

Supplementary Materials for

**Required chlorination doses to fulfill the credit value for
disinfection of enteric viruses in water: A critical review**

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Containing:

16 Figures and 1 page explanation about R analysis used in the main manuscript

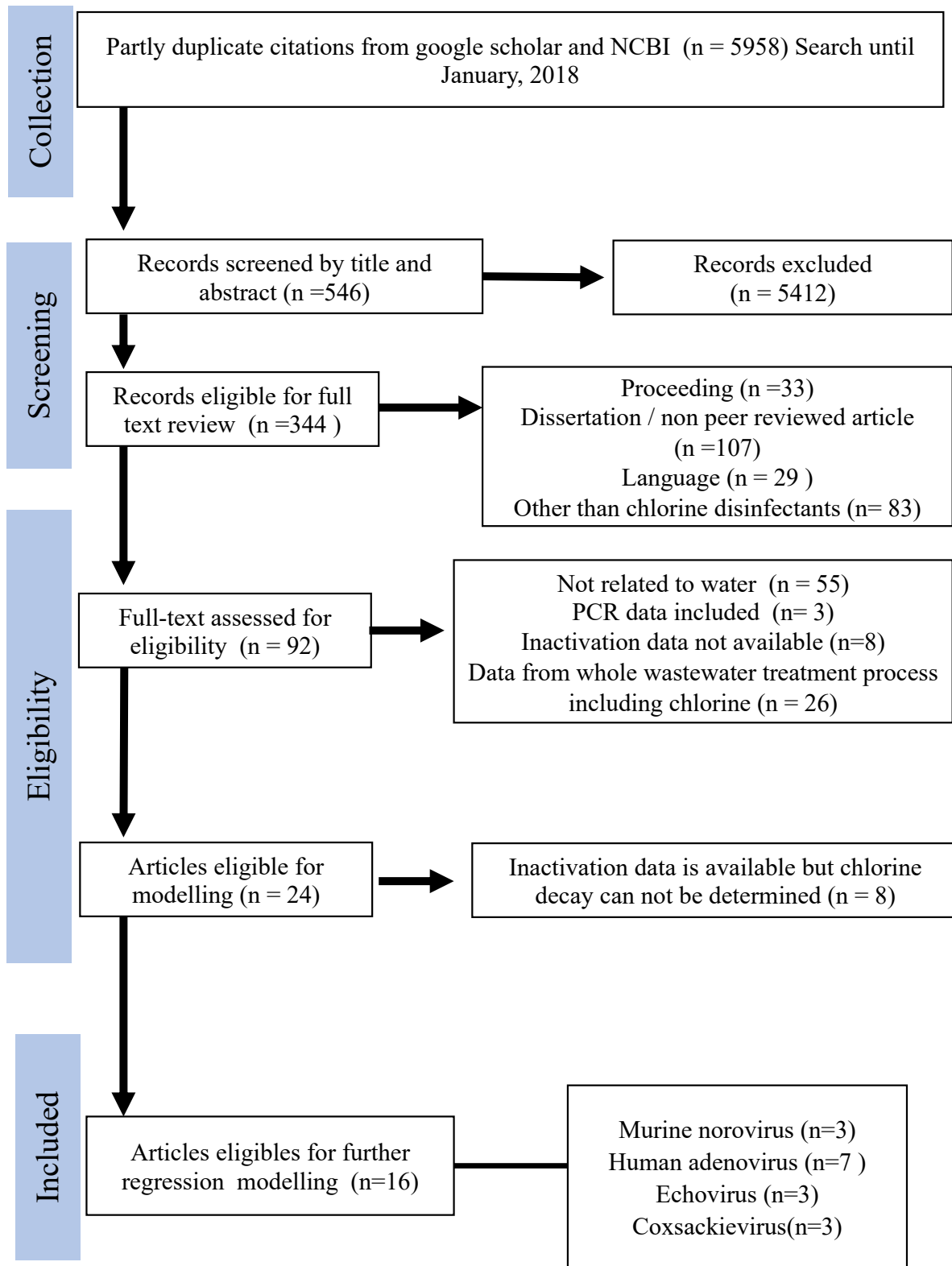


Figure S1. The flowchart of systematic review process used to select the appropriate studies

