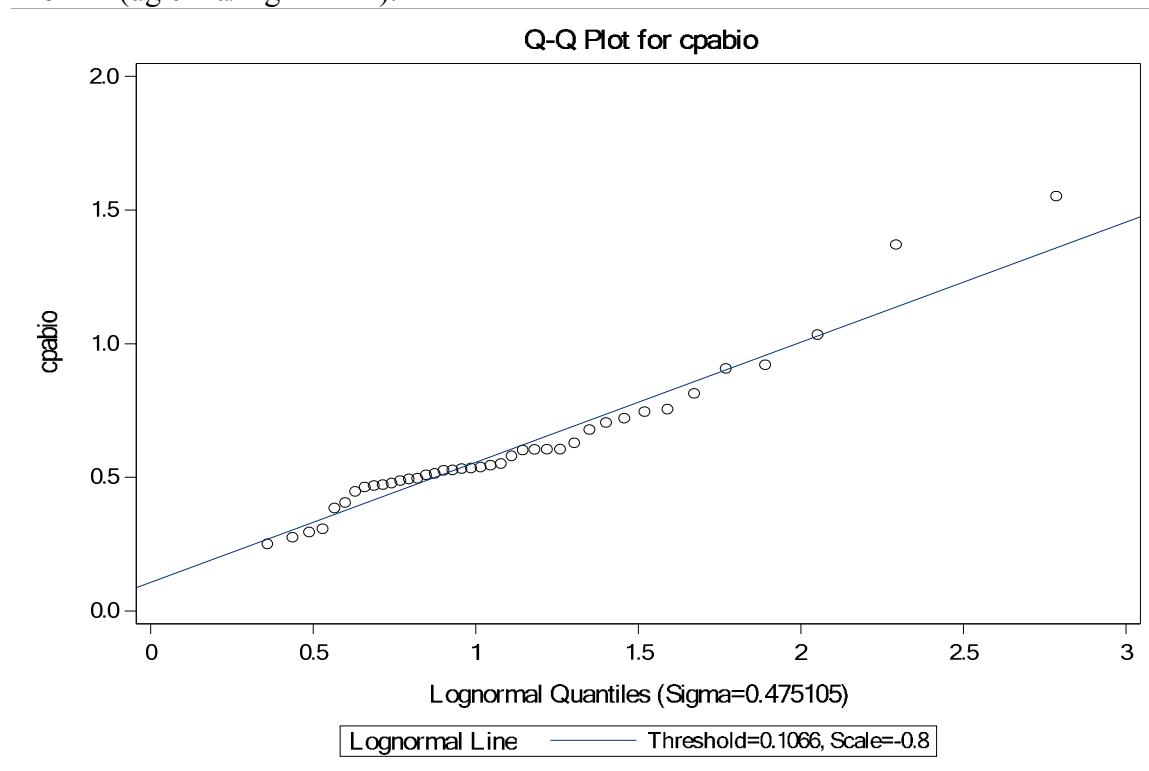


Figure S2B.5.4. Q-Q plot for gamma distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

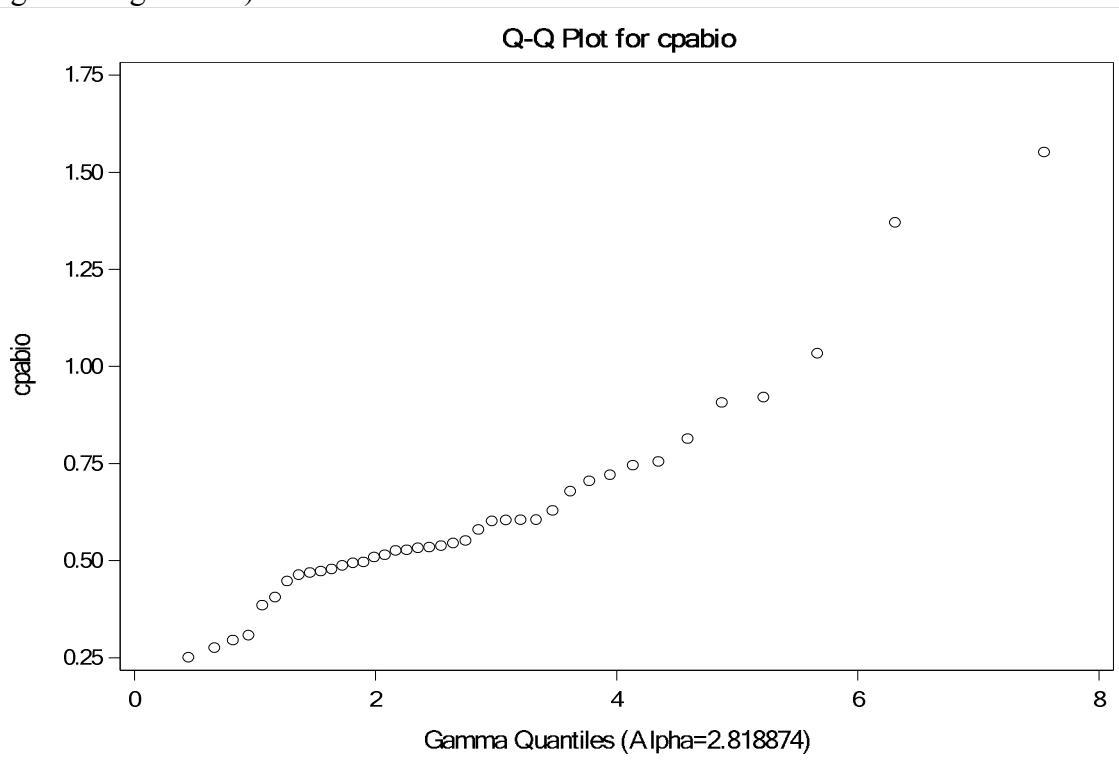


Figure S2B.5.5. Q-Q plot for Weibull distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

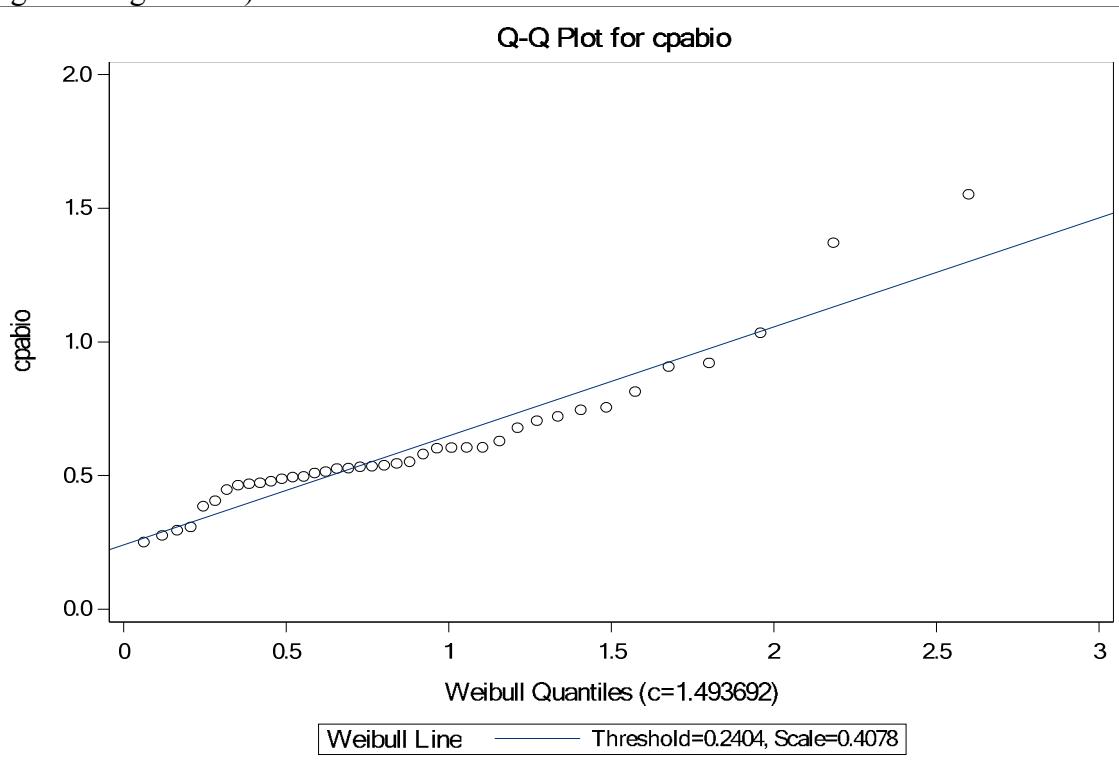


Table S2B.5.2. Parameter estimates for normal distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	0.608833
Std Dev	Sigma	0.26143

Table S2B.5.3. Results of tests for normality for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Tests for Normality				
Test	Statistic	p Value		
Shapiro-Wilk	W	0.827512	Pr < W	<0.0001
Kolmogorov-Smirnov	D	0.205034	Pr > D	<0.0100
Cramer-von Mises	W-Sq	0.375042	Pr > W-Sq	<0.0050
Anderson-Darling	A-Sq	2.10505	Pr > A-Sq	<0.0050

Table S2B.5.4. Parameter estimates for lognormal distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Parameters for Lognormal Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	0.10664
Scale	Zeta	-0.80005
Shape	Sigma	0.475105
Mean		0.60963
Std Dev		0.253115

Table S2B.5.5. Results of goodness-of-fit tests for lognormal distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Goodness-of-Fit Tests for Lognormal Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.13975260	Pr > D	0.016
Cramer-von Mises	W-Sq	0.13817906	Pr > W-Sq	0.010
Anderson-Darling	A-Sq	0.76686410	Pr > A-Sq	0.012

Table S2B.5.6. Parameter estimates for Weibull distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Parameters for Weibull Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	0.240424
Scale	Sigma	0.407832
Shape	C	1.493692
Mean		0.608782
Std Dev		0.251077

Goodness of fit test not available for Weibull distribution.

Table S2B.5.7. Parameter estimates for gamma distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Parameters for Gamma Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	0.201562
Scale	Sigma	0.14448
Shape	Alpha	2.818874
Mean		0.608833
Std Dev		0.242575

Table S2B.5.8. Results of goodness-of-fit tests for gamma distribution fit for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Goodness-of-Fit Tests for Gamma Distribution				
Test	Statistic		p Value	
Kolmogorov-Smirnov	D	0.13998724	Pr > D	0.022
Cramer-von Mises	W-Sq	0.15883162	Pr > W-Sq	0.006
Anderson-Darling	A-Sq	0.87611539	Pr > A-Sq	0.007

S2B.6 Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM)

Table S2B.6.1. Moments of response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

Moments			
N	40	Sum Weights	40
Mean	0.11900086	Sum Observations	4.76003424
Std Deviation	0.11007849	Variance	0.01211727
Skewness	1.20629661	Kurtosis	0.50234452
Uncorrected SS	1.03902182	Corrected SS	0.47257368
Coeff Variation	92.5022665	Std Error Mean	0.01740494

Figure S2B.6.1. Histogram of Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM) with fitted distribution curves.

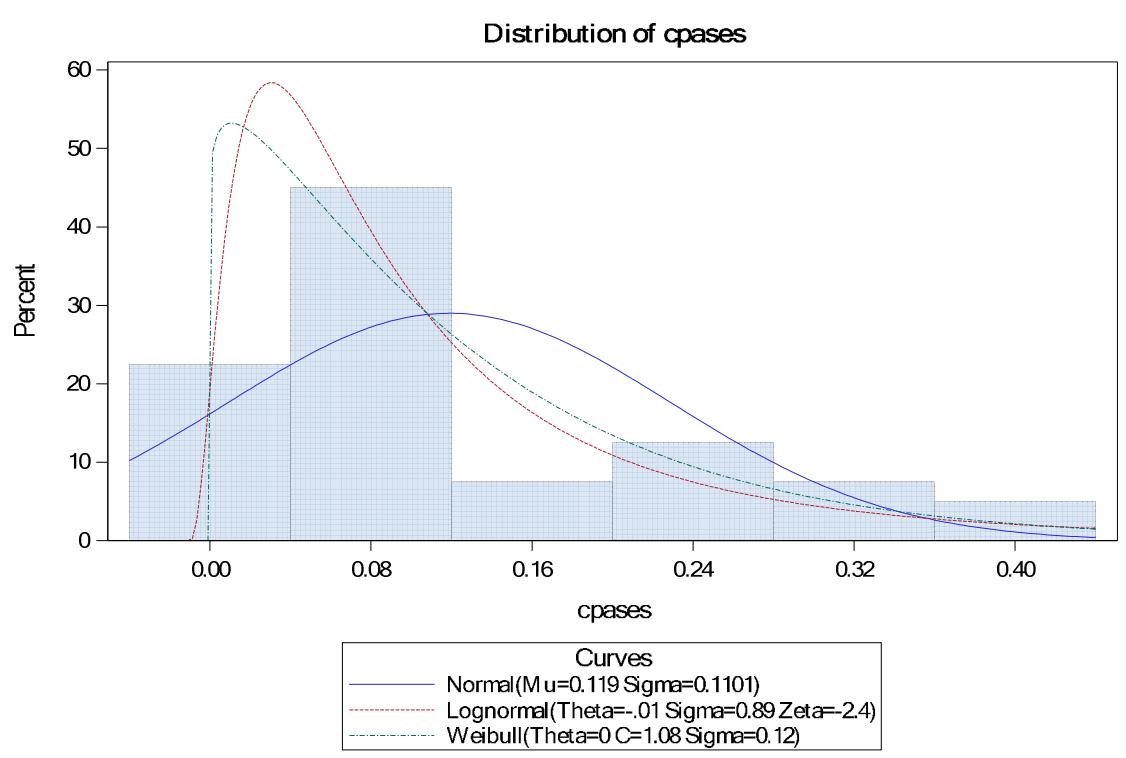


Figure S2B.6.2. Q-Q plot for normal distribution fit for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

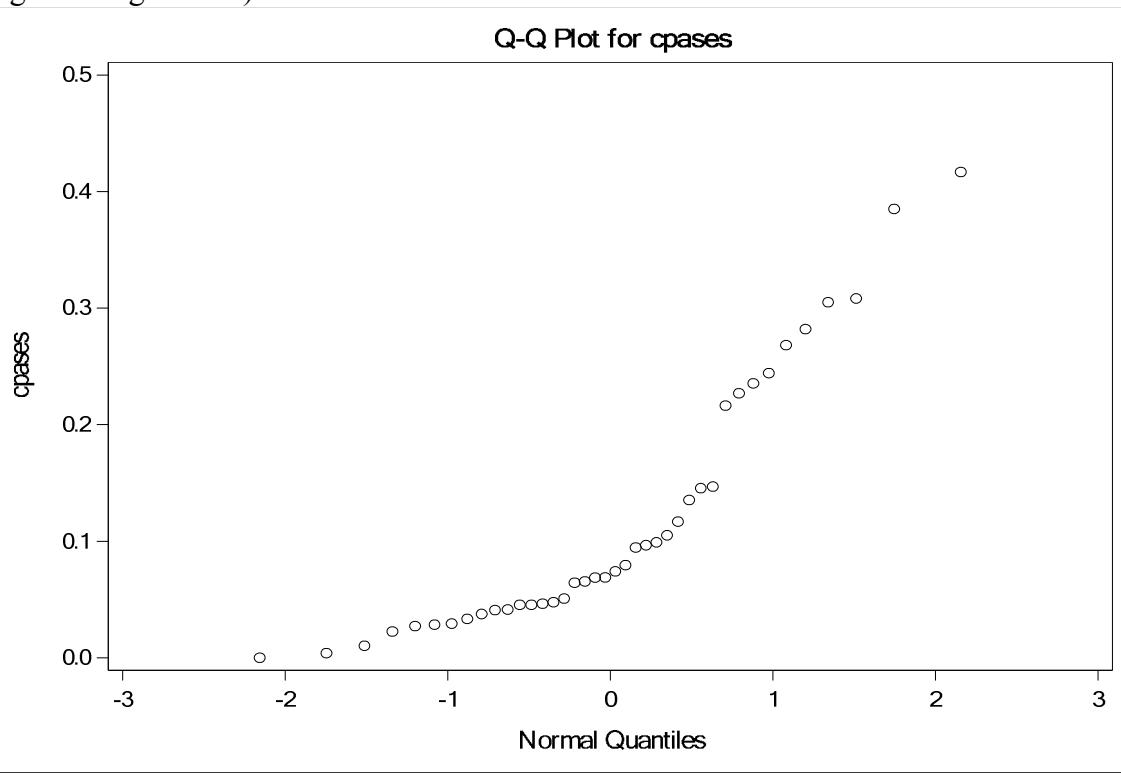


Figure S2B.6.3. Q-Q plot for lognormal distribution fit for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

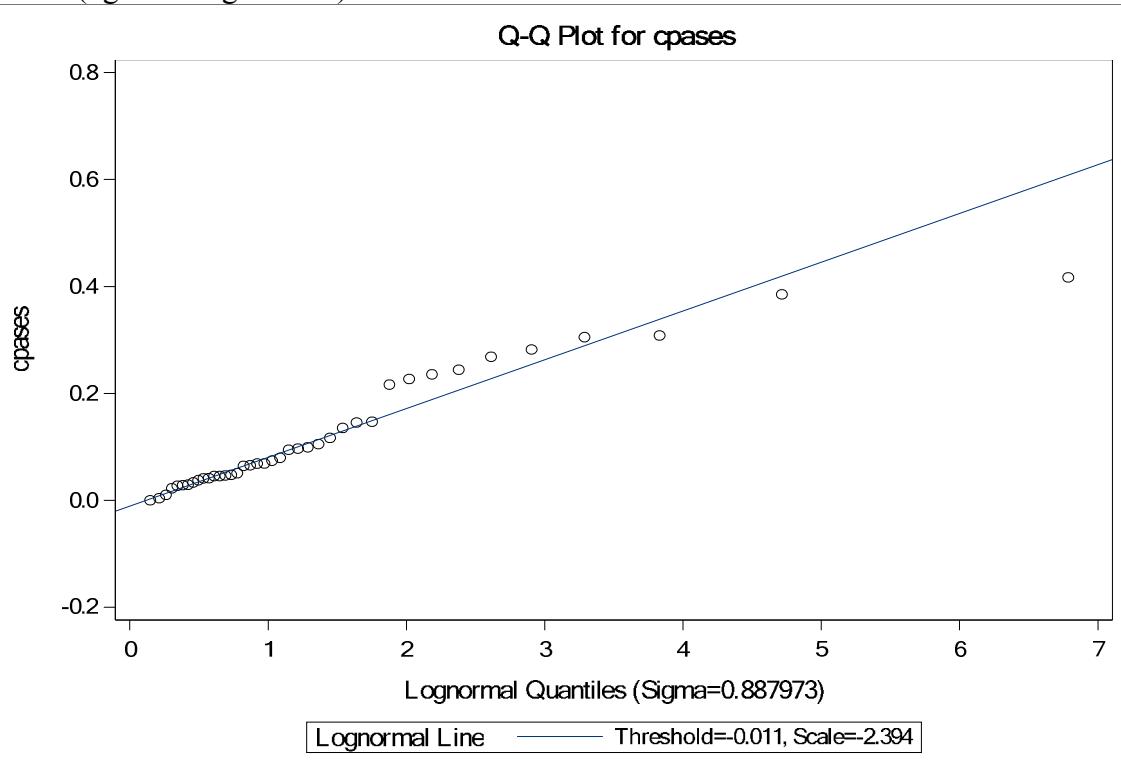


Figure S2B.6.4. Q-Q plot for Weibull distribution fit for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

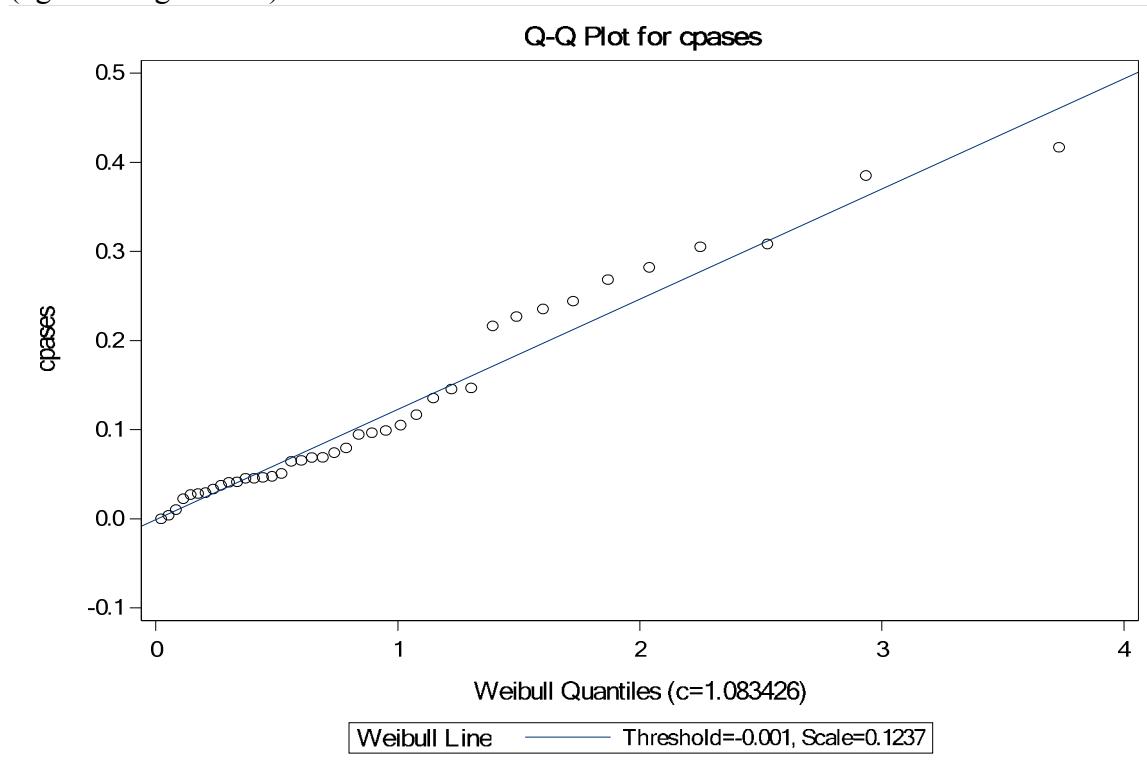


Table S2B.6.2. Parameter estimates for normal distribution fit for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	0.119001
Std Dev	Sigma	0.110078

Table S2B.6.3. Results of tests for normality for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

Tests for Normality				
Test	Statistic	p Value		
Shapiro-Wilk	W	0.842894	Pr < W	<0.0001
Kolmogorov-Smirnov	D	0.200401	Pr > D	<0.0100
Cramer-von Mises	W-Sq	0.450343	Pr > W-Sq	<0.0050
Anderson-Darling	A-Sq	2.43299	Pr > A-Sq	<0.0050

Table S2B.6.4. Parameter estimates for lognormal distribution fit for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

Parameters for Lognormal Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.0111
Scale	Zeta	-2.39362
Shape	Sigma	0.887973
Mean		0.12432
Std Dev		0.148351

Table S2B.6.5. Results of goodness-of-fit tests for lognormal distribution fit for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

Goodness-of-Fit Tests for Lognormal Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.09809380	Pr > D	>0.250
Cramer-von Mises	W-Sq	0.04707354	Pr > W-Sq	>0.250
Anderson-Darling	A-Sq	0.34914859	Pr > A-Sq	>0.250

Table S2B.6.6. Parameter estimates for Weibull distribution fit for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

Parameters for Weibull Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.001
Scale	Sigma	0.123742
Shape	C	1.083426
Mean		0.119011
Std Dev		0.110868

Goodness of fit test not available for Weibull distribution.

Gamma distribution could not be fit.