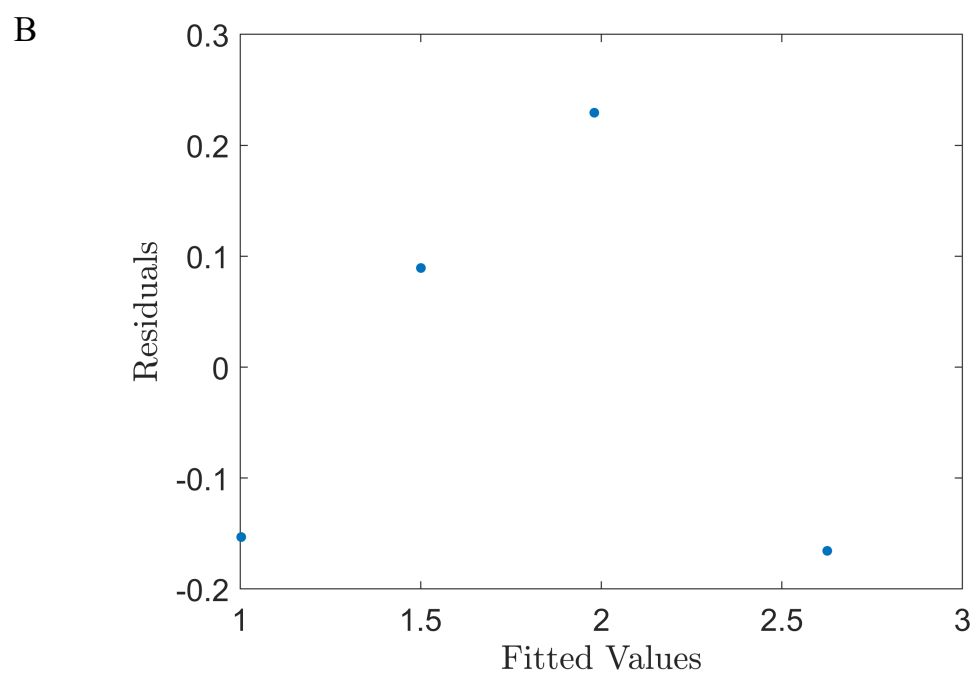
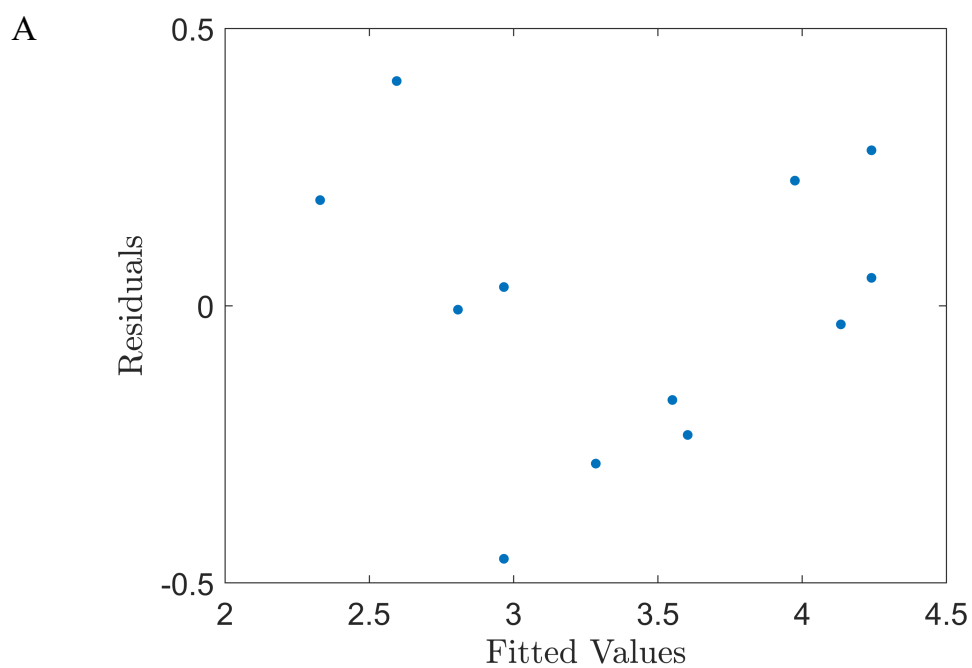


Figure S2. Linear regression model residuals for free chlorine inactivation of murine norovirus. Residuals are described as the different between observed and predicted values. Figures A and B represent the first and second dataset respectively.