S2B.7 Gross primary production – Biofilm (mg O₂/h/mg AFDM)

Table S2B.7.1. Moments of response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

Moments			
N	40	Sum Weights	40
Mean	155999.949	Sum Observations	6239997.97
Std Deviation	95826.2975	Variance	9182679283
Skewness	0.16141356	Kurtosis	-0.2754484
Uncorrected SS	1.33156E12	Corrected SS	3.58124E11
Coeff Variation	61.4271338	Std Error Mean	15151.468

Figure S2B.7.1. Histogram of Gross primary production – Biofilm (mg O₂/h/mg AFDM) with fitted distribution curves.

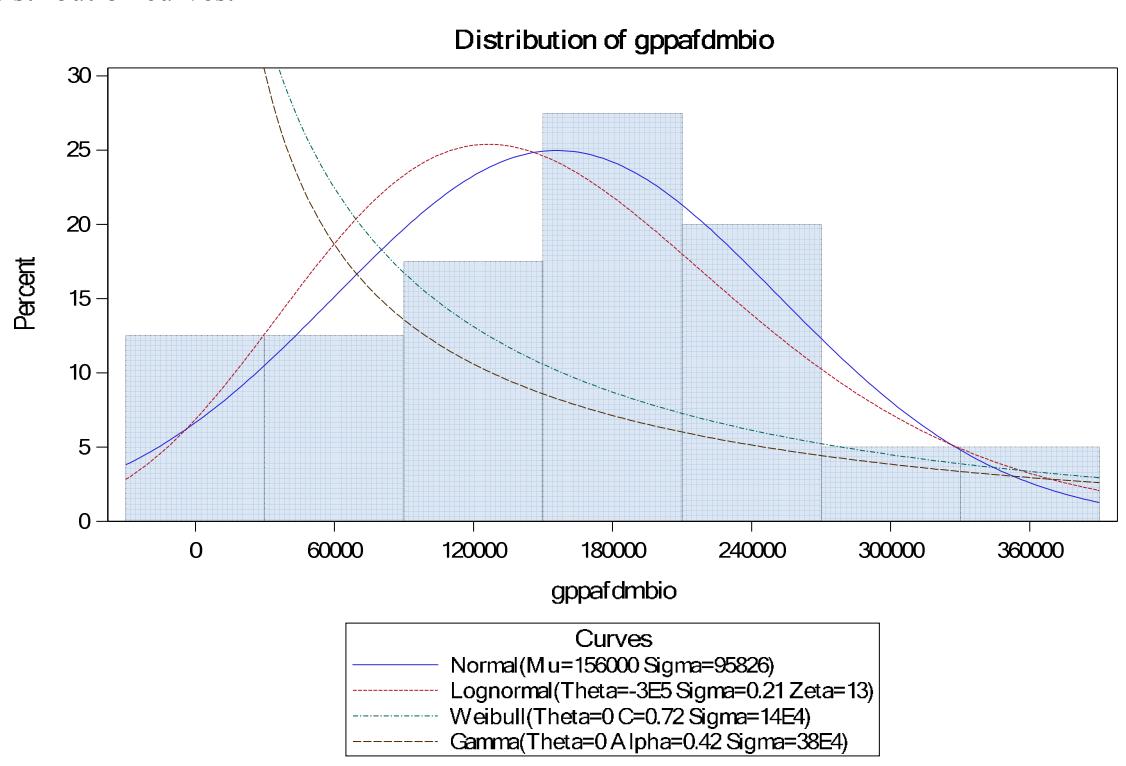


Figure S2B.7.2. Q-Q plot for normal distribution fit for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

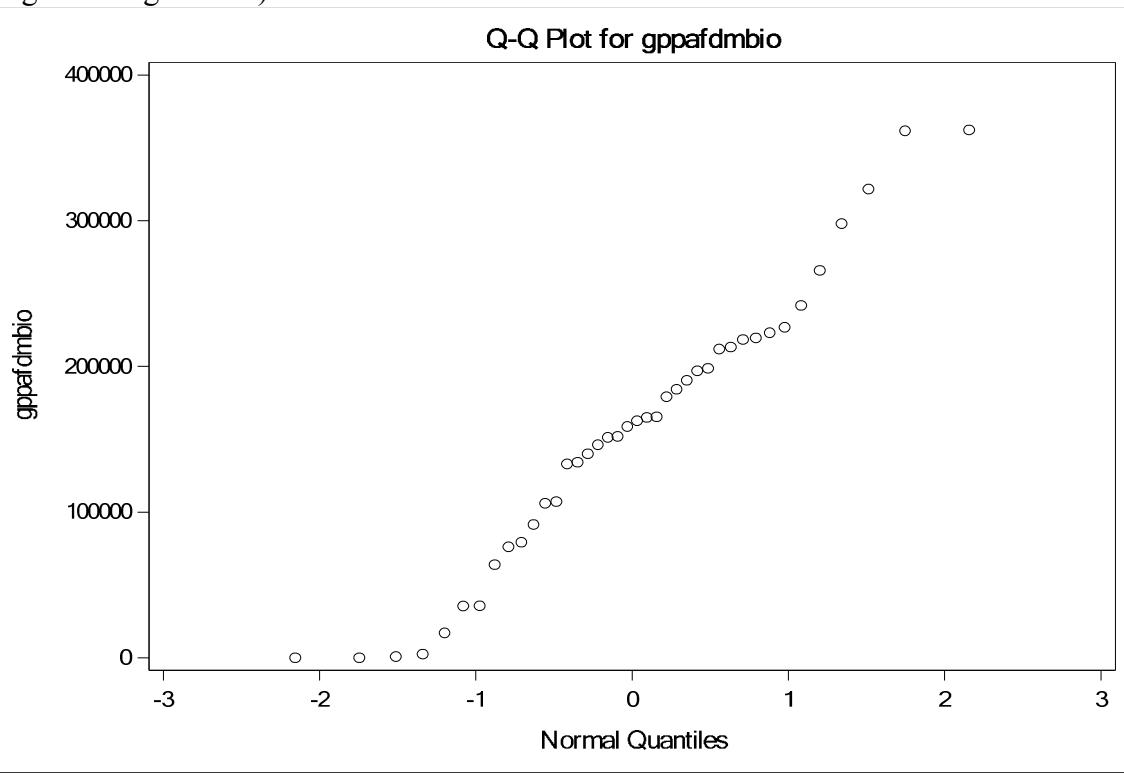


Figure S2B.7.3. Q-Q plot for lognormal distribution fit for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

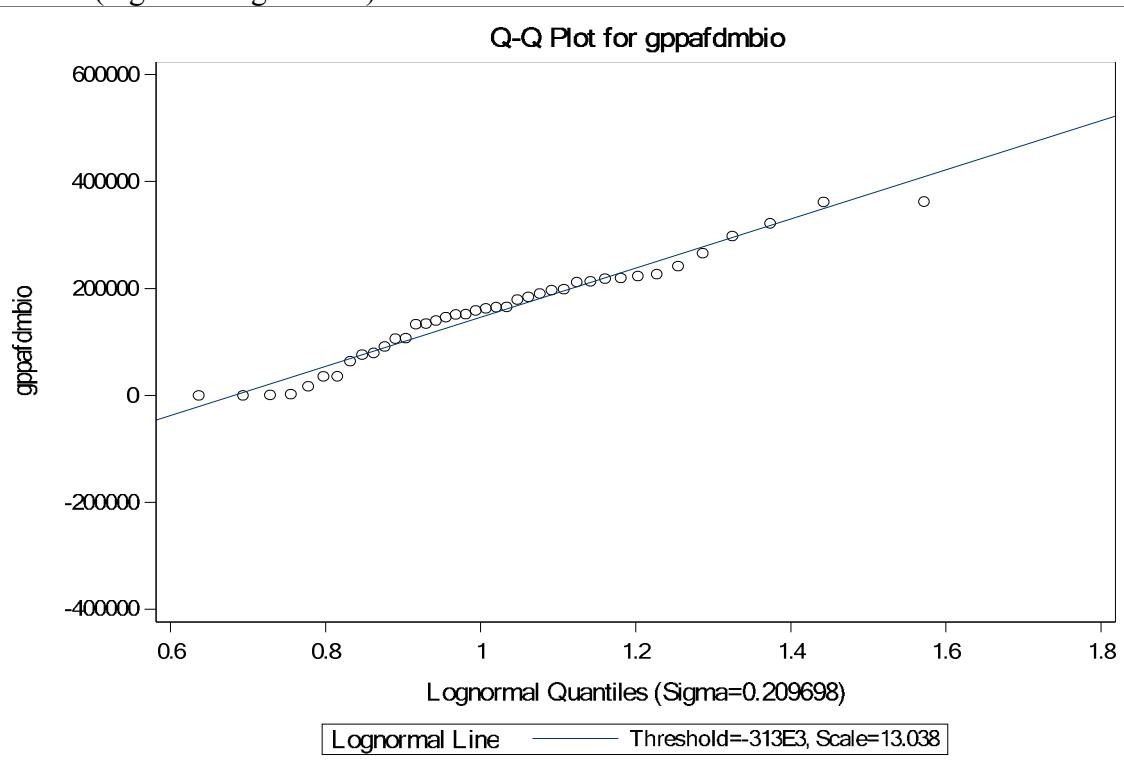


Figure S2B.7.4. Q-Q plot for gamma distribution fit for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

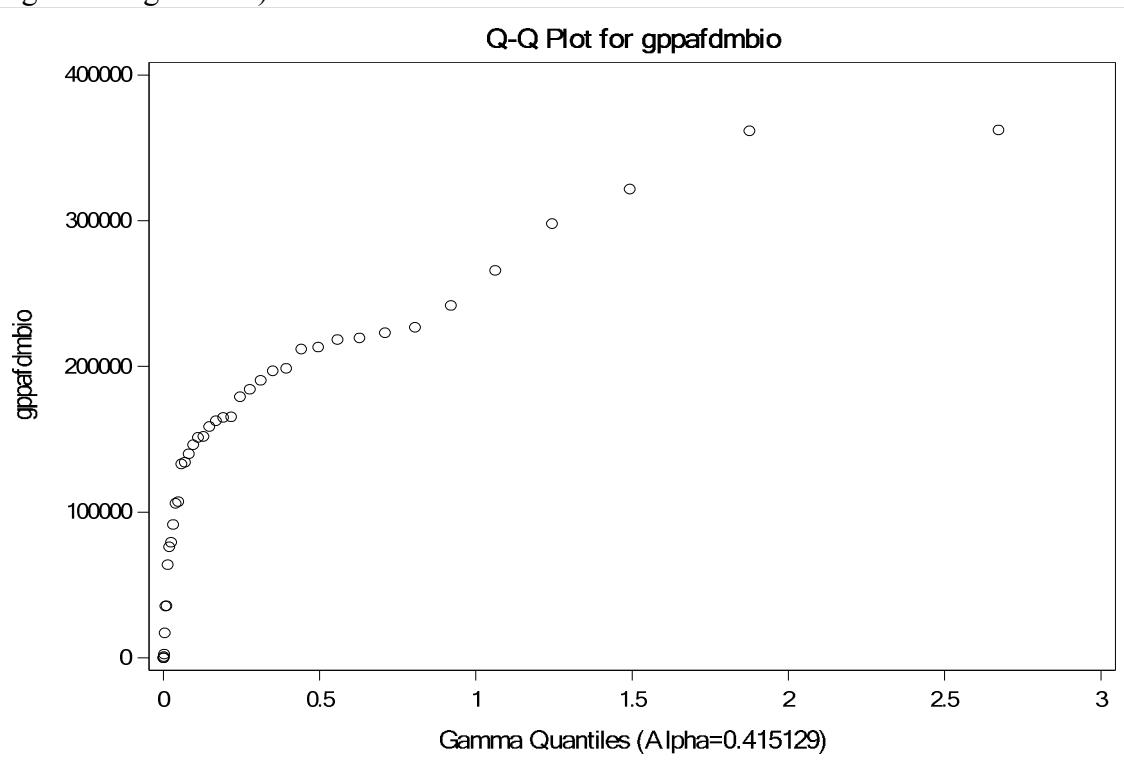


Figure S2B.7.5. Q-Q plot for Weibull distribution fit for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

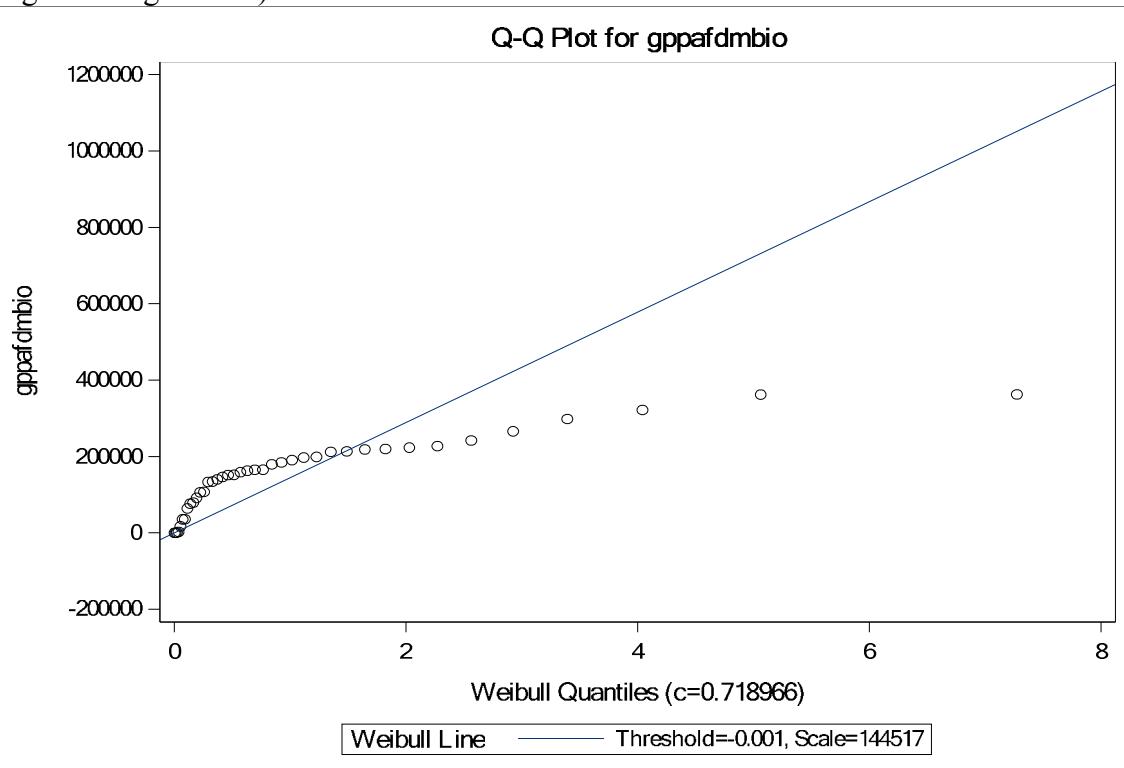


Table S2B.7.2. Parameter estimates for normal distribution fit for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	155999.9
Std Dev	Sigma	95826.3

Table S2B.7.3. Results of tests for normality for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

Tests for Normality				
Test	Statistic	p Value		
Shapiro-Wilk	W	0.965592	Pr < W	0.2588
Kolmogorov-Smirnov	D	0.080503	Pr > D	>0.1500
Cramer-von Mises	W-Sq	0.041133	Pr > W-Sq	>0.2500
Anderson-Darling	A-Sq	0.338648	Pr > A-Sq	>0.2500

Table S2B.7.4. Parameter estimates for lognormal distribution fit for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

Parameters for Lognormal Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-313293
Scale	Zeta	13.03802
Shape	Sigma	0.209698
Mean		156478.8
Std Dev		99602.99

Table S2B.7.5. Results of goodness-of-fit tests for lognormal distribution fit for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

Goodness-of-Fit Tests for Lognormal Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.11982677	Pr > D	0.071
Cramer-von Mises	W-Sq	0.08651319	Pr > W-Sq	0.080
Anderson-Darling	A-Sq	0.55434877	Pr > A-Sq	0.060

Table S2B.7.6. Parameter estimates for Weibull distribution fit for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

Parameters for Weibull Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.001
Scale	Sigma	144516.7
Shape	C	0.718966
Mean		178453.1
Std Dev		253141.5

Goodness of fit not available for Weibull distribution.

Table S2B.7.7. Parameter estimates for gamma distribution fit for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

Parameters for Gamma Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-1E-6
Scale	Sigma	375786.7
Shape	Alpha	0.415129
Mean		155999.9
Std Dev		242121.2

Goodness of fit not available for Gamma distribution.

S2B.8 Gross primary production – Seston (mg O₂/h/mg AFDM)

Table S2B.8.1. Moments of response variable Gross primary production – Seston (mg O₂/h/mg AFDM).

Moments			
N	40	Sum Weights	40
Mean	0.00098996	Sum Observations	0.03959858
Std Deviation	0.0010287	Variance	1.05822E-6
Skewness	0.90545286	Kurtosis	0.06881861
Uncorrected SS	0.00008047	Corrected SS	0.00004127
Coeff Variation	103.912749	Std Error Mean	0.00016265

Figure S2B.8.1. Histogram of Gross primary production – Seston (mg O₂/h/mg AFDM) with fitted distribution curves.

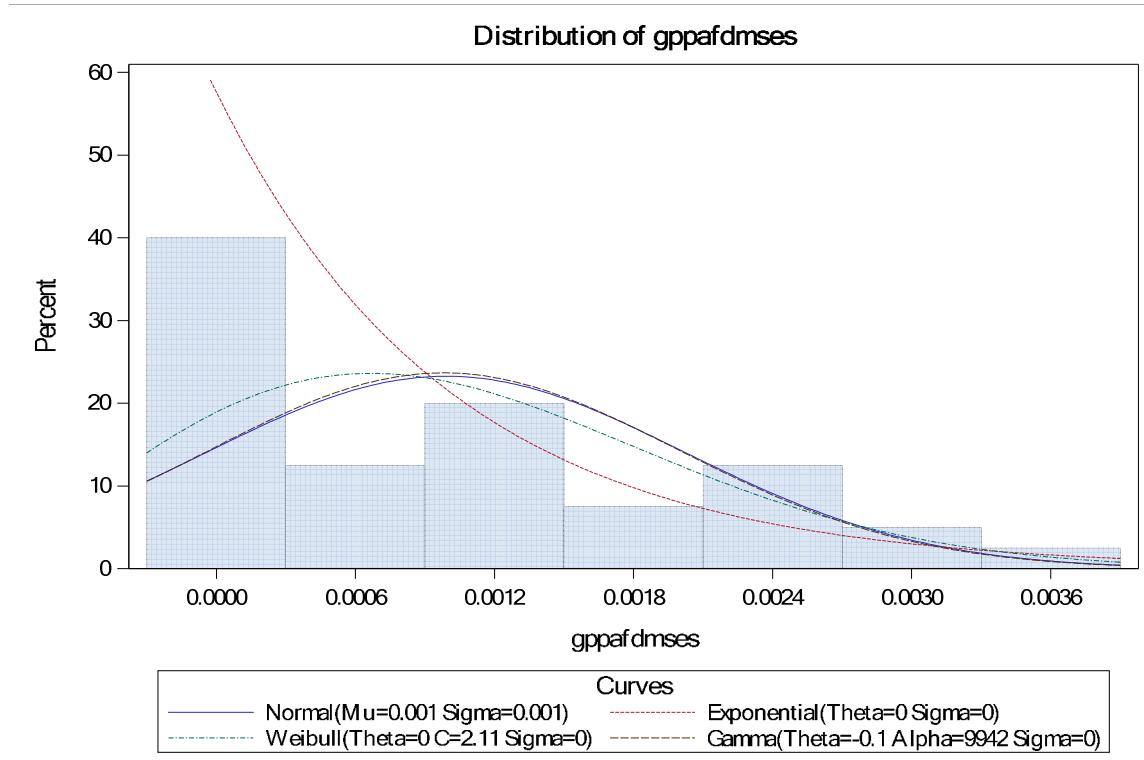


Figure S2B.8.2. Q-Q plot for normal distribution fit for response variable Gross primary production – Seston (mg O₂/h/mg AFDM).

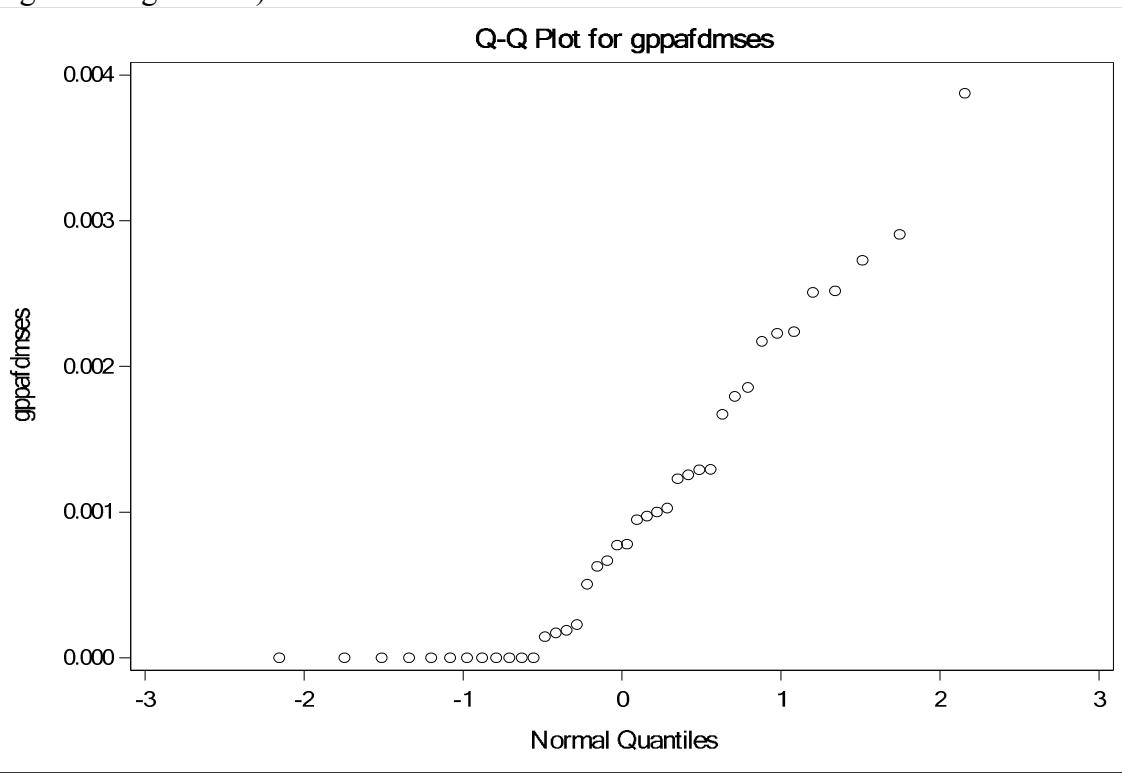


Figure S2B.8.3. Q-Q plot for gamma distribution fit for response variable Gross primary production – Seston (mg O₂/h/mg AFDM).

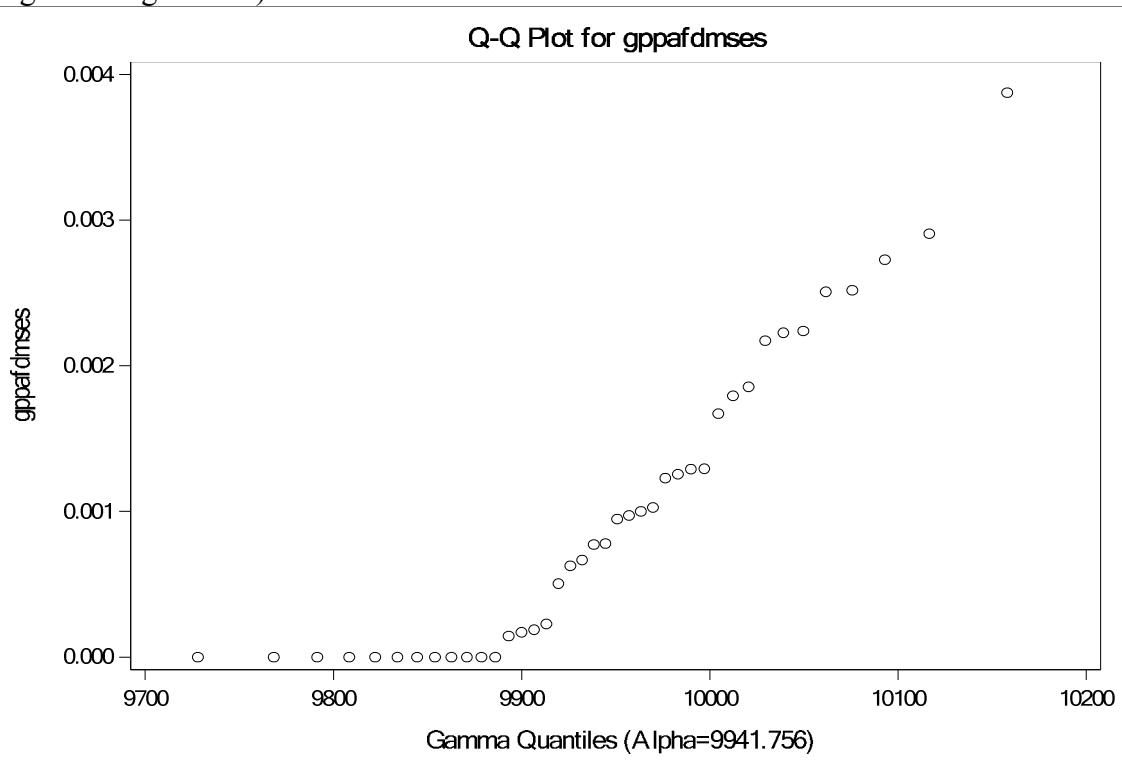


Figure S2B.8.4. Q-Q plot for Weibull distribution fit for response variable Gross primary production – Seston (mg O₂/h/mg AFDM).

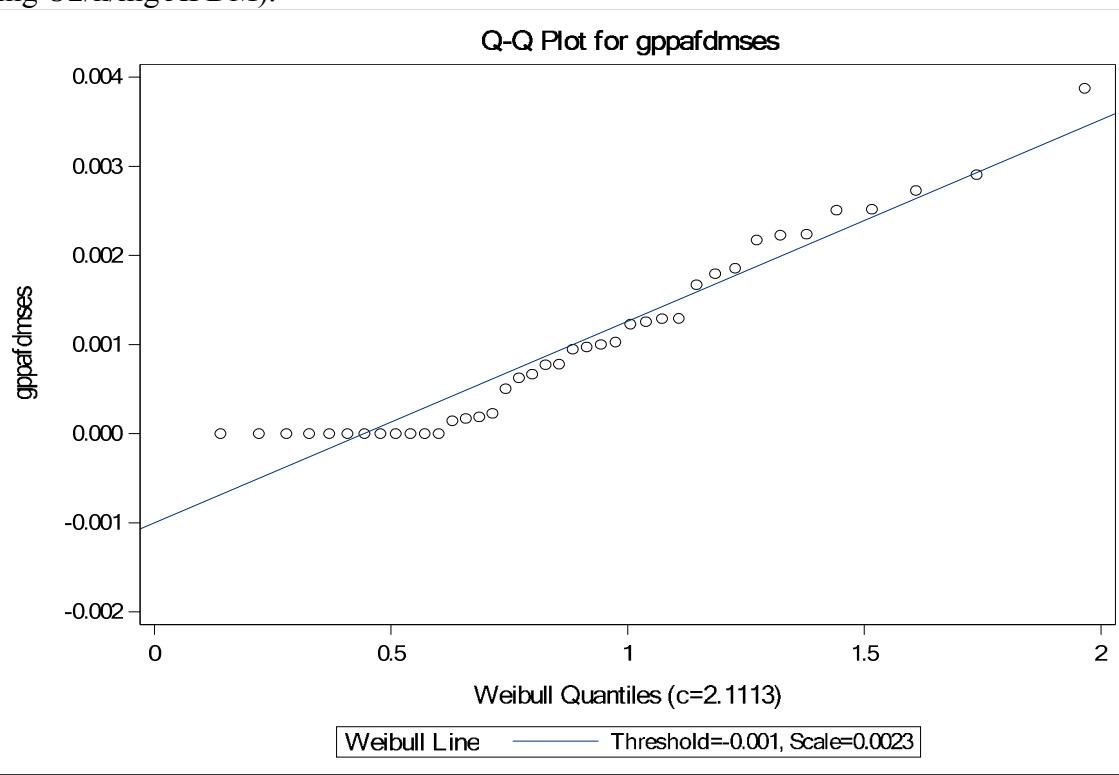


Figure S2B.8.5. Q-Q plot for exponential distribution fit for response variable Gross primary production – Seston (mg O₂/h/mg AFDM).

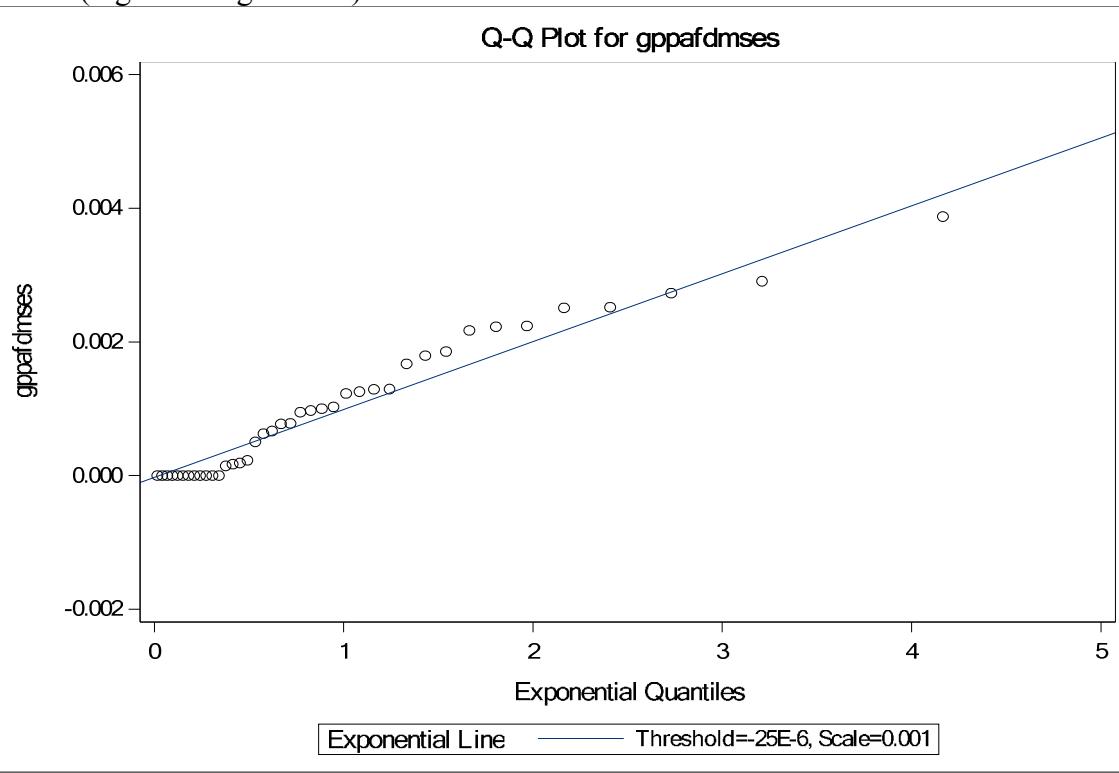


Table S2B.8.2. Parameter estimates for normal distribution fit for response variable Gross primary production – Seston (mg O₂/h/mg AFDM).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	0.00099
Std Dev	Sigma	0.001029

Table S2B.8.3. Results of tests for normality for response variable Gross primary production – Seston (mg O₂/h/mg AFDM).

Tests for Normality				
Test	Statistic	p Value		
Shapiro-Wilk	W	0.871712	Pr < W	0.0003
Kolmogorov-Smirnov	D	0.170609	Pr > D	<0.0100
Cramer-von Mises	W-Sq	0.258564	Pr > W-Sq	<0.0050
Anderson-Darling	A-Sq	1.676881	Pr > A-Sq	<0.0050

Lognormal distribution could not be fit.

S2B.9 Community respiration – Biofilm (mg O₂/h/mg AFDM)

Table S2B.9.1. Moments of response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

Moments			
N	40	Sum Weights	40
Mean	65091.0738	Sum Observations	2603642.95
Std Deviation	31554.1865	Variance	995666683
Skewness	1.88883655	Kurtosis	4.41939878
Uncorrected SS	2.08305E11	Corrected SS	3.8831E10
Coeff Variation	48.4769795	Std Error Mean	4989.15495

Figure S2B.9.1. Histogram of Community respiration – Biofilm (mg O₂/h/mg AFDM) with fitted distribution curves.

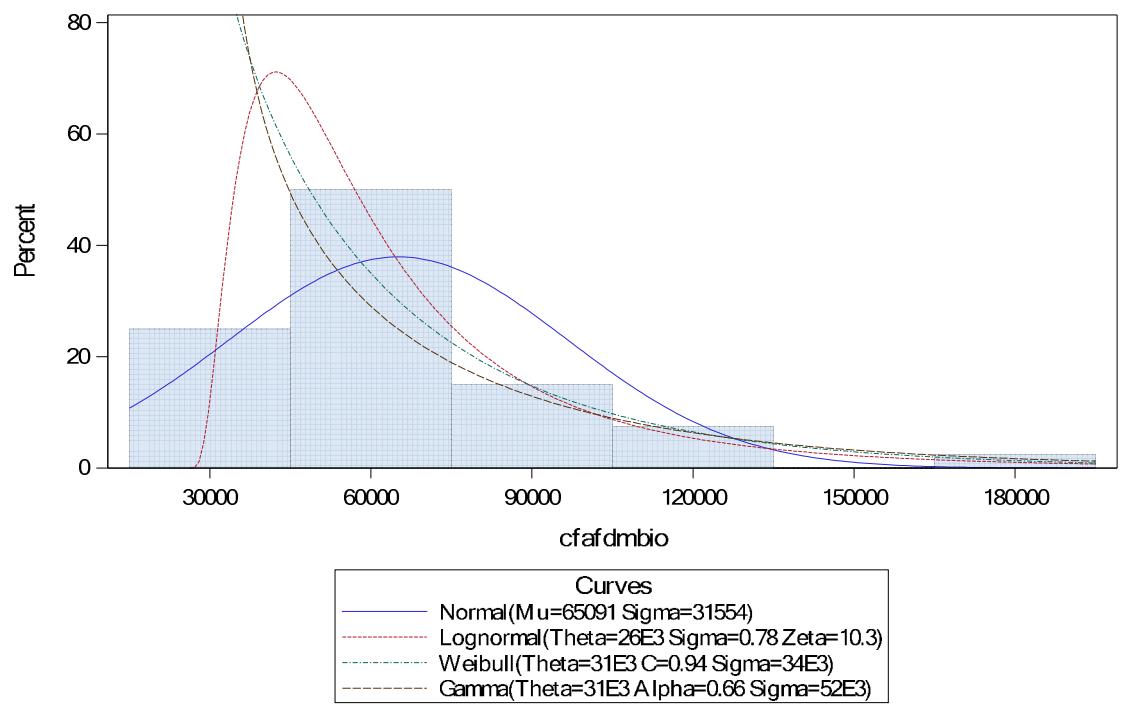


Figure S2B.9.2. Q-Q plot for normal distribution fit for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

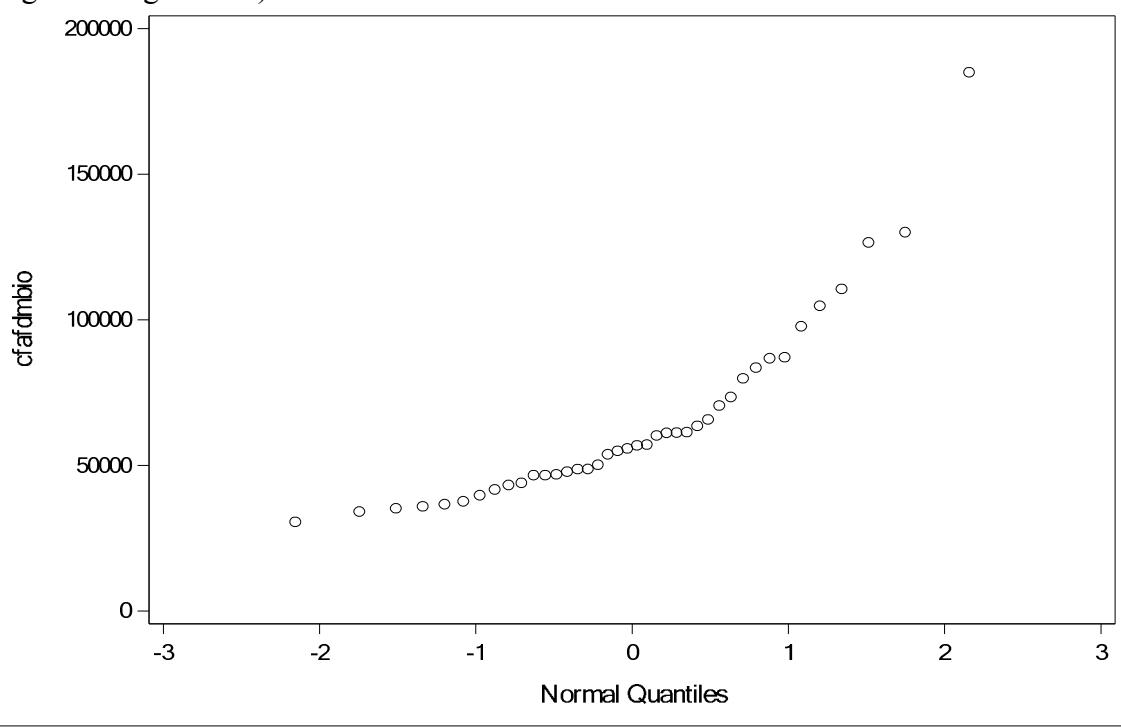


Figure S2B.9.3. Q-Q plot for lognormal distribution fit for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

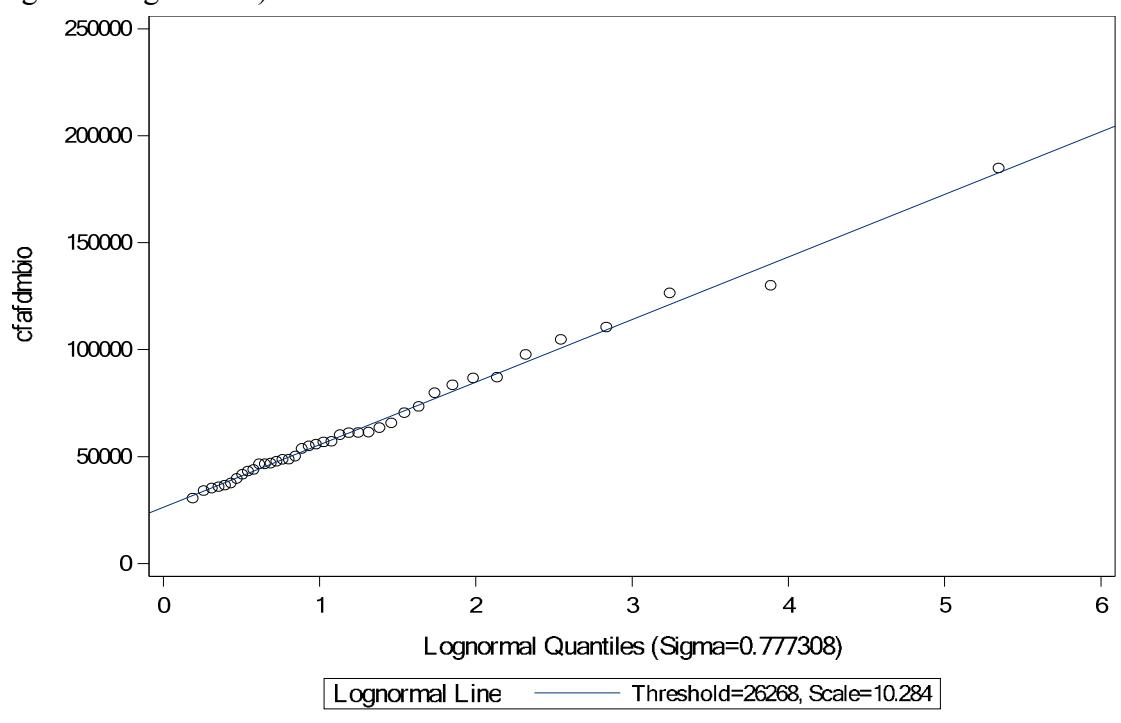


Figure S2B.9.4. Q-Q plot for gamma distribution fit for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

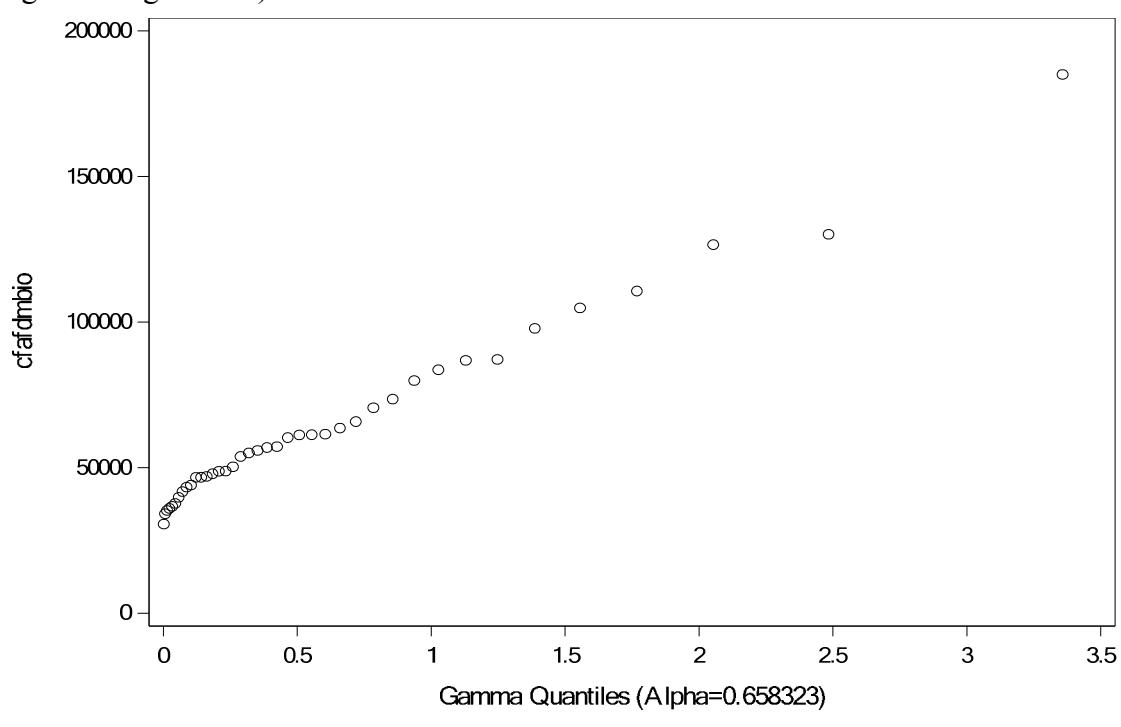


Figure S2B.9.5. Q-Q plot for Weibull distribution fit for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

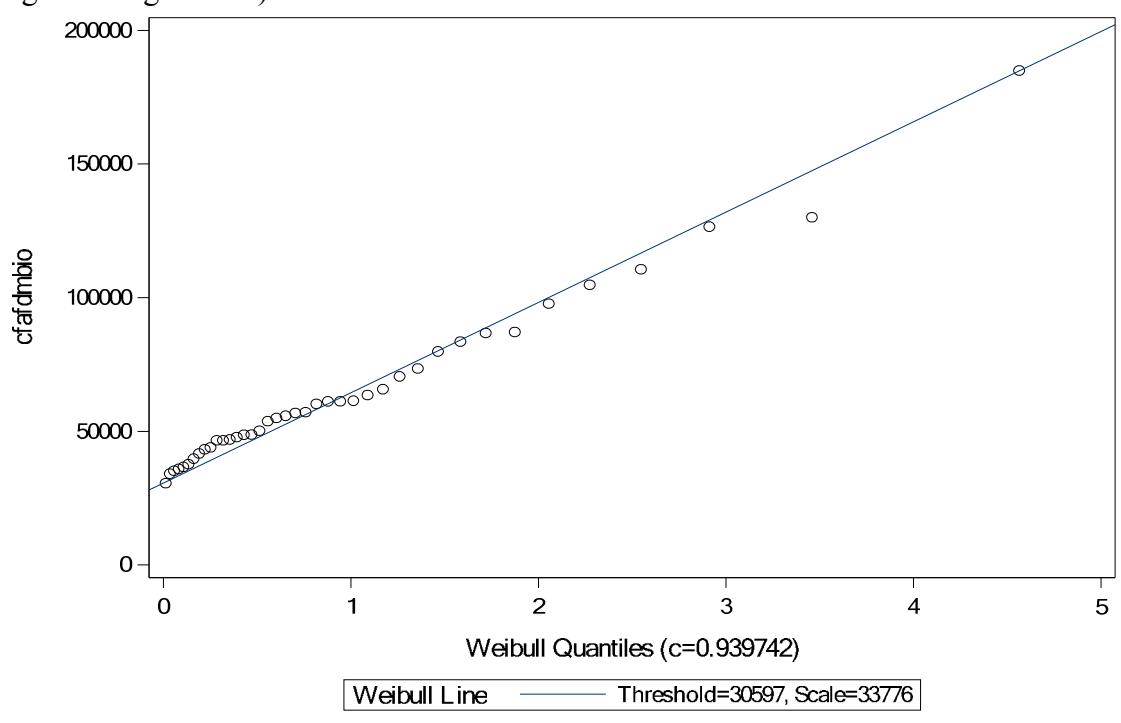


Table S2B.9.2. Parameter estimates for normal distribution fit for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	65091.07
Std Dev	Sigma	31554.19

Table S2B.9.3. Results of tests for normality for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

Tests for Normality				
Test	Statistic	p Value		
Shapiro-Wilk	W	0.821962	Pr < W	<0.0001
Kolmogorov-Smirnov	D	0.195944	Pr > D	<0.0100
Cramer-von Mises	W-Sq	0.365871	Pr > W-Sq	<0.0050
Anderson-Darling	A-Sq	2.070371	Pr > A-Sq	<0.0050

Table S2B.9.4. Parameter estimates for lognormal distribution fit for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

Parameters for Lognormal Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	26268.09
Scale	Zeta	10.28395
Shape	Sigma	0.777308
Mean		65847.13
Std Dev		36053.93

Table S2B.9.5. Results of goodness-of-fit tests for lognormal distribution fit for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

Goodness-of-Fit Tests for Lognormal Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.07081724	Pr > D	>0.500
Cramer-von Mises	W-Sq	0.02003962	Pr > W-Sq	>0.500
Anderson-Darling	A-Sq	0.12545535	Pr > A-Sq	>0.500

Table S2B.9.6. Parameter estimates for Weibull distribution fit for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

Parameters for Weibull Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	30596.68
Scale	Sigma	33775.84
Shape	C	0.939742
Mean		65346.13
Std Dev		36999.21

Goodness of fit not available for Weibull distribution.