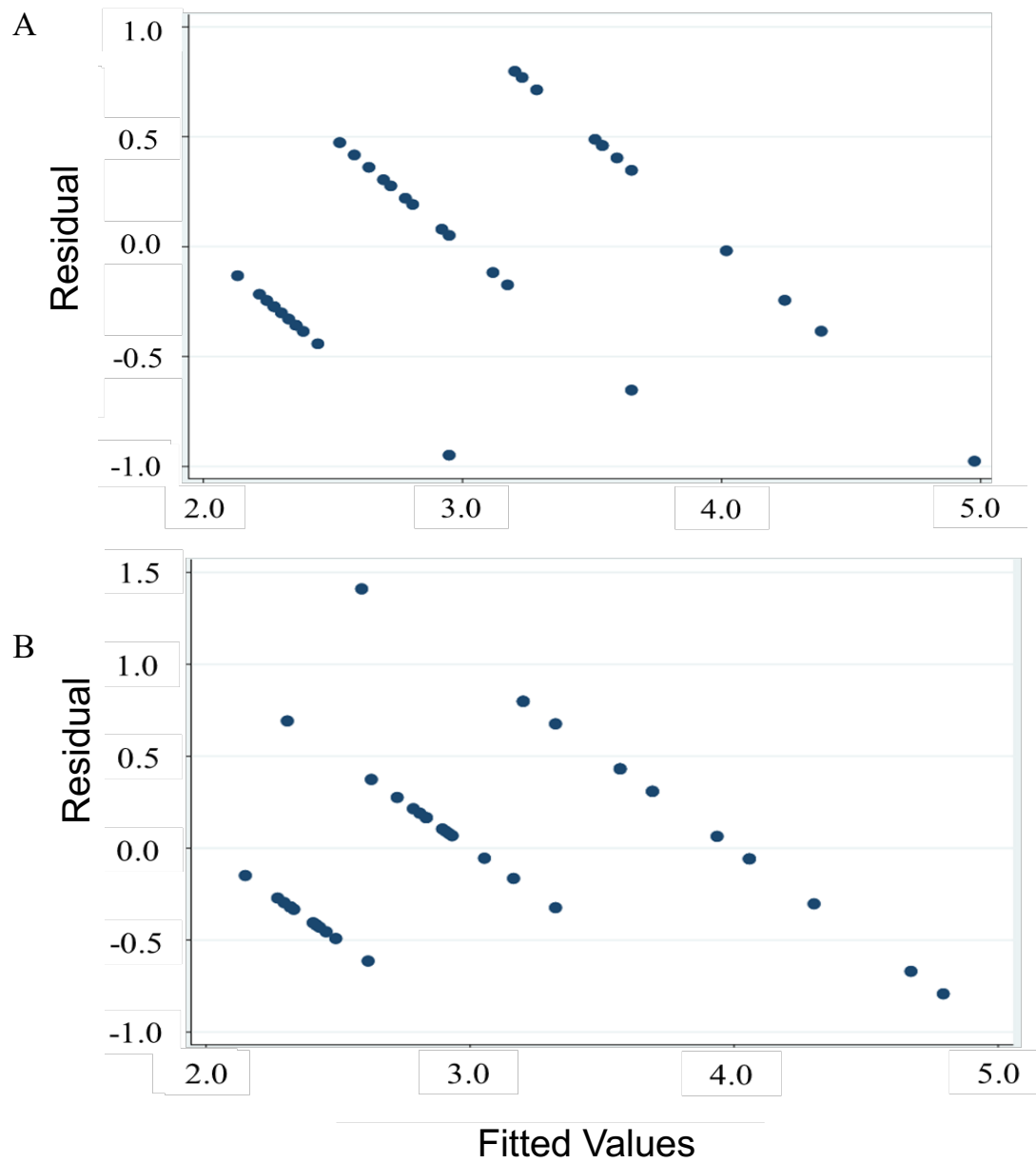


Figure S3. Linear regression model residuals for monochloramine inactivation of murine norovirus. Residuals are described as the different between observed and predicted values. Residuals are described as the different between observed and predicted values. Figures A and B represent the first (15° C) and second dataset (5° C) respectively.