Table S2B.9.7. Parameter estimates for gamma distribution fit for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

Parameters for Gamma Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	30596.68
Scale	Sigma	52397.33
Shape	Alpha	0.658323
Mean		65091.07
Std Dev		42513.7

Goodness of fit not available for Gamma distribution.

S2B.10 Community respiration – Seston (mg O₂/h/mg AFDM)

Table S2B.10.1. Moments of response variable Community respiration – Seston (mg O₂/h/mg AFDM).

Moments			
N	40	Sum Weights	40
Mean	0.00122462	Sum Observations	0.04898488
Std Deviation	0.00046309	Variance	2.14455E-7
Skewness	-0.1743026	Kurtosis	0.72533474
Uncorrected SS	0.00006835	Corrected SS	8.36376E-6
Coeff Variation	37.8151985	Std Error Mean	0.00007322

Figure S2B.10.1. Histogram of Community respiration – Seston (mg O₂/h/mg AFDM) with fitted distribution curves.

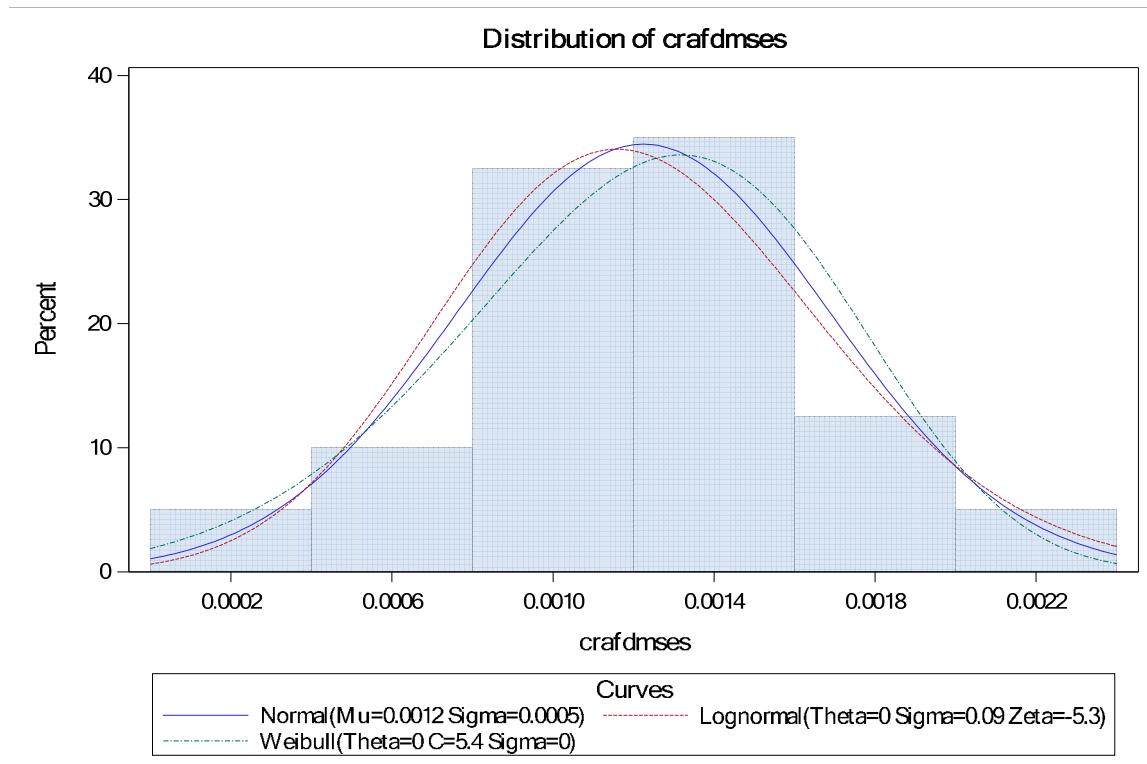


Figure S2B.10.2. Q-Q plot for normal distribution fit for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

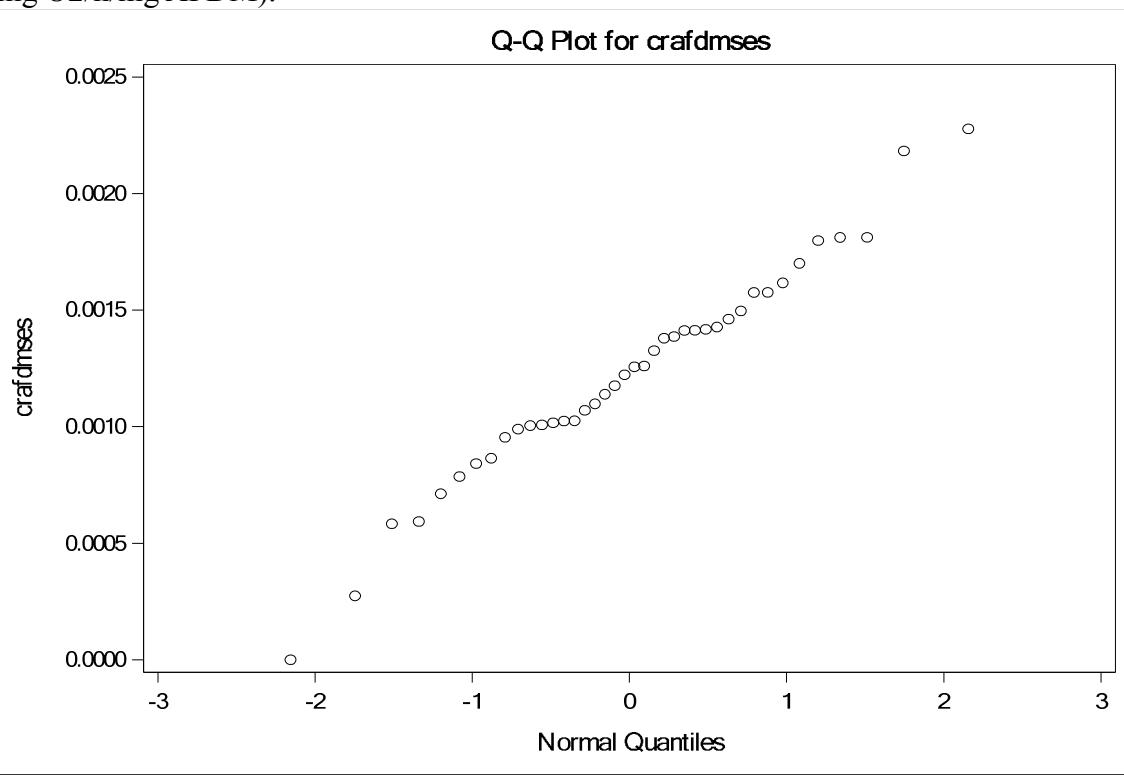


Figure S2B.10.3. Q-Q plot for lognormal distribution fit for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

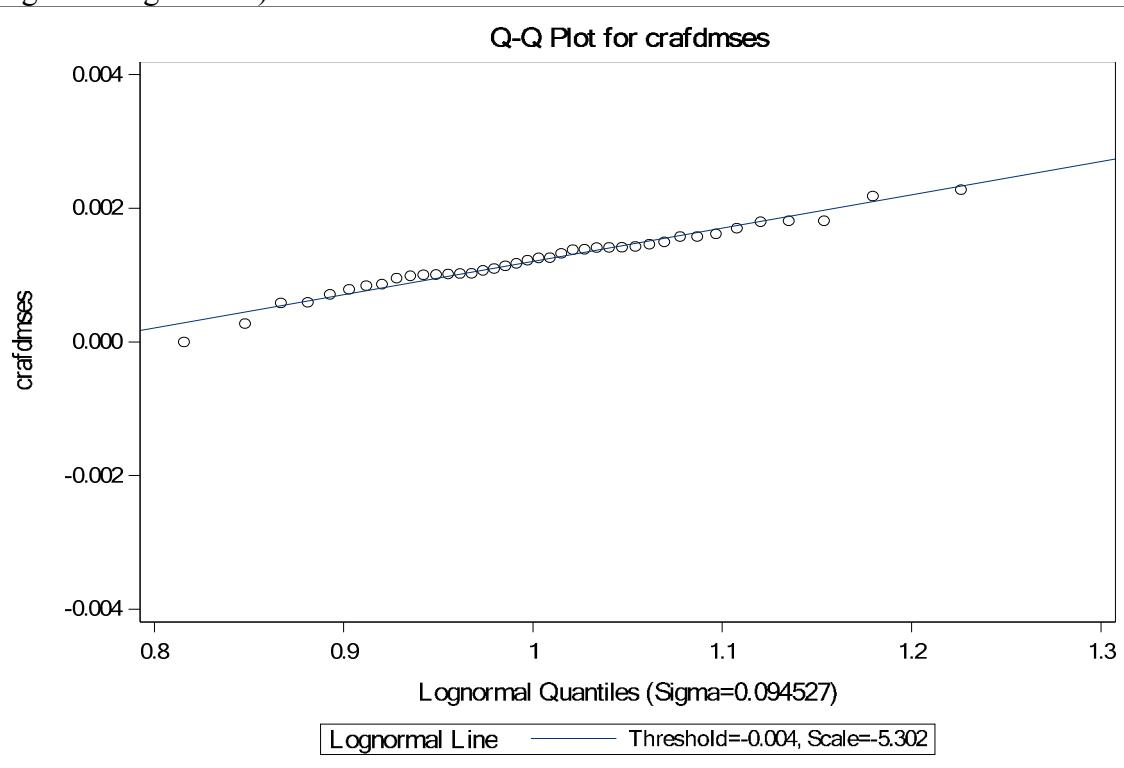


Figure S2B.10.4. Q-Q plot for Weibull distribution fit for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

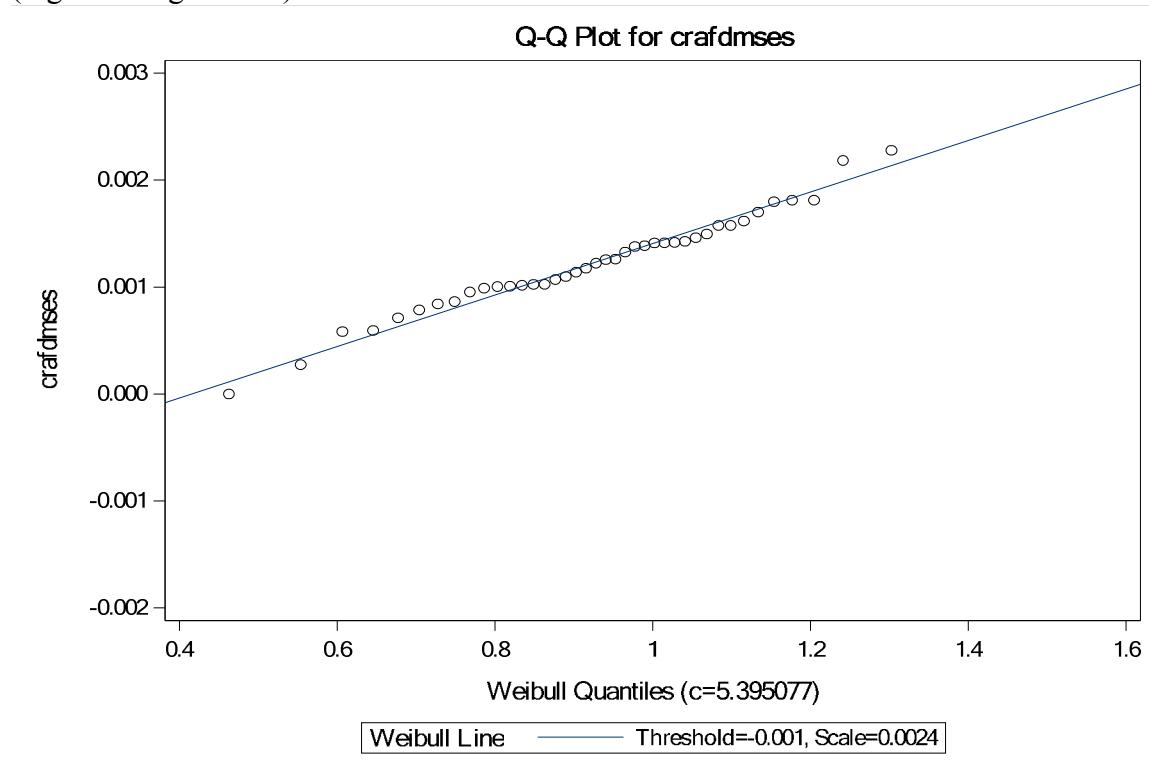


Table S2B.10.2. Parameter estimates for normal distribution fit for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	0.001225
Std Dev	Sigma	0.000463

Table S2B.10.3. Results of tests for normality for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

Tests for Normality				
Test	Statistic	p Value		
Shapiro-Wilk	W	0.983948	Pr < W	0.8308
Kolmogorov-Smirnov	D	0.08108	Pr > D	>0.1500
Cramer-von Mises	W-Sq	0.037397	Pr > W-Sq	>0.2500
Anderson-Darling	A-Sq	0.25973	Pr > A-Sq	>0.2500

Table S2B.10.4. Parameter estimates for lognormal distribution fit for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

Parameters for Lognormal Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.00378
Scale	Zeta	-5.30237
Shape	Sigma	0.094527
Mean		0.001226
Std Dev		0.000474

Table S2B.10.5. Results of goodness-of-fit tests for lognormal distribution fit for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

Goodness-of-Fit Tests for Lognormal Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.09656854	Pr > D	>0.250
Cramer-von Mises	W-Sq	0.05081130	Pr > W-Sq	>0.250
Anderson-Darling	A-Sq	0.35080389	Pr > A-Sq	>0.250

Table S2B.10.6. Parameter estimates for Weibull distribution fit for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

Parameters for Weibull Distribution		
Parameter	Symbol	Estimate
Threshold	Theta	-0.001
Scale	Sigma	0.002407
Shape	C	5.395077
Mean		0.00122
Std Dev		0.000474

Table S2B.10.7. Results of goodness-of-fit tests for Weibull distribution fit for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

Goodness-of-Fit Tests for Weibull Distribution				
Test	Statistic	p Value		
Kolmogorov-Smirnov	D	0.07737904	Pr > D	>0.500
Cramer-von Mises	W-Sq	0.04923077	Pr > W-Sq	>0.250
Anderson-Darling	A-Sq	0.34087509	Pr > A-Sq	>0.250

Gamma distribution could not be fit.

S2B.11 Invertebrate emergence (individuals)

Table S2B.11.1. Moments of response variable Invertebrate emergence (individuals).

Moments			
N	18	Sum Weights	18
Mean	85.3333333	Sum Observations	1536
Std Deviation	57.4916874	Variance	3305.29412
Skewness	0.9191108	Kurtosis	0.27741848
Uncorrected SS	187262	Corrected SS	56190
Coeff Variation	67.3730711	Std Error Mean	13.5509207

Table S2B.11.2. Parameter estimates for normal distribution fit for response variable Invertebrate emergence (individuals).

Parameters for Normal Distribution		
Parameter	Symbol	Estimate
Mean	Mu	85.33333
Std Dev	Sigma	57.49169

Table S2B.11.3. Results of tests for normality for response variable Invertebrate emergence (individuals).

Tests for Normality				
Test	Statistic	p Value		
Shapiro-Wilk	W	0.917404	Pr < W	0.1163
Kolmogorov-Smirnov	D	0.187226	Pr > D	0.0928
Cramer-von Mises	W-Sq	0.091201	Pr > W-Sq	0.1395
Anderson-Darling	A-Sq	0.54597	Pr > A-Sq	0.1418

Figure S2B.11.1. Histogram of Invertebrate emergence (individuals) with fitted normal distribution curve.

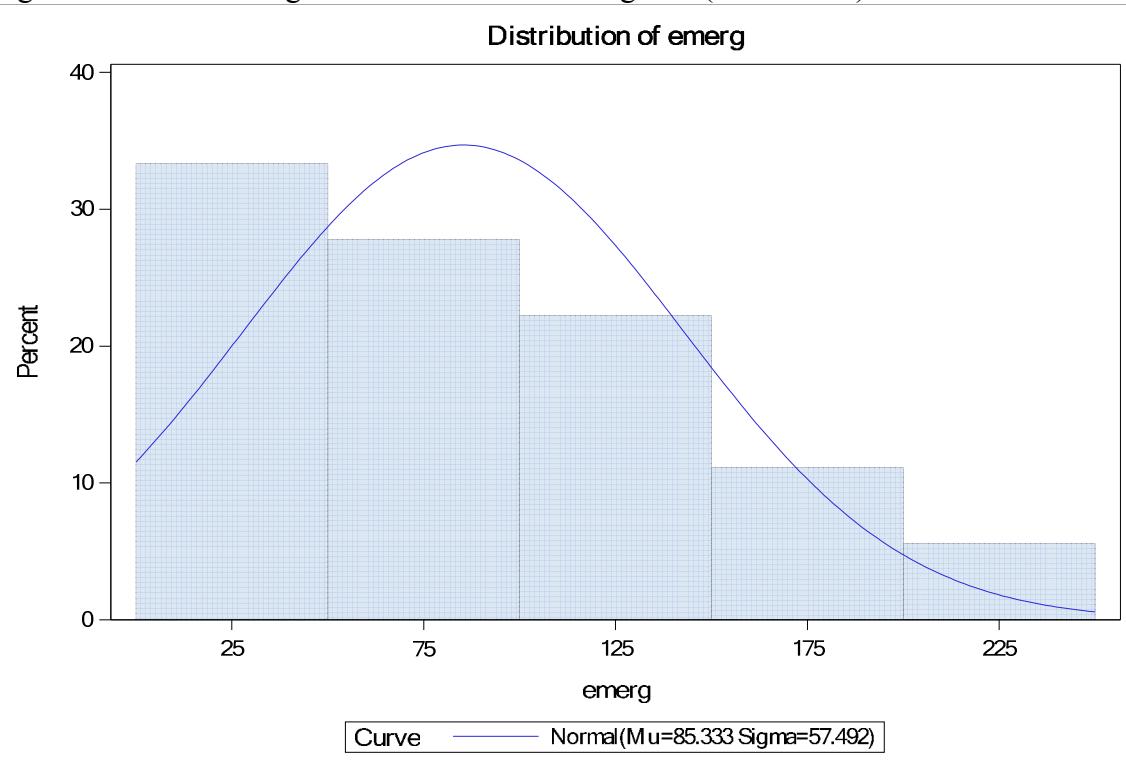


Figure S2B.11.2. Q-Q plot for normal distribution fit for response variable Invertebrate emergence (individuals).

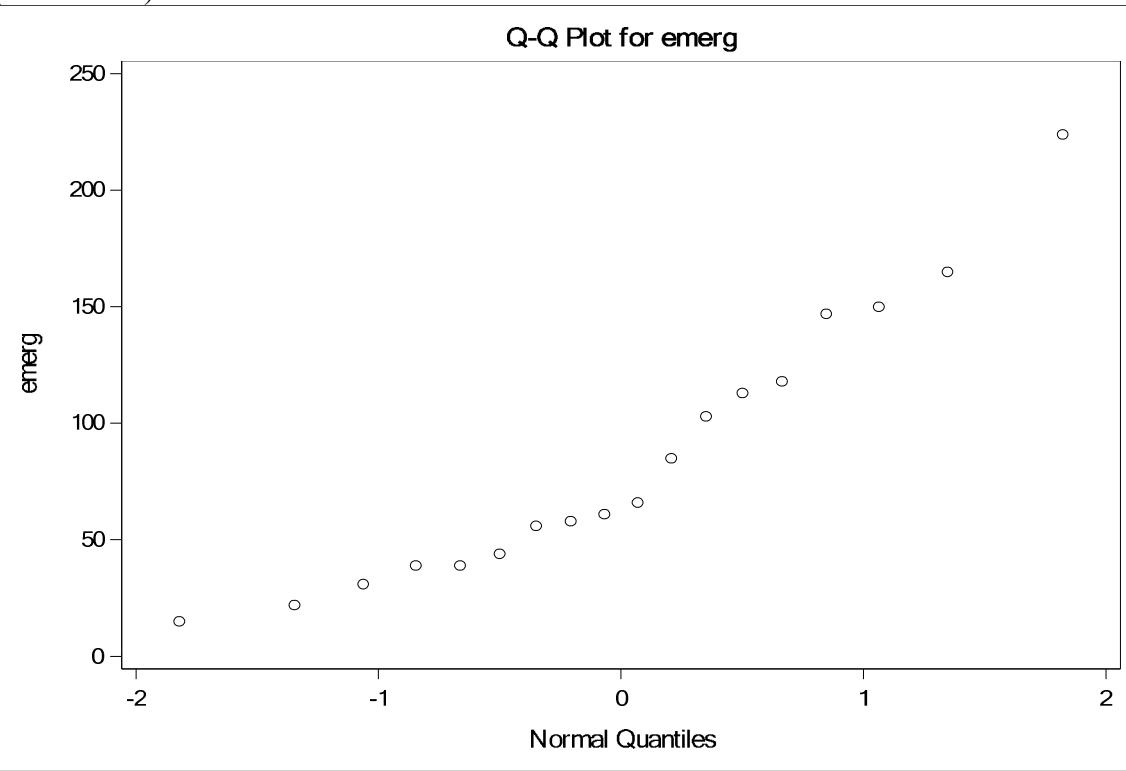


Table S2B.11.4. Maximum likelihood parameter estimates for poisson distribution fit for response variable Invertebrate emergence (individuals).

Poisson Distribution Analysis Of Maximum Likelihood Parameter Estimates						
Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square	Pr > ChiSq
Intercept	1	4.4466	0.0255	4.3966 4.4966	30369.7	<.0001
Scale	0	1.0000	0.0000	1.0000 1.0000		

Table S2B.11.5. Maximum likelihood parameter estimates for negative binomial distribution fit for response variable Invertebrate emergence (individuals).

Negative Binomial Distribution Analysis Of Maximum Likelihood Parameter Estimates						
Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square	Pr > ChiSq
Intercept	1	4.4466	0.1555	4.1418 4.7513	817.95	<.0001
Dispersion	1	0.4234	0.1371	0.2245 0.7986		

S2B.12 Selected distributions.

Table S2B.12.1 Distributions selected for analysis of response variables in generalized linear mixed models.

Variable	Distribution selected	Link	Notes
Chlorophyll a – Biofilm (ug/m ²)	Lognormal	Identity	
Chlorophyll a – Seston (ug/L)	Lognormal	Identity	
Ash-free dry mass – Biofilm (mg/m ²)	Lognormal	Identity	
Ash-free dry mass – Seston (mg/L)	Lognormal	Identity	
Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM)	Lognormal	Identity	
Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM)	Lognormal	Identity	
Gross primary production – Biofilm (mg O ₂ /h/mg AFDM)	Gamma	Log	GLMM with lognormal distribution fails residual diagnostics (See S2C-D).
Gross primary production – Seston (mg O ₂ /h/mg AFDM)	Lognormal	Identity	GLMM with exponential distribution fails to converge (See S2C-D).
Community respiration – Biofilm (mg O ₂ /h/mg AFDM)	Lognormal	Identity	
Community respiration – Seston (mg O ₂ /h/mg AFDM)	Lognormal	Identity	
Invertebrate emergence (individuals)	Gaussian	Identity	

S2C. SAS code for generalized linear mixed models (proc glimmix).

```
/**Designate working directory*/
libname amph1 '/folders/myfolders';

/**Call in metabolism dataset with chl a, AFDM, chl a per AFDM, GPP CR.
 Trt=AMPH=1 should appear first for correct simple effect comparisons
 and confidence interval calculations.*/
proc contents data=amph1.metdata;
run;

/**Testing the effect of treatments on each variable with generalized linear mixed models.
 Method = LaPlace = Maximum Likelihood
 Fixed factors = trt, day, trt*day
 Random factors = stream
 Distribution choice based on proc univariate and residuals diagnostics in proc glimmix**/

/**Chlorophyll a biofilm*/
ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model chlabio=trt day trt*day / dist=lognormal link=identity;
random intercept / subject=stream;
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

/**Chlorophyll a seston*/
ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model chlasses=trt day trt*day / dist=lognormal link=identity;
random intercept / subject=stream;
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

/**AFDM biofilm*/
ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model afdbio=trt day trt*day / dist=lognormal link=identity;
random intercept / subject=stream;
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

/**AFDM seston*/
```

```

ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model afdmses=trt day trt*day / dist=lognormal link=identity;
random intercept / subject=stream;
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

```

/**Chlorophyll a per AFDM biofilm**/

```

ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model cpabio=trt day trt*day / dist=lognormal link=identity;
random intercept / subject=stream;
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

```

/**Chlorophyll a per AFDM seston**/

```

ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model cpases=trt day trt*day / dist=lognormal link=identity;
random intercept / subject=stream;
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

```

/**GPP biofilm

Not Lognormal distribution due to poor residual fits.

Used Gamma distribution with log link.**/

```

ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model gppafdbio=trt day trt*day / dist=gamma link=log;
random intercept / subject=stream;
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

```

/**GPP seston lognormal distribution. Exponential distribution fails to converge.**/

```

ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model gppafdmse=trt day trt*day / dist=lognormal link=identity;
random intercept / subject=stream;

```

```

lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

/**CR biofilm*/
ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model crafdbio=trt day trt*day / dist=lognormal link=identity;
random intercept / subject=stream;
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

/**CR seston*/
ods graphics on;
proc glimmix data=amph1.metdata order=data method=laplace plots=residualpanel;
class trt day stream;
model crafdses=trt day trt*day / dist=lognormal link=identity;
random intercept / subject=stream;
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;

/**Datalines for Emergence*/
data amph1.emerg;
input trt stream day emerg;
/*NOTE: trt are control=1, amph=0*/
datalines;
0 4 7 165
0 5 7 150
0 6 7 44
1 1 7 31
1 2 7 147
1 3 7 39
0 4 14 56
0 5 14 39
0 6 14 103
1 1 14 22
1 2 14 85
1 3 14 118
0 4 21 224
0 5 21 61
0 6 21 66
1 1 21 15
1 2 21 58
1 3 21 113
;

```

```
/**GLMM for Emergence*/
/**NOTE: control=1, amph=0*/
ods graphics on;
proc glimmix data=amph1.emerg method=laplace plots=residualpanel;
class trt day stream;
model emerg=trt day trt*day / dist=gaussian;
random intercept / subject=stream;
random day / subject=stream*trt type=ar(1);
lsmeans trt*day / ilink cl alpha=0.1 slicediff=day slice=trt slicediff=trt adjust=tukey plot=meanplot(sliceby=trt
join ilink);
run;
```

S2D. Selected proc glimmix output.

S2D.1 Chlorophyll a – Biofilm (ug/m2)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable chlabio
 - Response Distribution Lognormal
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 40
- Convergence criterion (ABSGCONV=0.00001) satisfied.

Figure S2D.1.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Chlorophyll a – Biofilm ($\mu\text{g}/\text{m}^2$) on days 1, 4, 7, 14, and 21.

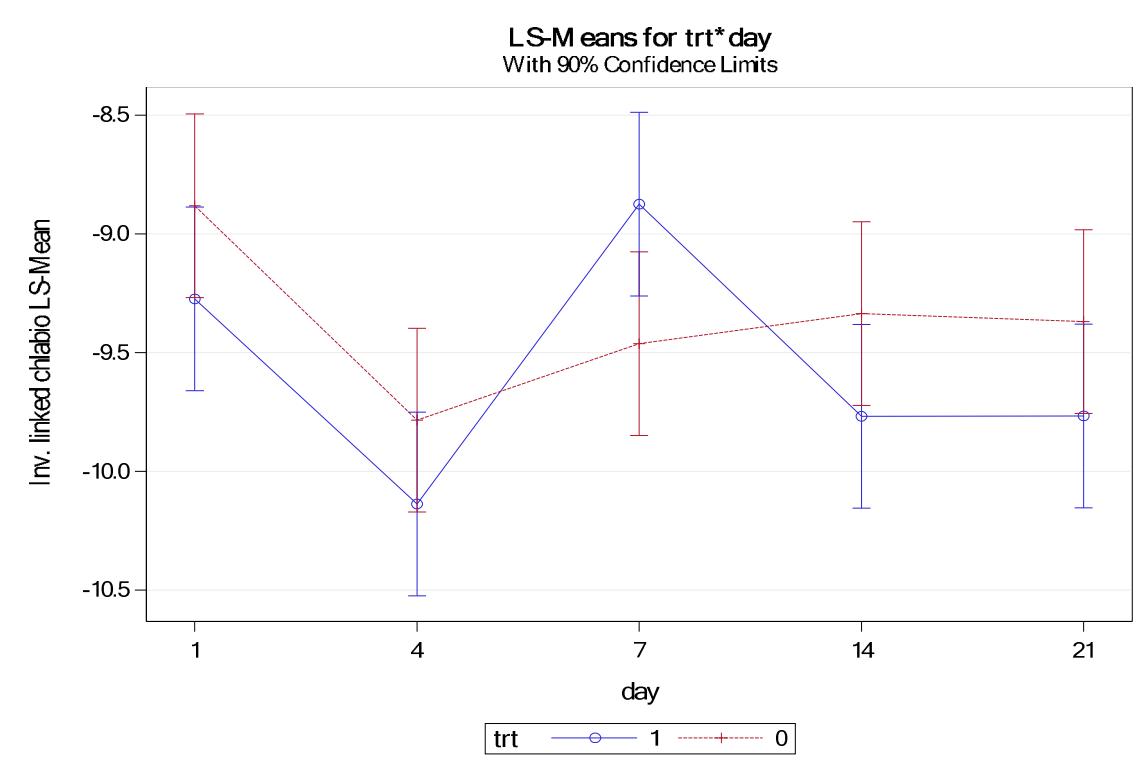


Figure S2D.1.2. GLMM results conditional residuals for response variable Chlorophyll a – Biofilm ($\mu\text{g}/\text{m}^2$).

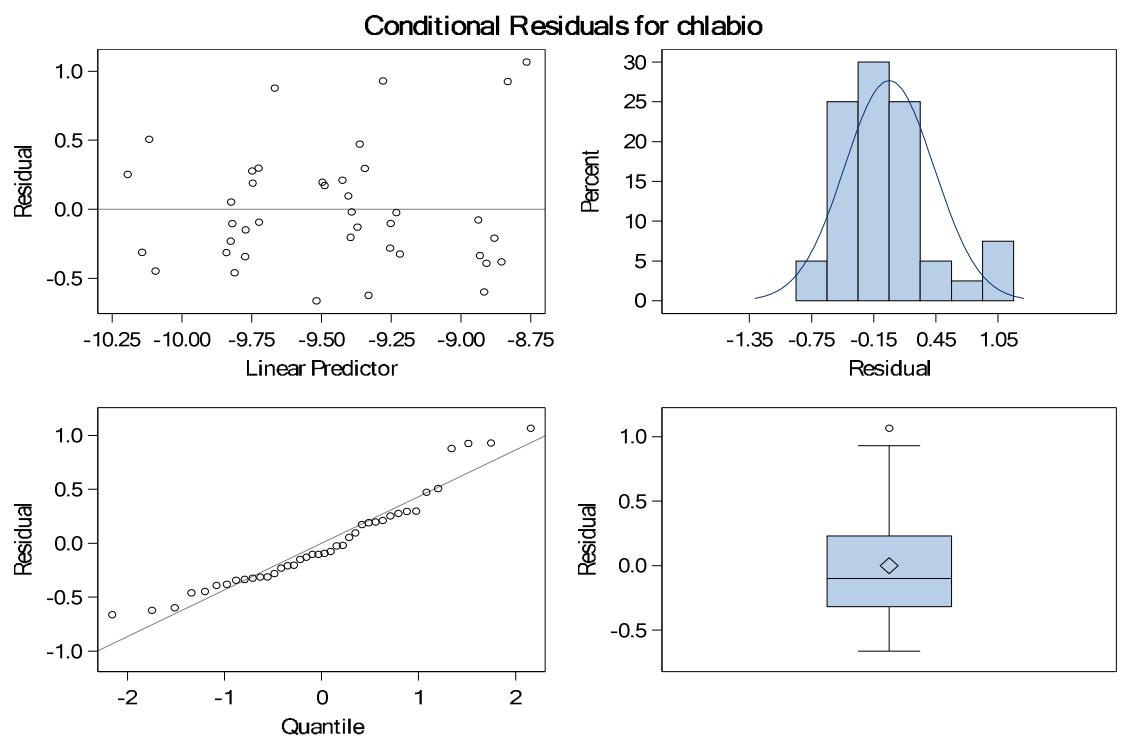


Table S2D.1.1. GLMM results Type III tests of fixed effects for response variable Chlorophyll a – Biofilm (ug/m²).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	24	1.53	0.2275
day	4	24	5.23	0.0036
trt*day	4	24	2.01	0.1249

Table S2D.1.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Chlorophyll a – Biofilm (ug/m²).

Simple Effect Comparisons of trt*day Least Squares Means By day										
Simple Effect Level	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 1	1	0	-0.3920	0.3197	24	-1.23	0.2320	0.1	-0.9389	0.1549
day 4	1	0	-0.3527	0.3197	24	-1.10	0.2809	0.1	-0.8996	0.1943
day 7	1	0	0.5870	0.3197	24	1.84	0.0787	0.1	0.04006	1.1339
day 14	1	0	-0.4320	0.3197	24	-1.35	0.1891	0.1	-0.9790	0.1149
day 21	1	0	-0.3975	0.3197	24	-1.24	0.2257	0.1	-0.9445	0.1494

S2D.2 Chlorophyll a – Seston (ug/L)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable chlases
 - Response Distribution Lognormal
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 39
- Convergence criterion (GCONV=1E-8) satisfied.

Figure S2D.2.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Chlorophyll a – Seston (ug/L) on days 1, 4, 7, 14, and 21.

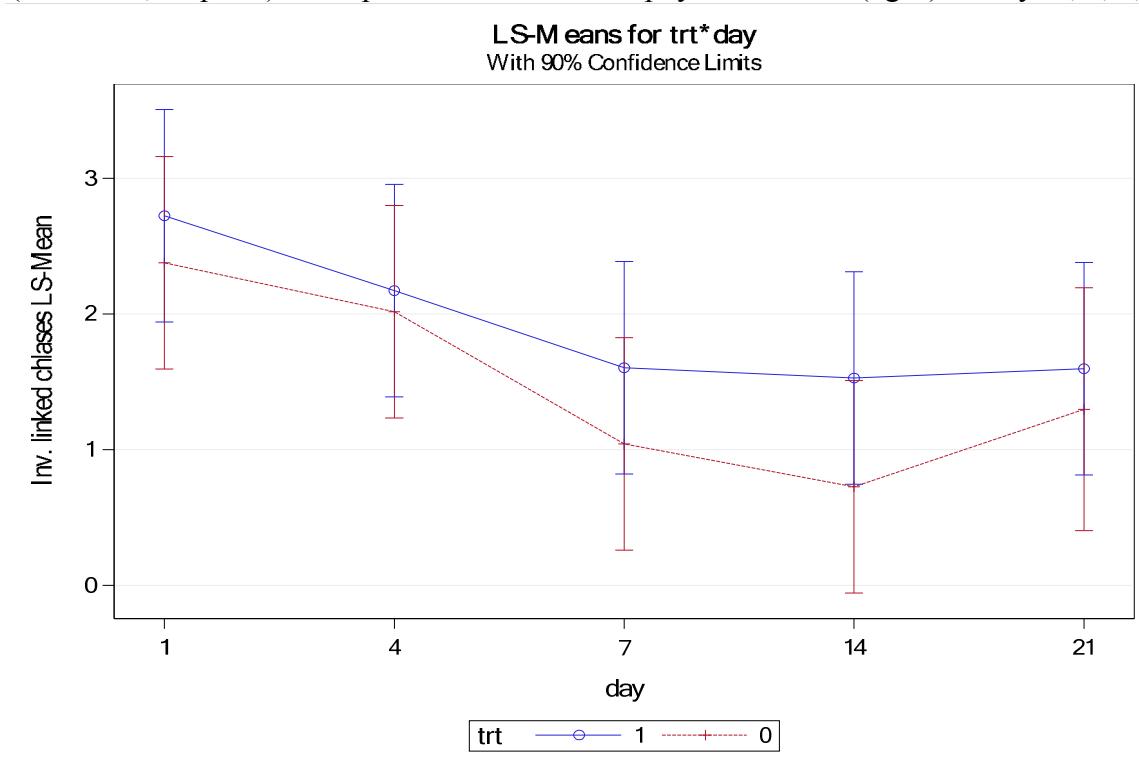


Figure S2D.2.2. GLMM results conditional residuals for response variable Chlorophyll a – Seston (ug/L).

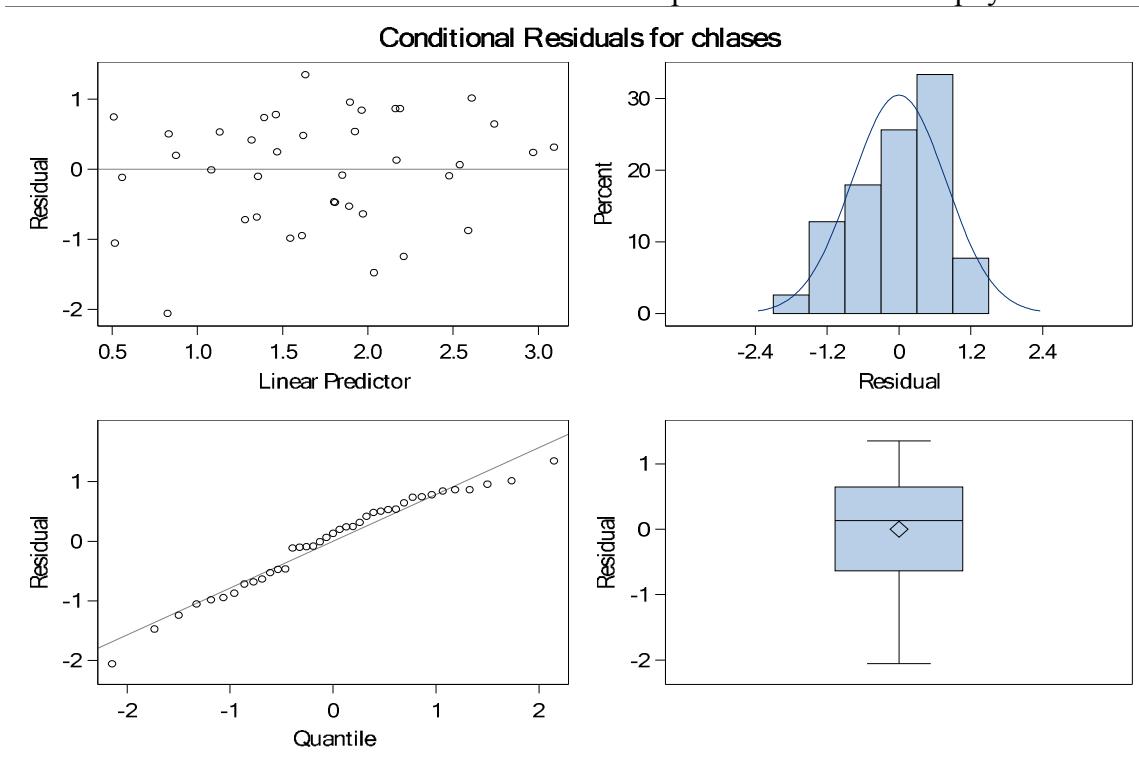


Table S2D.2.1. GLMM results Type III tests of fixed effects for response variable Chlorophyll a – Seston (ug/L).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	23	1.25	0.2750
day	4	23	4.16	0.0112
trt*day	4	23	0.19	0.9428

Table S2D.2.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Chlorophyll a – Seston (ug/L).

Simple Effect Comparisons of trt*day Least Squares Means By day										
Simple Effect Level	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
1.4548	1	0	0.3474	0.6461	23	0.54	0.5960	0.1	-0.7600	
day 4	1	0	0.1552	0.6461	23	0.24	0.8123	0.1	-0.9522	1.2626
day 7	1	0	0.5623	0.6461	23	0.87	0.3931	0.1	-0.5451	1.6698
day 14	1	0	0.8021	0.6461	23	1.24	0.2270	0.1	-0.3053	1.9095
day 21	1	0	0.2987	0.6943	23	0.43	0.6710	0.1	-0.8912	1.4886

S2D.3 Ash-free dry mass – Biofilm (mg/m²)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable afdbio
 - Response Distribution Lognormal
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 40
- Convergence criterion (ABSGCONV=0.00001) satisfied.

Figure S2D.3.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Ash-free dry mass – Biofilm (mg/m²) on days 1, 4, 7, 14, and 21.

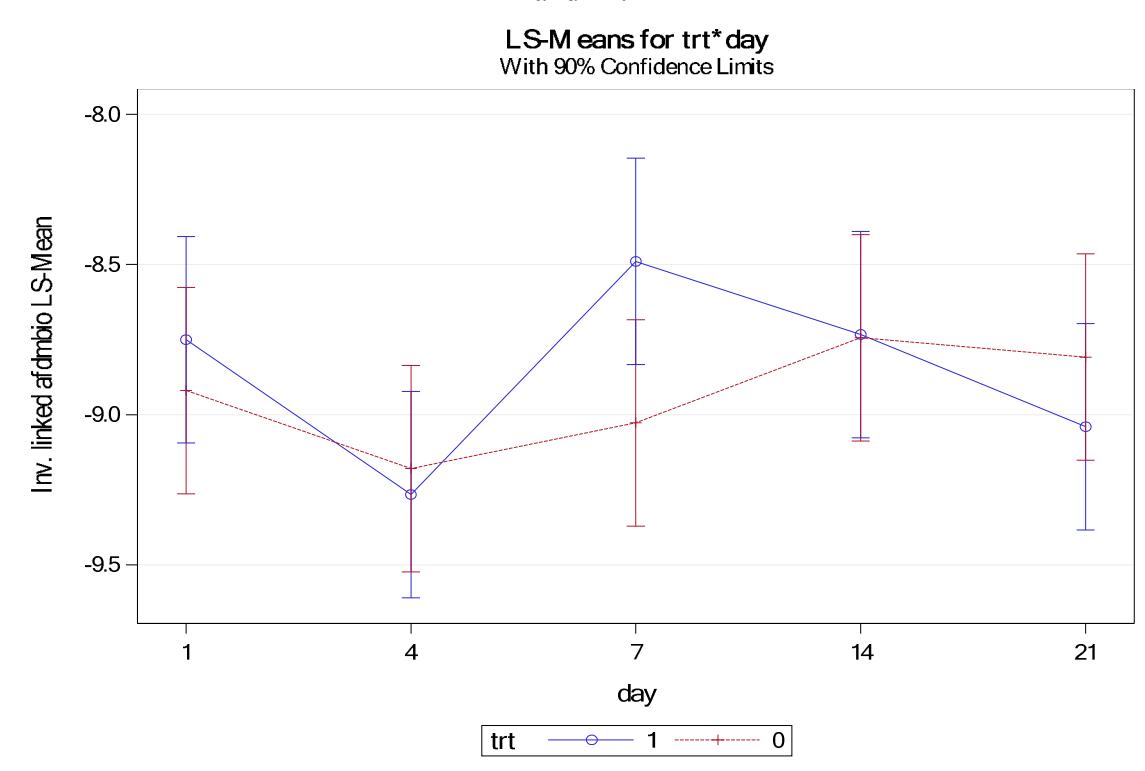


Figure S2D.3.2. GLMM results conditional residuals for response variable Ash-free dry mass – Biofilm (mg/m²).

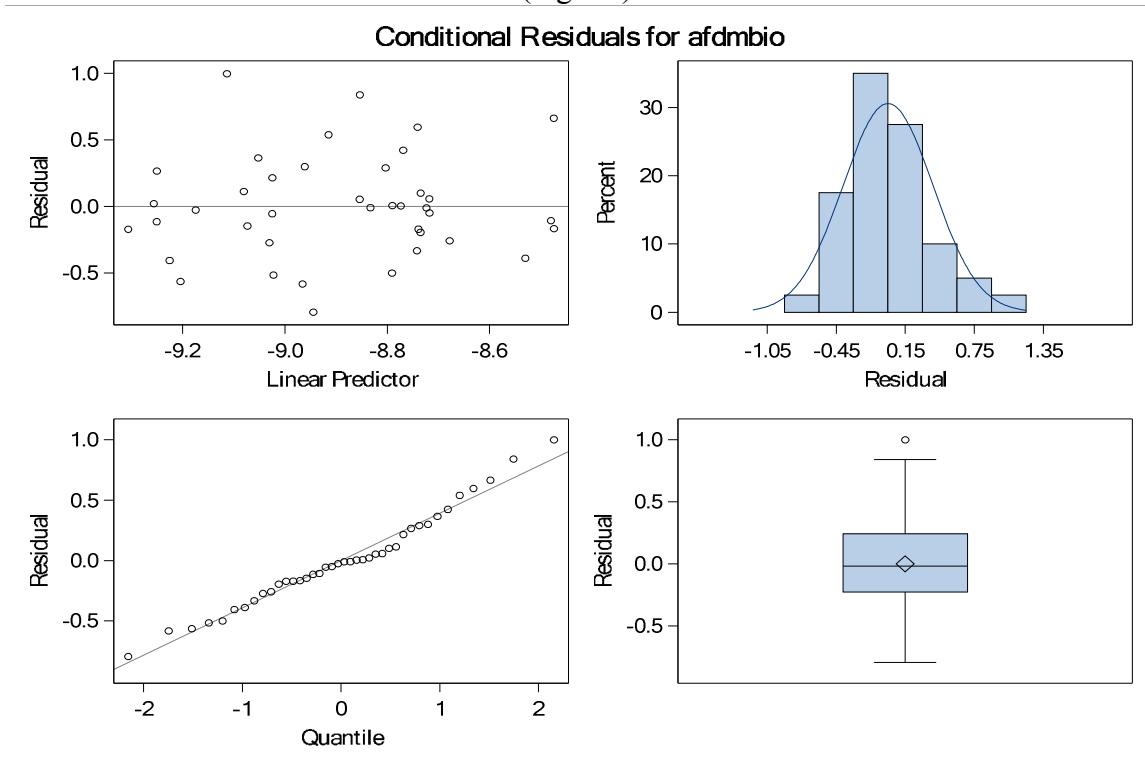


Table S2D.3.1. GLMM results Type III tests of fixed effects for response variable Ash-free dry mass – Biofilm (mg/m²).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	24	0.34	0.5652
day	4	24	2.00	0.1262
trt*day	4	24	1.12	0.3692

Table S2D.3.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Ash-free dry mass – Biofilm (mg/m²).

Simple Effect Comparisons of trt*day Least Squares Means By day										
Simple Effect Level	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 1	1	0	0.1694	0.2840	24	0.60	0.5564	0.1	-0.3165	0.6554
day 4	1	0	-0.08655	0.2840	24	-0.30	0.7632	0.1	-0.5725	0.3994
day 7	1	0	0.5378	0.2840	24	1.89	0.0704	0.1	0.05181	1.0237
day 14	1	0	0.01103	0.2840	24	0.04	0.9694	0.1	-0.4749	0.4970
day 21	1	0	-0.2321	0.2840	24	-0.82	0.4219	0.1	-0.7180	0.2539

S2D.4 Ash-free dry mass – Seston (mg/L)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable afdmse
 - Response Distribution Lognormal
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 40
- Convergence criterion (GCONV=1E-8) satisfied.

Figure S2D.4.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Ash-free dry mass – Seston (mg/L) on days 1, 4, 7, 14, and 21.