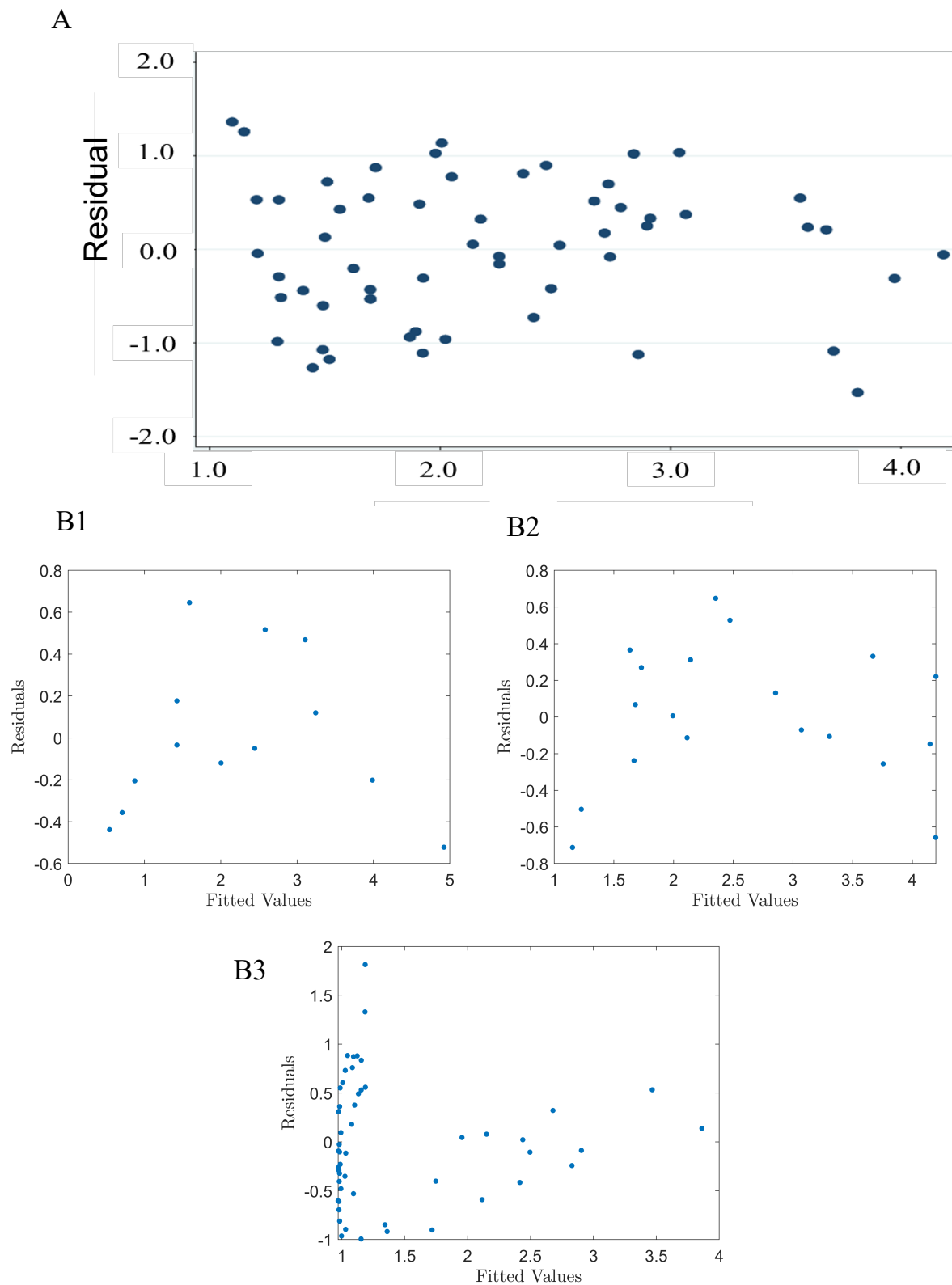


Figure S4. Residuals plots for adenovirus inactivation using free chlorine (A) (Figure 2A) and monochloramine at 5° C and pH 6,7 , and 8 respectively (Figure 2.B1, B2, and B3) regression model. Residuals are described as the different between observed and predicted values.