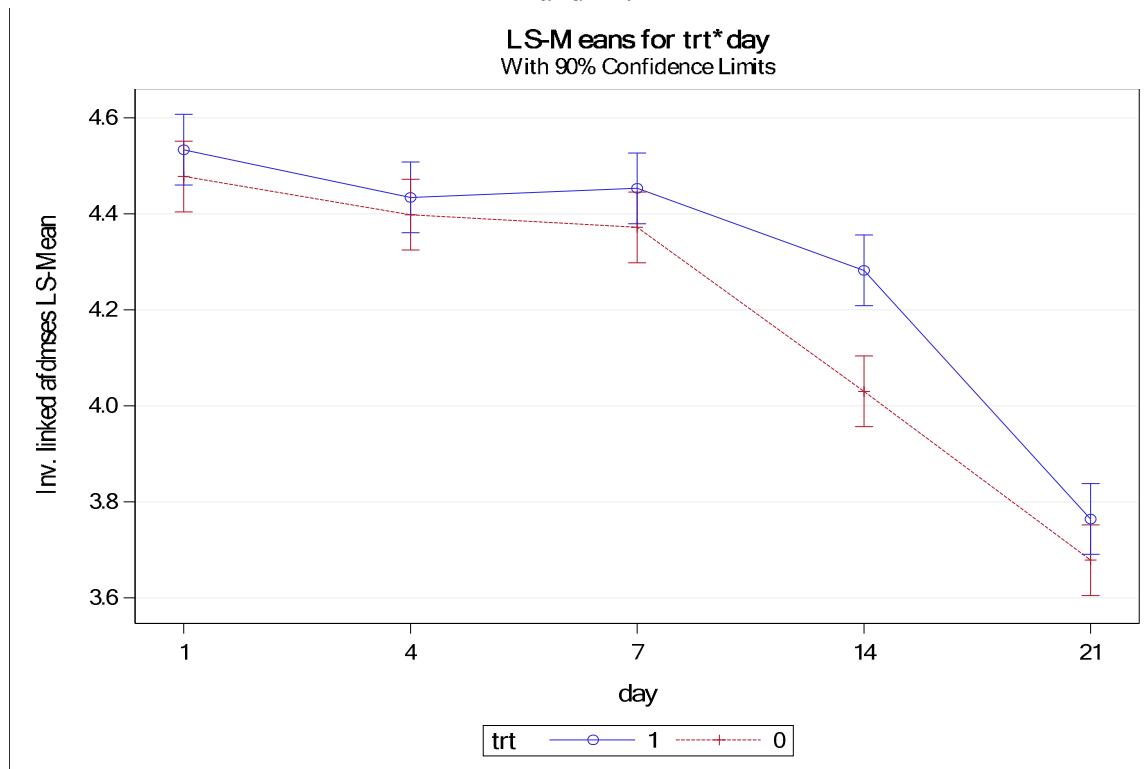


Figure S2D.4.2. GLMM results conditional residuals for response variable Ash-free dry mass – Seston (mg/L).

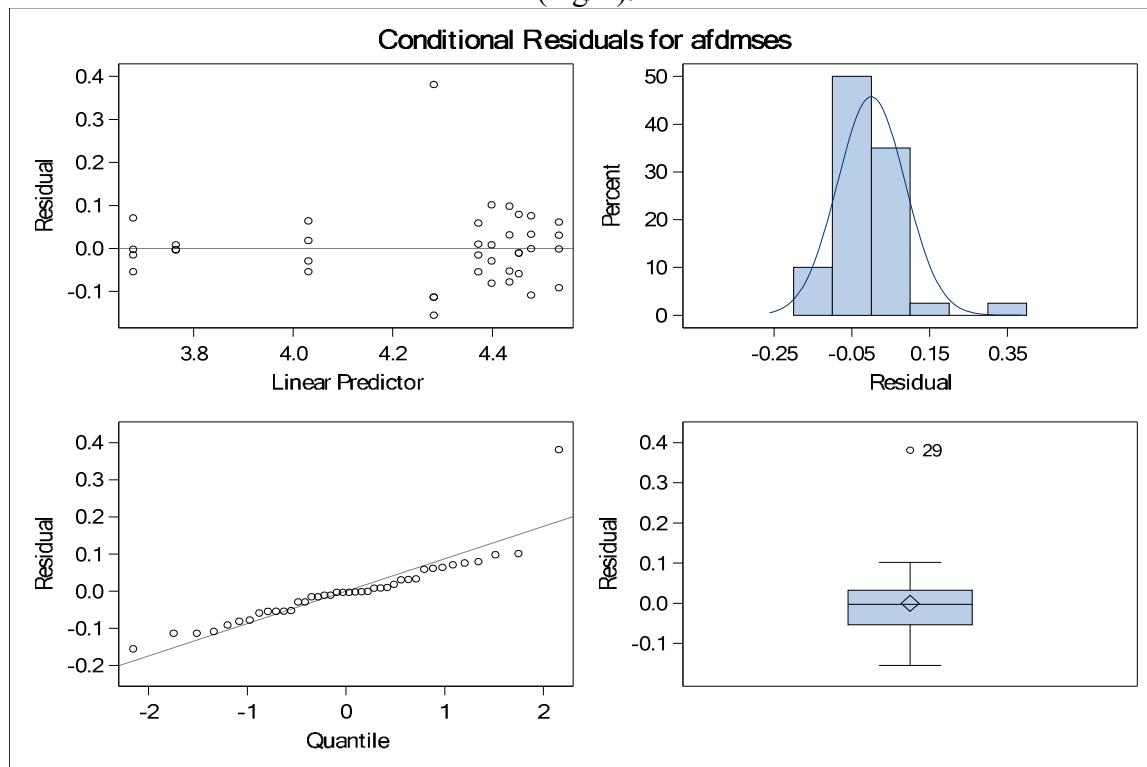


Table S2D.4.1. GLMM results Type III tests of fixed effects for response variable Ash-free dry mass – Seston (mg/L).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	24	14.06	0.0010
day	4	24	109.81	<.0001
trt*day	4	24	2.00	0.1267

Table S2D.4.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Ash-free dry mass – Seston (mg/L).

Simple Effect Comparisons of trt*day Least Squares Means By day										
Simple Effect Level	trt	-trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 1	1	0	0.05580	0.06092	24	0.92	0.3688	0.1	-0.04843	0.1600
day 4	1	0	0.03594	0.06092	24	0.59	0.5607	0.1	-0.06828	0.1402
day 7	1	0	0.08133	0.06092	24	1.33	0.1944	0.1	-0.02290	0.1856
day 14	1	0	0.2520	0.06092	24	4.14	0.0004	0.1	0.1478	0.3562
day 21	1	0	0.08566	0.06092	24	1.41	0.1725	0.1	-0.01856	0.1899

S2D.5 Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable cpabio
 - Response Distribution Lognormal
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 40
- Convergence criterion (ABSGCONV=0.00001) satisfied.

Figure S2D.5.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM) on days 1, 4, 7, 14, and 21.

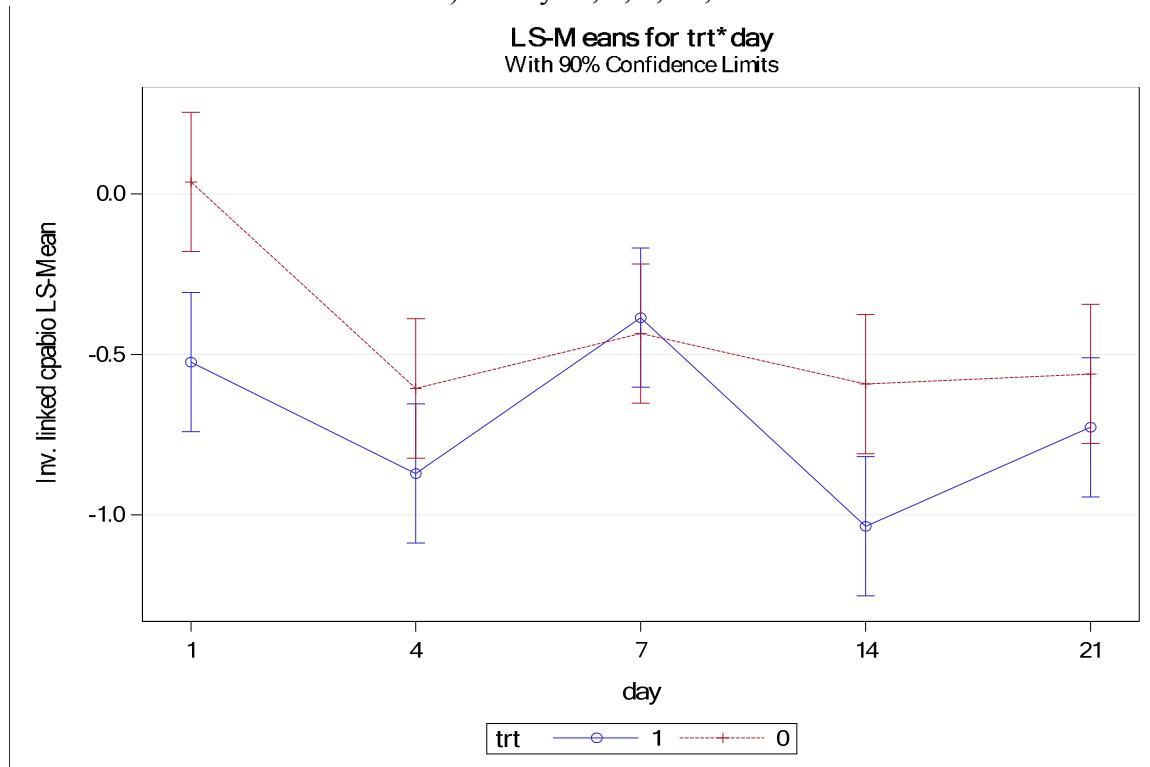


Figure S2D.5.2. GLMM results conditional residuals for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

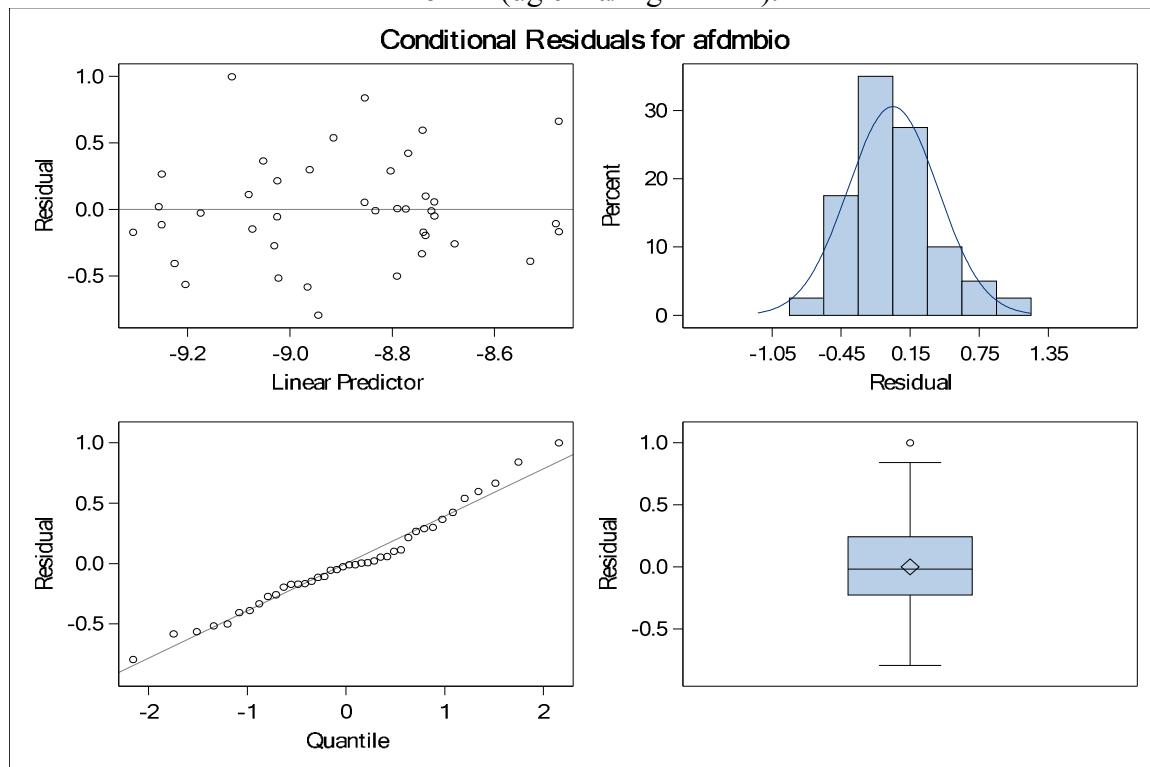


Table S2D.5.1. GLMM results Type III tests of fixed effects for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	24	11.70	0.0022
day	4	24	7.06	0.0007
trt*day	4	24	1.78	0.1659

Table S2D.5.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Chlorophyll a per AFDM – Biofilm (ug chl a/mg AFDM).

Simple Effect Comparisons of trt*day Least Squares Means By day										
Simple Effect Level	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 1	1	0	-0.5616	0.1793	24	-3.13	0.0045	0.1	-0.8683	-0.2549
day 4	1	0	-0.2652	0.1793	24	-1.48	0.1521	0.1	-0.5719	0.04154
day 7	1	0	0.04937	0.1793	24	0.28	0.7854	0.1	-0.2573	0.3561
day 14	1	0	-0.4429	0.1793	24	-2.47	0.0210	0.1	-0.7496	-0.1362
day 21	1	0	-0.1660	0.1793	24	-0.93	0.3637	0.1	-0.4727	0.1407

S2D.6 Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable chlases
 - Response Distribution Lognormal
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 39
- Convergence criterion (GCONV=1E-8) satisfied.

Figure S2D.6.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM) on days 1, 4, 7, 14, and 21.

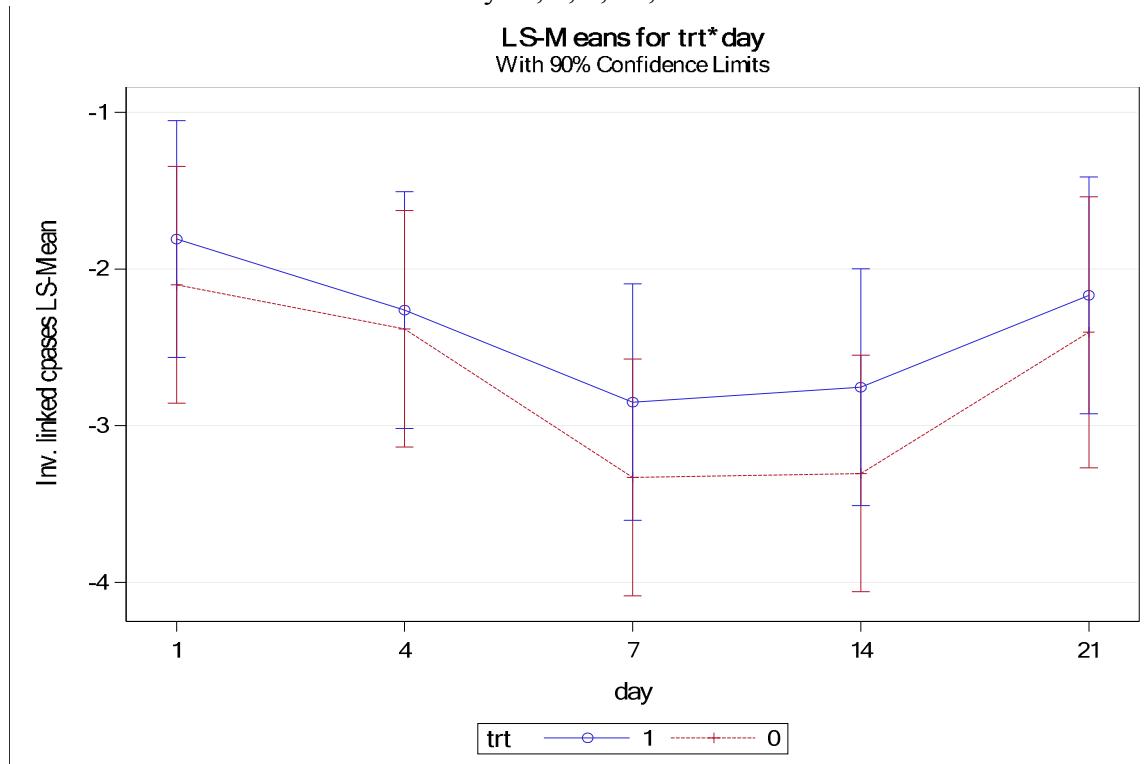


Figure S2D.6.2. GLMM results conditional residuals for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

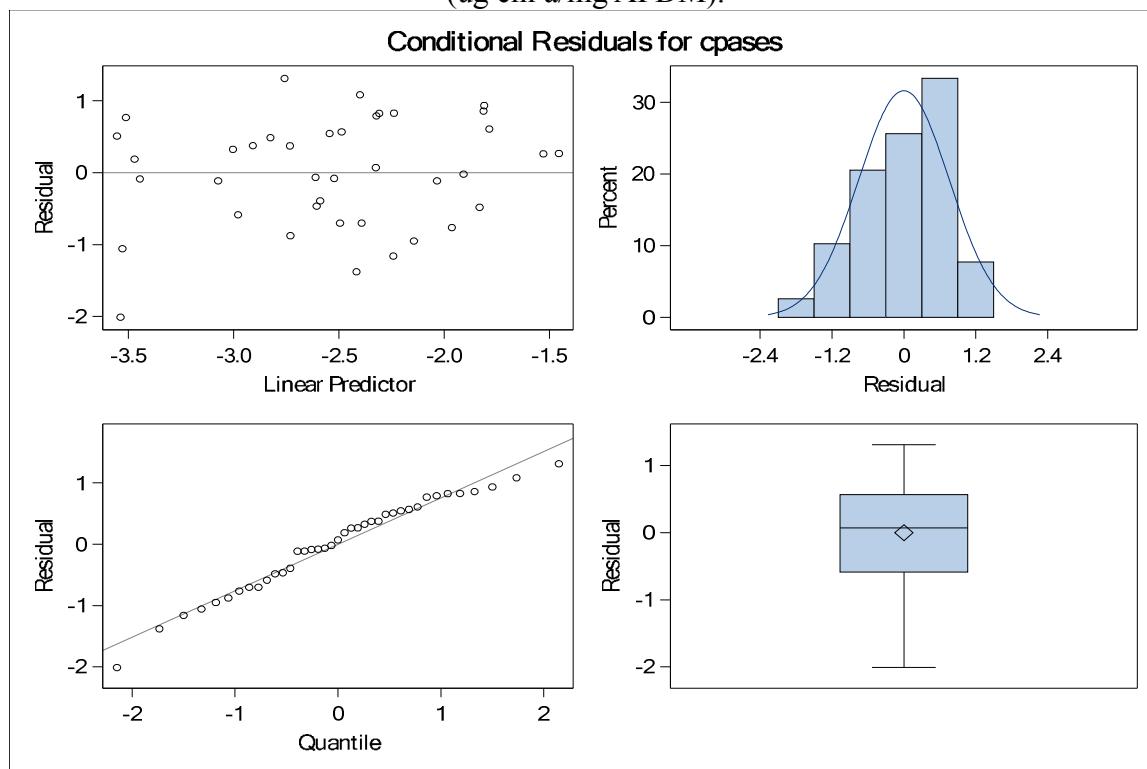


Table S2D.6.1. GLMM results Type III tests of fixed effects for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	23	0.81	0.3787
day	4	23	3.14	0.0336
trt*day	4	23	0.10	0.9817

Table S2D.6.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Chlorophyll a per AFDM – Seston (ug chl a/mg AFDM).

Simple Effect Comparisons of trt*day Least Squares Means By day										
Simple Effect Level	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 1	1	0	0.2916	0.6231	23	0.47	0.6442	0.1	-0.7763	1.3594
day 4	1	0	0.1193	0.6231	23	0.19	0.8499	0.1	-0.9486	1.1871
day 7	1	0	0.4810	0.6231	23	0.77	0.4480	0.1	-0.5868	1.5489
day 14	1	0	0.5501	0.6231	23	0.88	0.3865	0.1	-0.5178	1.6179
day 21	1	0	0.2359	0.6697	23	0.35	0.7278	0.1	-0.9118	1.3836

S2D.7 Gross primary production – Biofilm (mg O₂/h/mg AFDM)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable gppafdbio
 - Response Distribution Gamma
 - Link Function Log
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 38
- Convergence criterion (GCONV=1E-8) satisfied.

Figure S2D.7.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM) on days 1, 4, 7, 14, and 21.

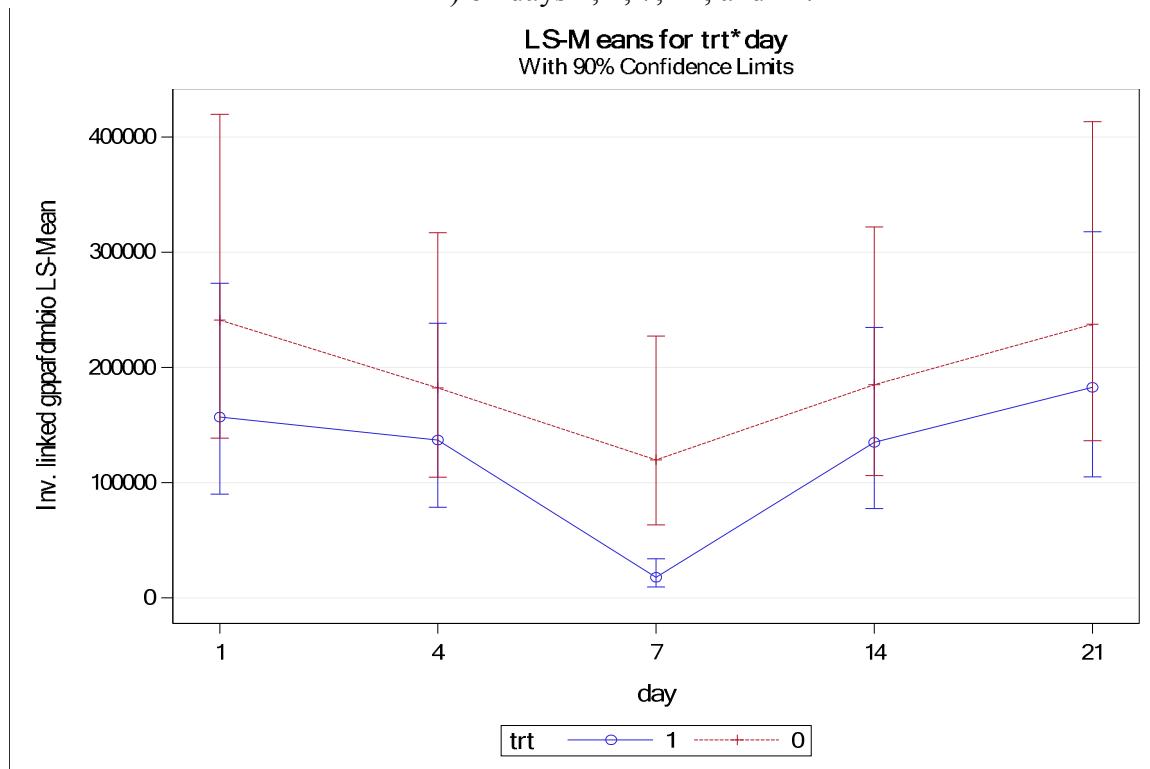


Figure S2D.7.2. GLMM results conditional residuals for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

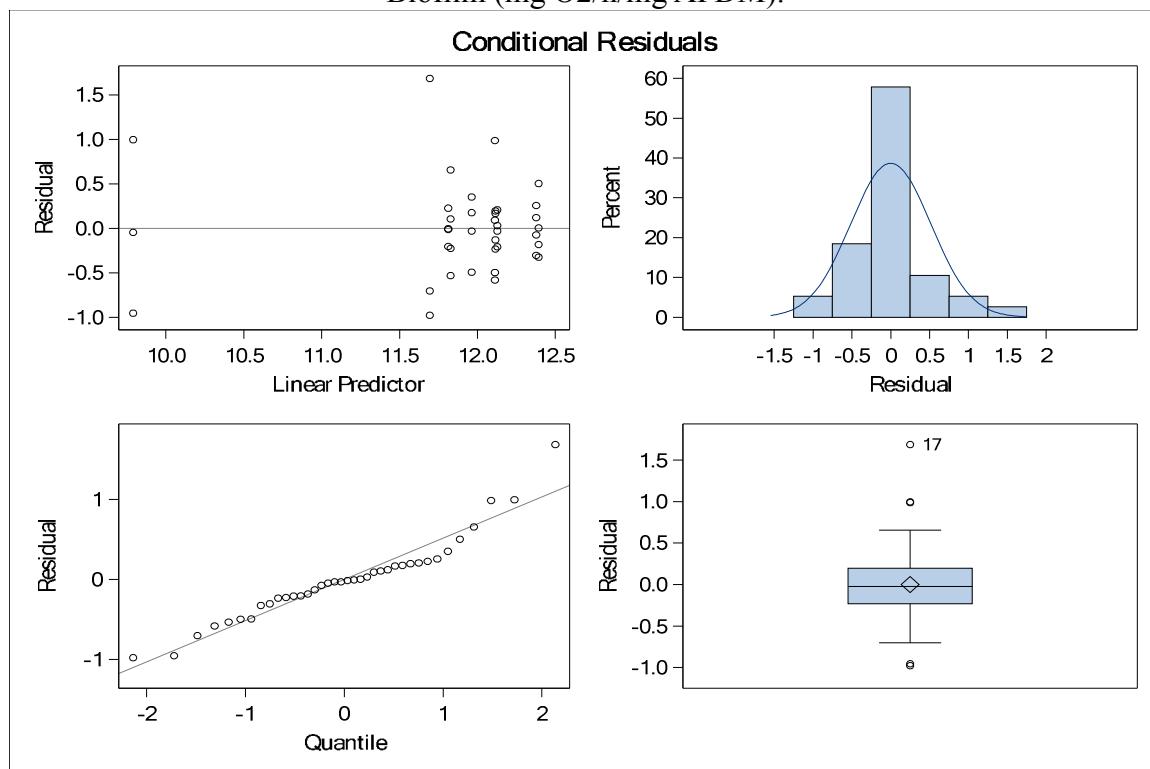


Table S2D.7.1. GLMM results Type III tests of fixed effects for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	22	9.19	0.0061
day	4	22	5.81	0.0024
trt*day	4	22	1.91	0.1437

Table S2D.7.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Gross primary production – Biofilm (mg O₂/h/mg AFDM).