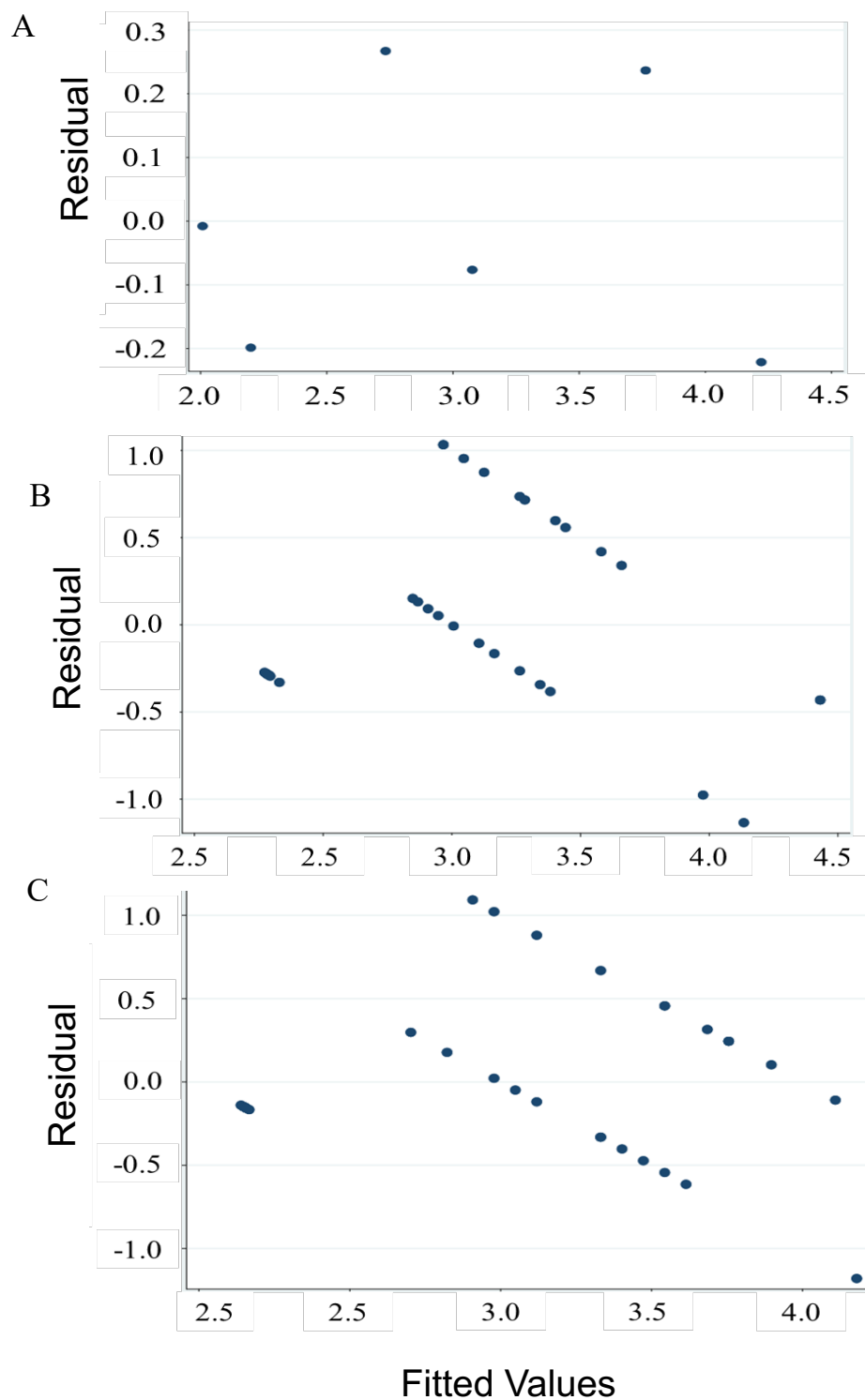


Figure S5. (A) Linear regression model residuals for free chlorine inactivation of echovirus from Figure 3A. Residuals are described as the different between observed and predicted values. Figures B and C, represent linear regression model residuals for monochloramine inactivation of echovirus at 15° C and 5° C, respectively (Figure 3B).