Simple Effect Comparisons of trt*day Least Squares Means By day										
Simple Effect Level	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 1	1	0	-0.4301	0.4563	22	-0.94	0.3562	0.1	-1.2137	0.3535
day 4	1	0	-0.2846	0.4563	22	-0.62	0.5393	0.1	-1.0682	0.4990
day 7	1	0	-1.9038	0.5271	22	-3.61	0.0015	0.1	-2.8088	-0.9988
day 14	1	0	-0.3149	0.4563	22	-0.69	0.4974	0.1	-1.0984	0.4687
day 21	1	0	-0.2621	0.4564	22	-0.57	0.5717	0.1	-1.0458	0.5217

S2D.8 Gross primary production – Seston (mg O₂/h/mg AFDM)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable gppafdmses
 - Response Distribution Lognormal
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 28
- Convergence criterion (GCONV=1E-8) satisfied.

Figure S2D.8.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Gross primary production – Seston (mg O₂/h/mg AFDM) on days 1, 4, 14, and 21. Day 7 not estimated because response=0.

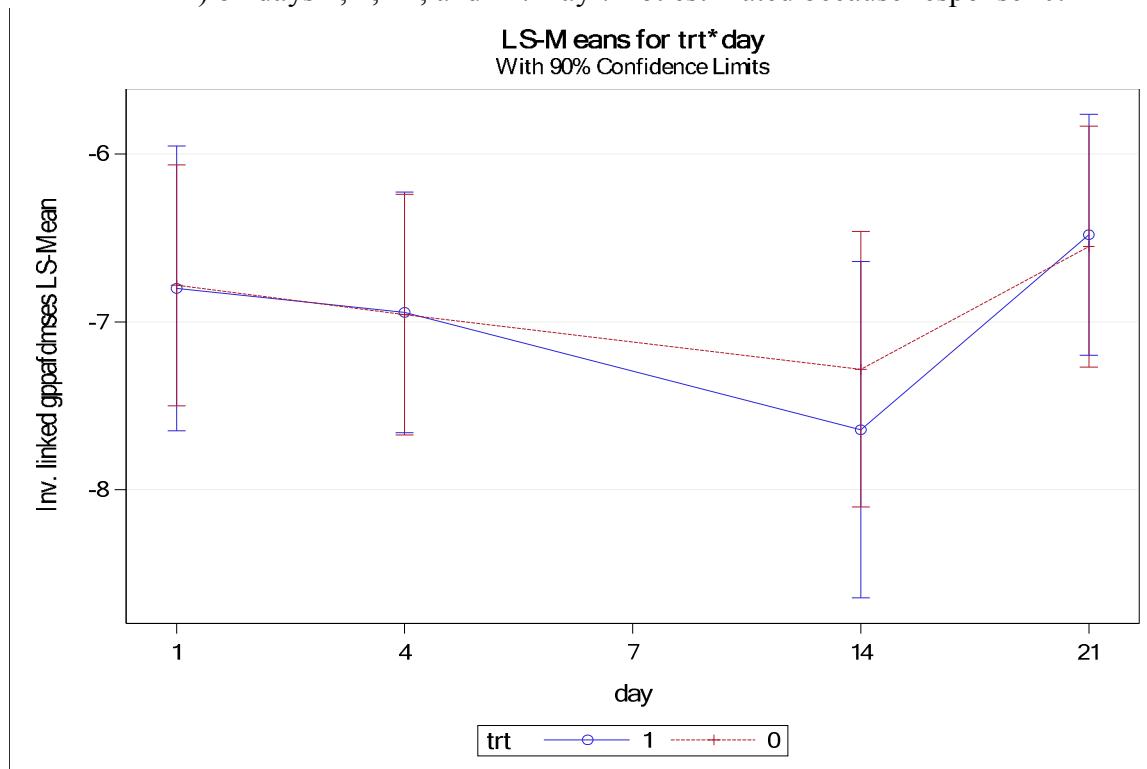


Figure S2D.8.2. GLMM results conditional residuals for response variable Gross primary production – Seston (mg O₂/h/mg AFDM).

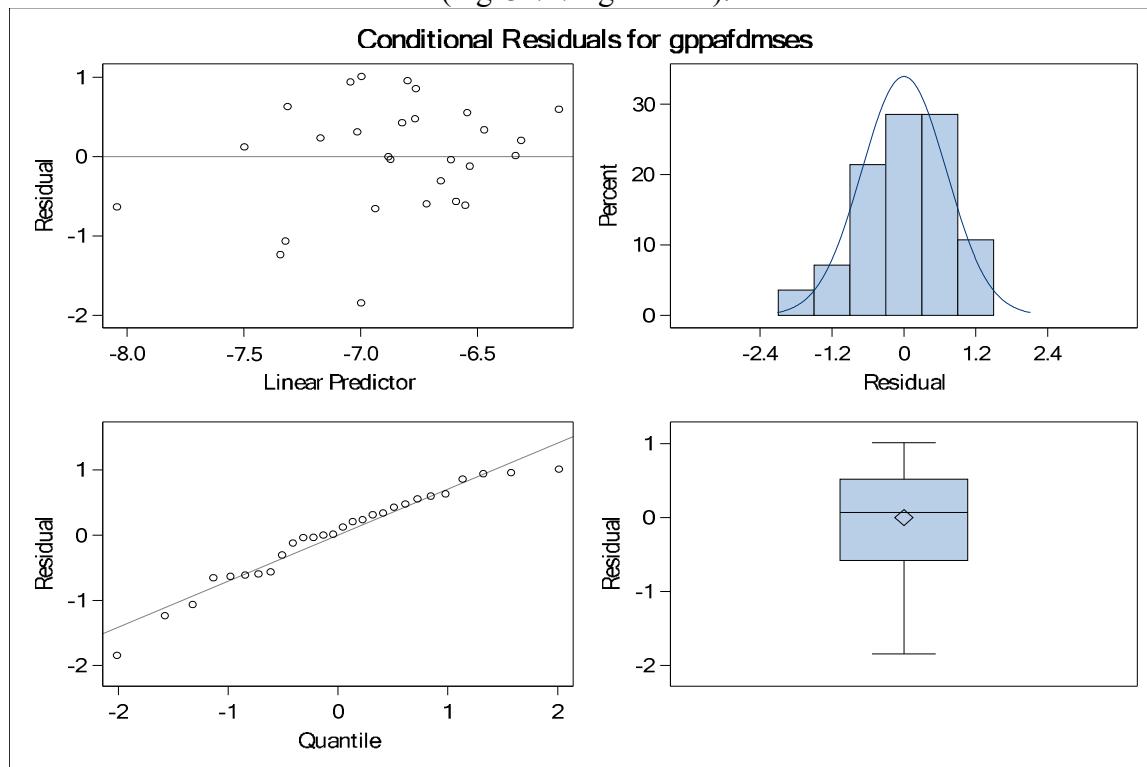


Table S2D.8.1. GLMM results Type III tests of fixed effects for response variable Gross primary production – Seston (mg O₂/h/mg AFDM).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	14	0.04	0.8481
day	3	14	1.63	0.2281
trt*day	3	14	0.09	0.9645

Table S2D.8.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Gross primary production – Seston (mg O₂/h/mg AFDM). Day 7 not estimated because response=0.

Simple Effect Comparisons of trt*day Least Squares Means By day Adjustment for Multiple Comparisons: Tukey										
Simple Effect Level	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 1	1	0	-0.01840	0.6304	14	-0.03	0.9771	0.1	-1.1287	1.0919
day 4	1	0	0.01323	0.5758	14	0.02	0.9820	0.1	-1.0010	1.0275
day 7*	1	0	Non-est	0.1	.	.
day 14	1	0	-0.3604	0.7348	14	-0.49	0.6314	0.1	-1.6547	0.9338
day 21	1	0	0.07086	0.5758	14	0.12	0.9038	0.1	-0.9434	1.0851

*day 7 gppafdmse was zero for all streams.

S2D.9 Community respiration – Biofilm (mg O₂/h/mg AFDM)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable crafdbio
 - Response Distribution Lognormal
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 40
- Convergence criterion (ABSGCONV=0.00001) satisfied.

Figure S2D.9.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Community respiration – Biofilm (mg O₂/h/mg AFDM) on days 1, 4, 7, 14, and 21.

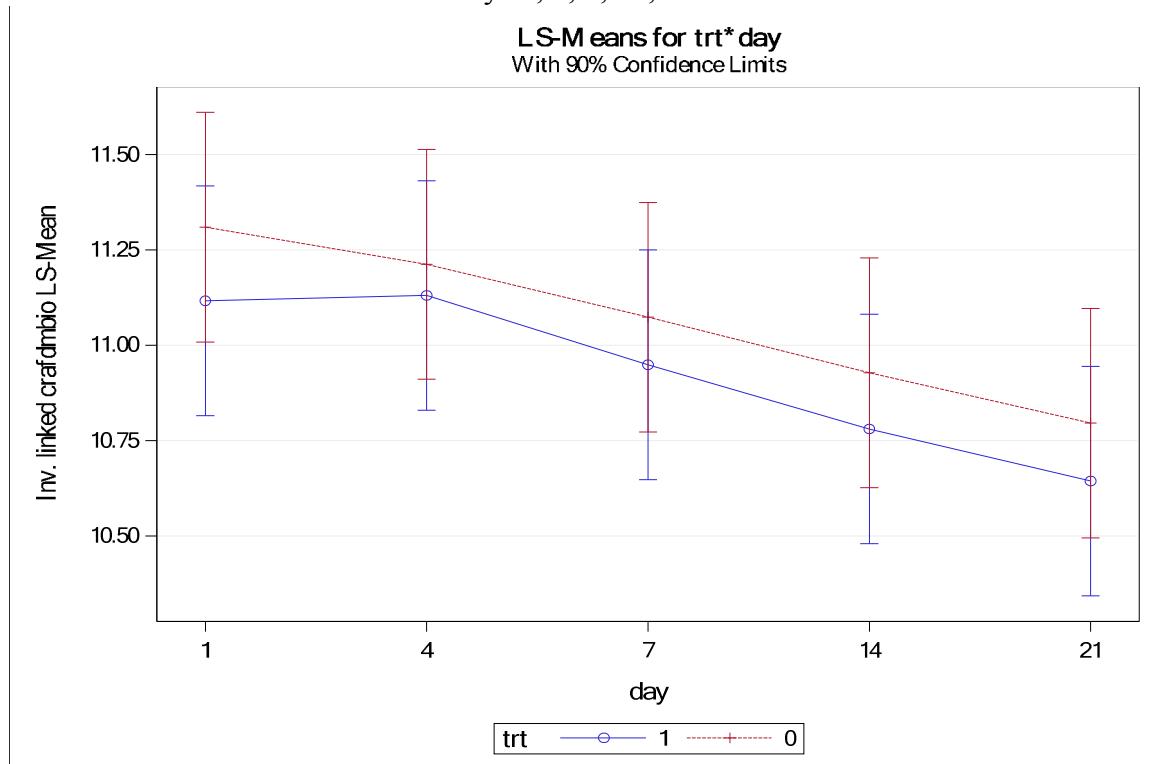


Figure S2D.9.2. GLMM results conditional residuals for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

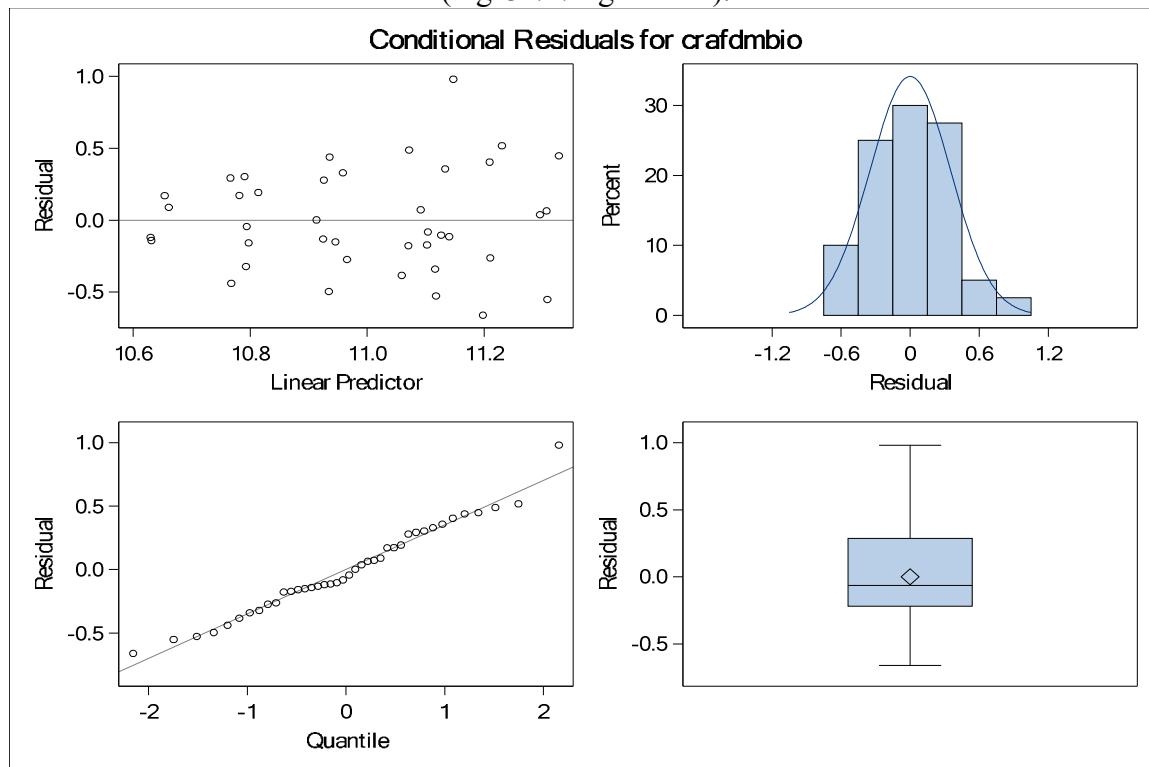


Table S2D.9.1. GLMM results Type III tests of fixed effects for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	24	1.48	0.2361
day	4	24	2.87	0.0449
trt*day	4	24	0.03	0.9985

Table S2D.9.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Community respiration – Biofilm (mg O₂/h/mg AFDM).

Simple Effect Comparisons of trt*day Least Squares Means By day										
Simple Effect Level	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 1	1	0	-0.1930	0.2487	24	-0.78	0.4453	0.1	-0.6186	0.2326
day 4	1	0	-0.08172	0.2487	24	-0.33	0.7454	0.1	-0.5073	0.3439
day 7	1	0	-0.1246	0.2487	24	-0.50	0.6210	0.1	-0.5502	0.3010
day 14	1	0	-0.1470	0.2487	24	-0.59	0.5600	0.1	-0.5726	0.2786
day 21	1	0	-0.1517	0.2487	24	-0.61	0.5477	0.1	-0.5773	0.2739

S2D.10 Community respiration – Seston (mg O₂/h/mg AFDM)

- Model Information
 - Data Set AMPH1.METDATA
 - Response Variable crafdfmses
 - Response Distribution Lognormal
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0
 - day 5 levels values: 1 4 7 14 21
 - stream 8 levels values: 5 6 7 8 1 2 3 4
- Number of Observations Read 40
- Number of Observations Used 39
- Convergence criterion (GCONV=1E-8) satisfied.

Figure S2D.10.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (control=0, amph=1) on response variable Community respiration – Seston (mg O₂/h/mg AFDM) on days 1, 4, 7, 14, and 21.

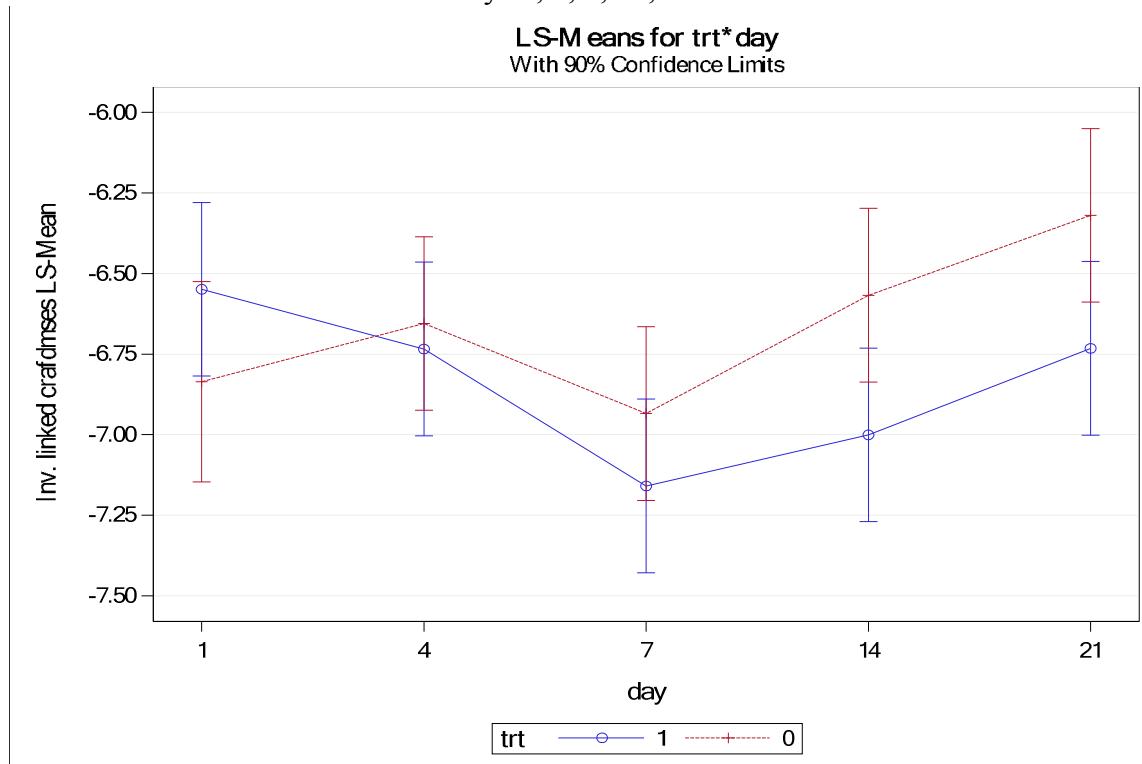


Figure S2D.10.2. GLMM results conditional residuals for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

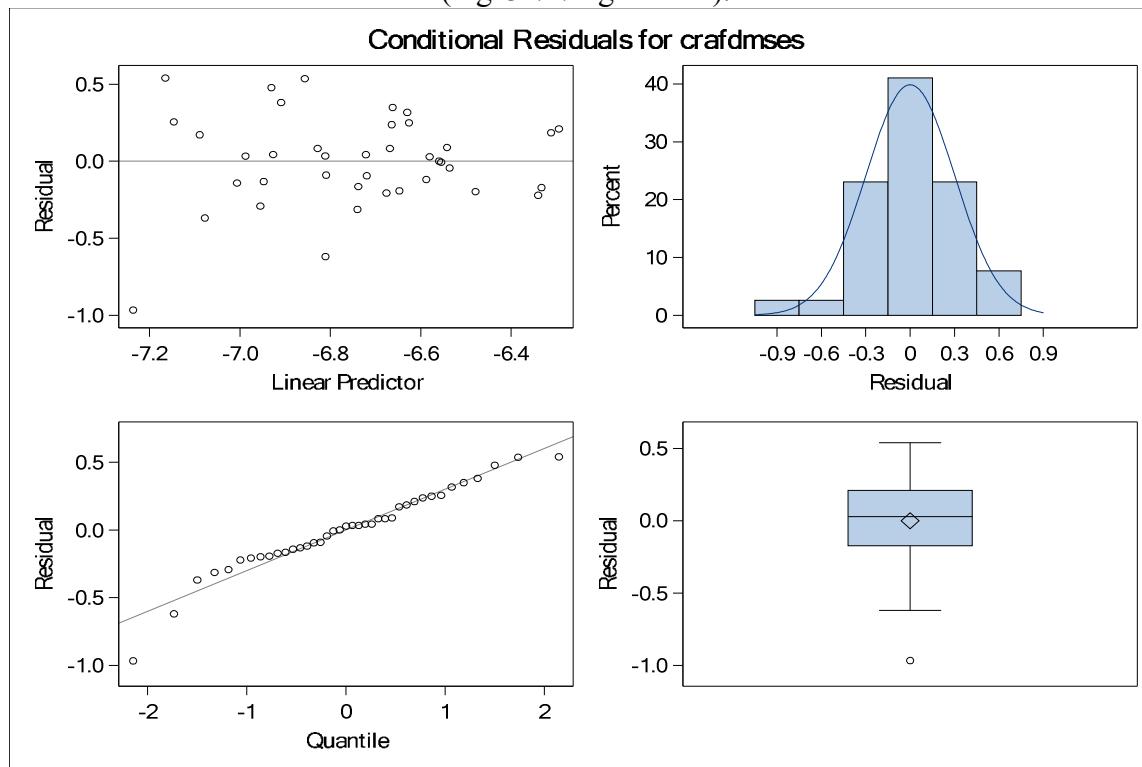


Table S2D.10.1. GLMM results Type III tests of fixed effects for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	23	2.34	0.1397
day	4	23	3.14	0.0337
trt*day	4	23	1.71	0.1828

Table S2D.10.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Community respiration – Seston (mg O₂/h/mg AFDM).

Simple Effect Level	Simple Effect Comparisons of trt*day Least Squares Means By day Adjustment for Multiple Comparisons: Tukey									
	trt	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 1	1	0	0.2874	0.2399	23	1.20	0.2433	0.1	-0.1239	0.6986
day 4	1	0	-0.07894	0.2222	23	-0.36	0.7257	0.1	-0.4598	0.3020
day 7	1	0	-0.2247	0.2222	23	-1.01	0.3225	0.1	-0.6056	0.1562
day 14	1	0	-0.4333	0.2222	23	-1.95	0.0635	0.1	-0.8142	-0.05237
day 21	1	0	-0.4126	0.2222	23	-1.86	0.0762	0.1	-0.7935	-0.03171

- Variable: Invertebrate emergence (individuals)
- Model Information
 - Data Set AMPH1.EMERG
 - Response Variable emerg
 - Response Distribution Gaussian
 - Link Function Identity
 - Variance Function Default
 - Variance Matrix Blocked By stream
 - Estimation Technique Maximum Likelihood
 - Likelihood Approximation Laplace
 - Degrees of Freedom Method Containment
- Class Level Information (variable name, levels, values)
 - trt 2 levels values: 1 0 *Note: trt 0=AMPH, trt 1=Control
 - day 3 levels values: 7 14 21
 - stream 6 levels values: 1 2 3 4 5 6
- Number of Observations Read 18
- Number of Observations Used 18
- Convergence criterion (GCONV=1E-8) satisfied.

Figure S2D.11.1. GLMM results inverse linked least square means with 90% confidence intervals – effect of treatments (Note: control=1, amph=0) on response variable Invertebrate emergence on days 7, 14, and 21 (cumulative number of individuals collected during weeks 1, 2, and 3).

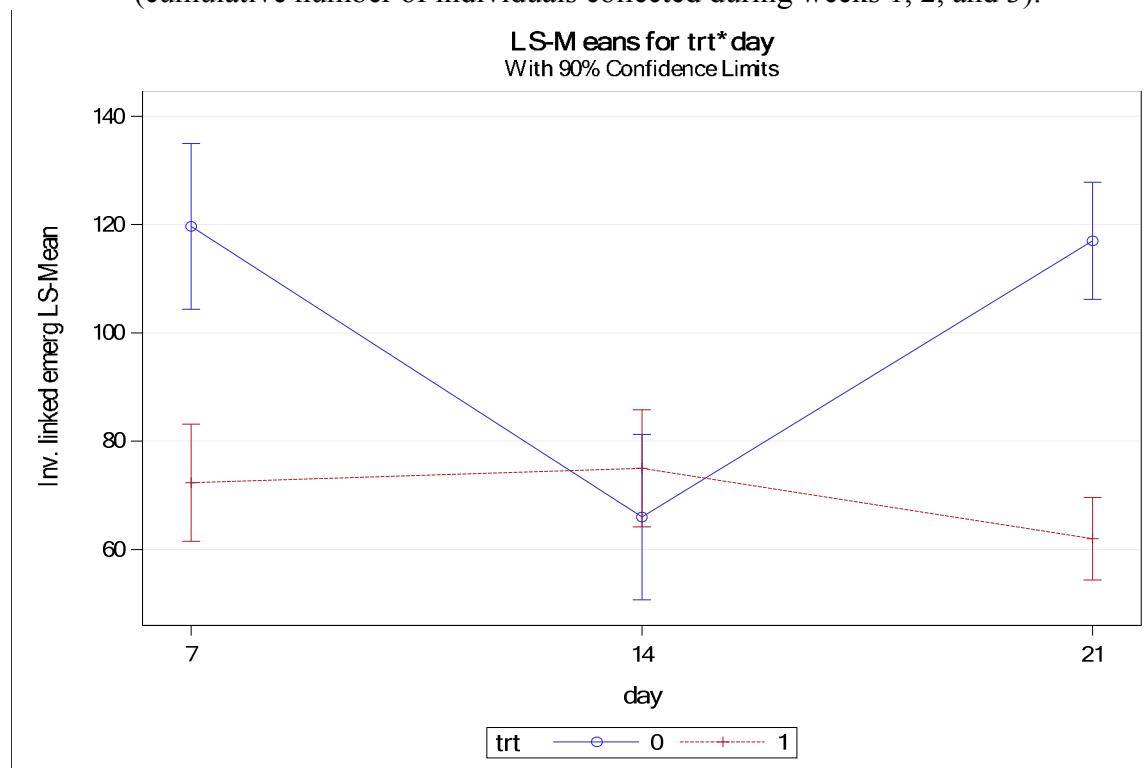


Figure S2D.11.2. GLMM results conditional residuals for response variable Invertebrate emergence.

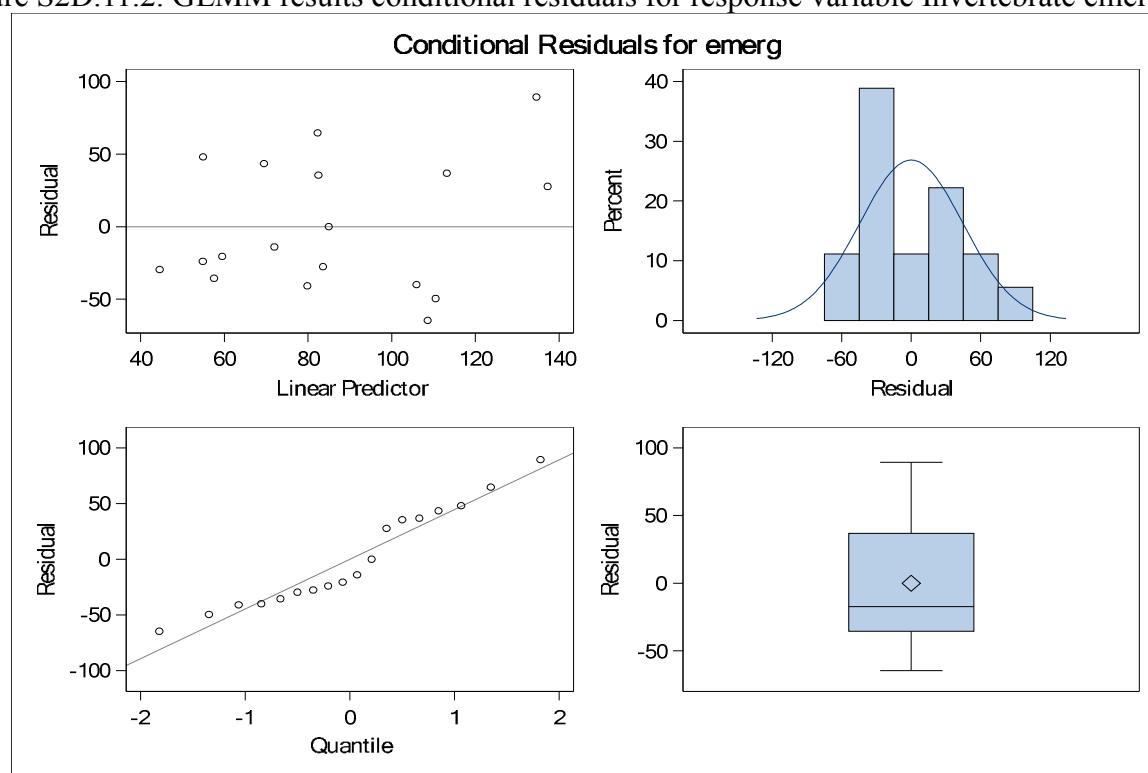


Table S2D.11.1. GLMM results Type III tests of fixed effects for response variable Invertebrate emergence.

Type III Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
trt	1	8	46.92	0.0001
day	2	8	9.47	0.0078
trt*day	2	8	122.89	<.0001

Table S2D.11.2. GLMM results simple effect comparisons of treatment by day interaction least square means, sliced by day, for response variable Invertebrate emergence.

Simple Effect Level	Simple Effect Comparisons of trt*day Least Squares Means By day									
	trt*	_trt	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
day 7	1	0	47.3338	5.8115	8	8.14	<.0001	0.1	36.5269	58.1406
day 14	1	0	-9.0001	5.8106	8	-1.55	0.1600	0.1	-19.8052	1.8050
day 21	1	0	54.9991	4.1088	8	13.39	<.0001	0.1	47.3586	62.6395

*Note: trt 0=AMPH, trt 1=Control

Supporting Information 3

Power Analysis (post-hoc).

Power analysis for k=2 groups, n=4 replicates, f=0.8 large effect size, sig.level=0.05:

```
> pwr.anova.test(k=2, n=4, f=0.8, sig.level=0.05, power=NULL)
```

Balanced one-way analysis of variance power calculation

```
k = 2  
n = 4  
f = 0.8  
sig.level = 0.05  
power = 0.4761509
```

NOTE: n is number of streams in each treatment group

Power analysis for k=2 groups, n=4 replicates, f=0.8 large effect size, sig.level=0.1:

```
> pwr.anova.test(k=2, n=4, f=0.8, sig.level=0.1, power=NULL)
```

Balanced one-way analysis of variance power calculation

```
k = 2  
n = 4  
f = 0.8  
sig.level = 0.1  
power = 0.6386771
```

NOTE: n is number of streams in each treatment group

References

Stephane Champely (2015). pwr: Basic Functions for Power Analysis. R package version 1.1-2. <http://CRAN.R-project.org/package=pwr>

Supporting Information 4 Bacterial and Diatom Community Analysis

S4 Table 1. SIMPER and ANOVA analyses of bacterial communities in control and AMPH-exposed artificial streams after 3 weeks of exposure (n=4 replicates per treatment).^a

OTU	Phylum	Class	Order	Family	Genus	Contr ol abund . %	AMP H abund . %	Diss/ SD	Contri b%	ANOV A p
OTU0 93	Bacteroidetes	Flavobacteria	Flavobacte riales	Flavobacte riaceae	<i>Cloacibacte rium</i>	0.01	1.44	4.4†	3.01	0.007*
OTU0 14	Gemmatimo nadetes	Gemmatimona detes	Gemmatimo nadales	Gemmation adaceae	<i>Gemmatio nas</i>	5.89	3.66	2.13†	2.39	0.264
OTU0 61	Proteobacteri a	Gammaproteob acteria	Pseudomon ales	Pseudomonad aceae	<i>Pseudomon as</i>	2.44	0.57	1.18	2.19	0.242
OTU0 55	Proteobacteri a	Betaproteobact eria	Burkholderia les	Oxalobacterac eae	unclassified	0.31	2.03	1.2	2.15	0.165
OTU0 54	Proteobacteri a	Betaproteobact eria	Burkholderia les	Oxalobacterac eae	<i>Massilia</i>	0.5	1.61	1.45	1.87	0.234
OTU0 11	Proteobacteri a	Betaproteobact eria	Burkholderia les	Comamonada ceae	unclassified	5.09	2.69	1.49	1.72	0.053•
OTU0 67	Firmicutes	Bacilli	Bacillales	Bacillales_In certae_Sedis_X II	<i>Exiguobacte rium</i>	0.22	1.04	1.48	1.71	0.174
OTU0 78	Bacteroidetes	Flavobacteria	Flavobacte riales	Flavobacte riaceae	<i>Chryseobact erium</i>	0.53	1.54	1.01	1.48	0.309
OTU0 04	Proteobacteri a	Betaproteobact eria	Burkholderia les	unclassified	unclassified	4.27	2.77	1.6	1.35	0.106
OTU0 09	Proteobacteri a	Gammaproteob acteria	Alteromonad ales	Alteromonada ceae	<i>Haliea</i>	2.91	2.68	1.46	1.35	0.835
OTU0 71	Proteobacteri a	Alphaproteoba cteria	Caulobactera les	Caulobacterac eae	<i>Caulobacter</i>	0.13	0.82	1.1	1.34	0.219

OTU0 06	Proteobacteri a	Alphaproteoba cteria	Rhizobiales	unclassified	unclassified	3.08	3.99	1.44	1.26	0.438
OTU0 13	Bacteroidetes	unclassified	unclassified	unclassified	unclassified	4.75	3.96	1.36	1.22	0.529
OTU0 19	Proteobacteri a	Alphaproteoba cteria	Caulobactera les	Caulobacterac eae	<i>Brevundimo nas</i>	2.03	2.36	1.35	1.21	0.715
OTU0 01	unclassified	unclassified	unclassified	unclassified	unclassified	12.84	12.68	1.42	1.19	0.941
OTU0 07	Proteobacteri a	unclassified	unclassified	unclassified	unclassified	4.06	3.5	1.31	1.18	0.627
OTU0 22	Bacteroidetes	Sphingobacteri a	Sphingobact eriales	unclassified	unclassified	1.61	1.12	1.66	1.01	0.213
OTU0 66	Bacteroidetes	Sphingobacteri a	Sphingobact eriales	Chitinophagac eae	<i>Sediminibac terium</i>	0.14	0.63	1.04	1.01	0.381
OTU0 42	Proteobacteri a	Betaproteobact eria	Rhodocyclal es	Rhodocyclace ae	unclassified	0.59	0.64	1.56	0.93	0.890
OTU0 08	Proteobacteri a	Betaproteobact eria	unclassified	unclassified	unclassified	4.11	3.28	1.79	0.88	0.254
OTU0 47	Proteobacteri a	Gammaproteob acteria	Xanthomona dales	Xanthomonad aceae	<i>Luteimonas</i>	0.64	0.23	2.38†	0.86	0.011*
OTU0 29	Proteobacteri a	Gammaproteob acteria	Xanthomona dales	Xanthomonad aceae	<i>Arenimonas</i>	0.56	0.71	1.91	0.85	0.627
OTU0 18	Proteobacteri a	Alphaproteoba cteria	Rhodobacter ales	Rhodobactera ceae	<i>Rhodobacte r</i>	1.1	1.65	1.57	0.83	0.189
OTU0 12	Planctomycet es	Planctomyceta cia	Planctomycet ales	Planctomycet aceae	unclassified	1.13	1.56	1.6	0.8	0.168
OTU0 17	Proteobacteri a	Alphaproteoba cteria	Sphingomon adales	Sphingomona daceae	<i>Sandaracino bacter</i>	0.61	1.05	1.68	0.8	0.347
OTU0 03	Proteobacteri a	Alphaproteoba cteria	Sphingomon adales	Sphingomona daceae	unclassified	4.58	4.56	1.4	0.79	0.978
OTU0 02	Proteobacteri a	Alphaproteoba cteria	Rhodobacter ales	Rhodobactera ceae	unclassified	5.54	5.49	1.24	0.75	0.954
OTU0	Proteobacteri a	Alphaproteoba cteria	unclassified	unclassified	unclassified	3.01	3.42	1.56	0.74	0.521

05	a	cteria								
OTU0 28	Proteobacteri a	Alphaproteoba cteria	Rhizobiales	Hyphomicrobi aceae	unclassified	0.73	1.15	1.32	0.73	0.220
OTU0 15	Bacteroidetes	Sphingobacteri a	Sphingobact riales	Chitinophagac eae	unclassified	2.55	2.27	1.7	0.72	0.614
OTU0 49	Proteobacteri a	Betaproteobact eria	Methylophil ales	Methylophilac eae	<i>Methylophil us</i>	2.05	1.84	1.52	0.69	0.676
OTU1 04	Deinococcus -Thermus	Deinococci	Deinococcale s	Trueperaceae	<i>Truepera</i>	0.53	0.28	1.54	0.67	0.186
OTU0 58	Proteobacteri a	Gammaproteob acteria	Aeromonadal es	Aeromonadac eae	<i>Aeromonas</i>	0.18	0.15	1.65	0.65	0.770

^a Taxa listed in order of mean % contribution to dissimilarities between all pairs of inter-group samples (i.e., every sample in control paired with every sample in AMPH) = Contrib %. Total average dissimilarity between treatments = 21.1.

Mean relative abundance (%) in control and AMPH-exposed streams = Control abund. % and AMPH abund. %, respectively.

Taxa that are good discriminating species (i.e., consistently higher or lower in relative abundance in control or AMPH samples) have higher mean dissimilarity divided by standard deviation of dissimilarities = Diss/SD. Daggers (†) indicate top 3 Diss/SD.

ANOVA comparing relative abundances of each taxon in control vs. AMPH streams was conducted using R version 3.1.3 (R Core Team 2015) and the *p*-values = ANOVA *p*. Asterisks indicate *p*<0.05 and filled circles indicate *p*<0.1.

S4 Table 2. SIMPER and ANOVA analyses of diatom communities in control and AMPH-exposed artificial streams after 3 weeks of exposure (n=4 replicates per treatment).^a

Taxon code	Nomenclature	Control abund. %	AMPH abund. %	Contrib% Diss/SD	ANOVA <i>p</i>
COPLAPLA	<i>Cocconeis placentula sensu lato</i> Ehrenberg 1838	2.38	9.52	12.09	1.86† 0.018*
ACMINMIN	<i>Achnanthidium minutissimum</i> (Kützing) Czarnecki 1994	78.56	66.73	11.29	1.22 0.064•
SEATOATO	<i>Sellaphora atomoides</i> (Grunow) C.E. Wetzel et Van de Vijver 2015	8.19	5.69	10.46	1.66 0.514
AMPEDPED	<i>Amphora pediculus</i> (Kützing) Grunow in Schmidt 1875	0.94	2.84	6.35	1.72 0.207
CABACBAC	<i>Caloneis bacillum</i> (Grunow) Cleve 1894	0	0.98	6.23	1.32 0.142
COPEDPED	<i>Cocconeis pediculus</i> Ehrenberg 1838	1.03	2.61	5.27	1.23 0.195
REUNIUNI	<i>Reimeria uniseriata</i> Sala, Guerrero and Ferrario 1993	0.57	1.07	5.07	2.16† 0.361
ACPYRPYR	<i>Achnanthidium pyrenaicum</i> (Hustedt) Kobayasi 1997	5.12	5.1	4.9	1.4 0.099•
NATRITRI	<i>Navicula tripunctata</i> (O.F. Müller) Bory 1822	0.12	0.58	4.51	1.63 0.227
MEVARVAR	<i>Melosira varians</i> Agardh 1827	0.08	0.58	4.07	1.5 0.135
KAPLOGES	<i>Karayevia ploenensis</i> var. <i>gessneri</i> (Hustedt) Bukhtiyarova 1999	0.08	0.37	3.48	1.38 0.128
PABAHBAH	<i>Platessa bahlsii</i> Potapova 2012	0.2	0.41	3.13	1.18 0.996
NAANTANT	<i>Navicula antonii</i> Lange-Bertalot 2000	0.25	0.25	3.1	1.16 0.993
NIINCINC	<i>Nitzschia inconspicua</i> Grunow 1862	0.41	0.25	2.96	1.36 0.491
CYCFHELV	<i>Cymbella cf. helvetica</i>	0	0.17	2.67	1.61 0.051•
GOCFMINU	<i>Gomphonema cf. minuta</i>	0.17	0.21	2.58	1.15 0.811

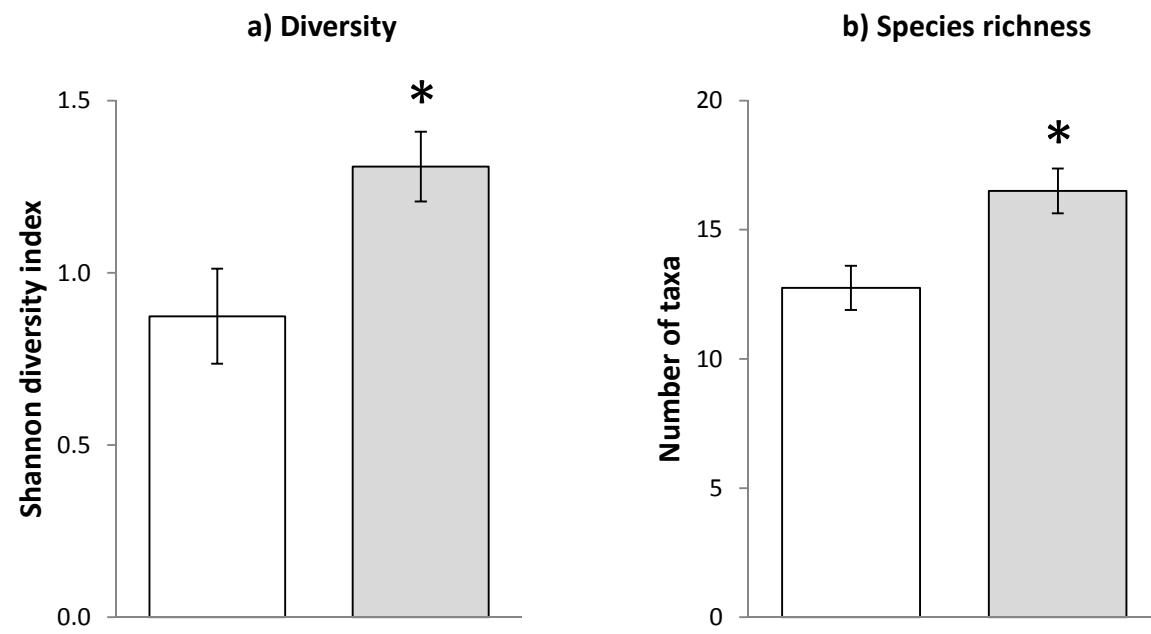
RHABBABB	<i>Rhoicosphenia abbreviata</i> (Agardh) Lange-Bertalot 1980	0.29	0.46	2.37	1.21	0.373
RESINSIN	<i>Reimeria sinuata</i> (Gregory) Kocielek and Stoermer 1987	1.36	1.82	2.1	1.27	0.26
AHSUBKRA	<i>Achnanthes subhudsonis</i> var. <i>kraeusei</i> (Cholnoky) Cholnoky 1956	0.04	0.17	1.96	0.77	0.169
NAVENVEN	<i>Navicula veneta</i> Kützing 1844	0	0.12	1.9	0.95	0.17
ACRIVRIV	<i>Achnanthidium rivulare</i> Potapova et Ponader 2004	0.12	0	1.88	0.94	0.492
PLFREFRE	<i>Planothidium frequentissimum</i> (Lange-Bertalot in Krammer and Lange-Bertalot) Lange-Bertalot 1999	0.08	0.08	1.64	0.75	0.359

^a Taxa listed in order of mean % contribution to dissimilarities between all pairs of inter-group samples (i.e., every sample in control paired with every sample in AMPH) = Contrib %. Total average dissimilarity between treatments = 24.8.

Mean relative abundance (%) in control and AMPH-exposed streams = Control abund. % and AMPH abund. %, respectively.

Taxa that are good discriminating species (i.e., consistently higher or lower in relative abundance in control or AMPH samples) have higher mean dissimilarity divided by standard deviation of dissimilarities = Diss/SD. Daggers (†) indicate top 2 Diss/SD.

ANOVA comparing relative abundances of each taxon in control vs. AMPH streams was conducted using R version 3.1.3 (R Core Team 2015) and the *p*-values = ANOVA *p*. Asterisk indicates *p*<0.05 and filled circles indicate *p*<0.1.



S4 Figure 1. Diversity and species richness of diatom communities in control (white bars) and AMPH-exposed (gray bars) artificial streams after the 3-week experiment ($n=4$ replicates per treatment). Asterisks indicate greater Shannon diversity (a) (ANOVA $df=1, 6, F=6.41, p=0.045$) and species richness (b) (ANOVA $df=1, 6, F= 9.51, p=0.022$) in the AMPH streams relative to control streams. ANOVA was conducted using R version 3.1.3 (R Core Team 2015).