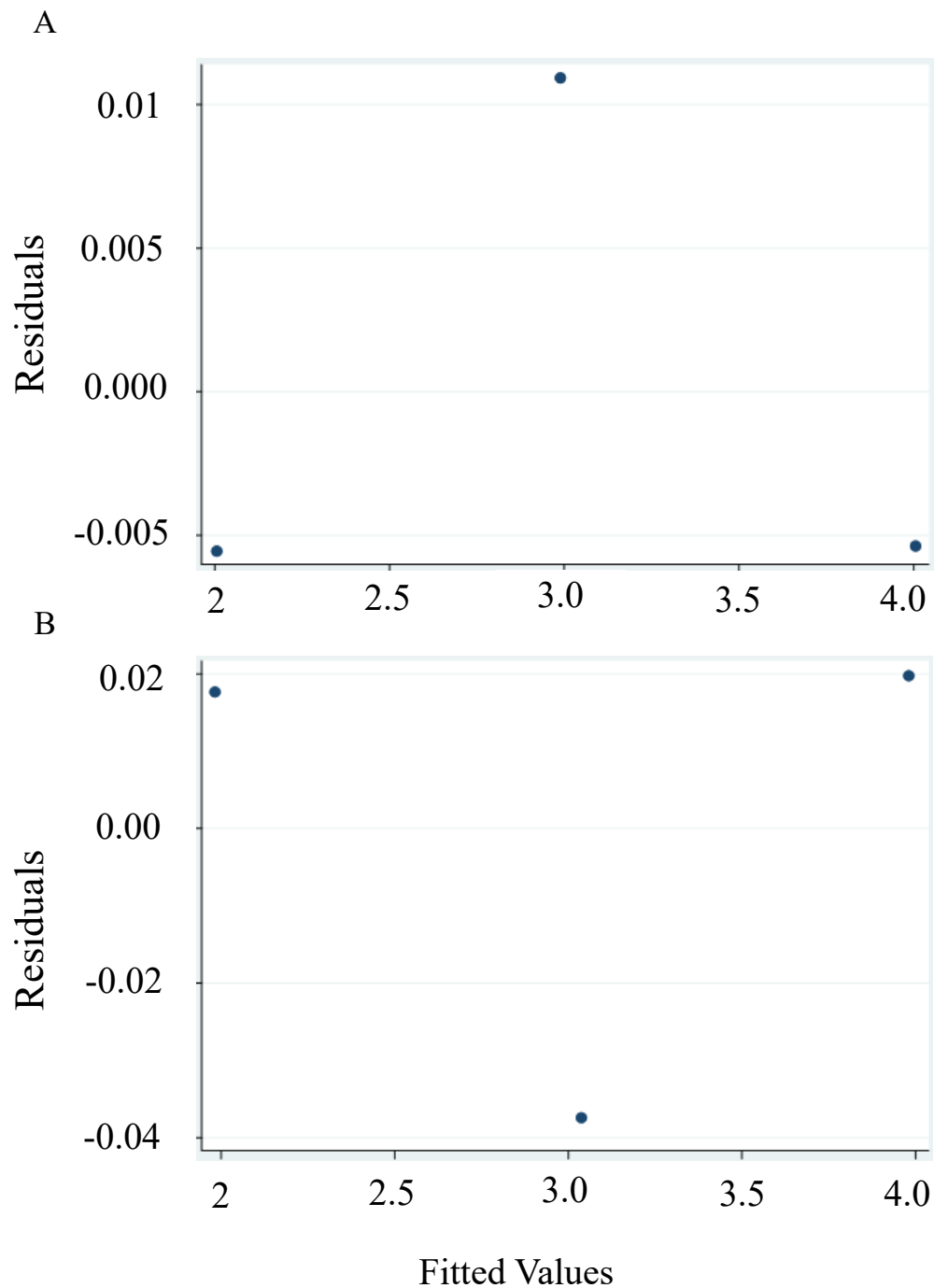


Figure S6. Linear regression model residuals for free chlorine inactivation of coxsakievirus. (Figure 4A). Residuals are described as the different between observed and predicted values. Figures A and B represent the first (pH 7.5) and second dataset (pH 9) respectively.

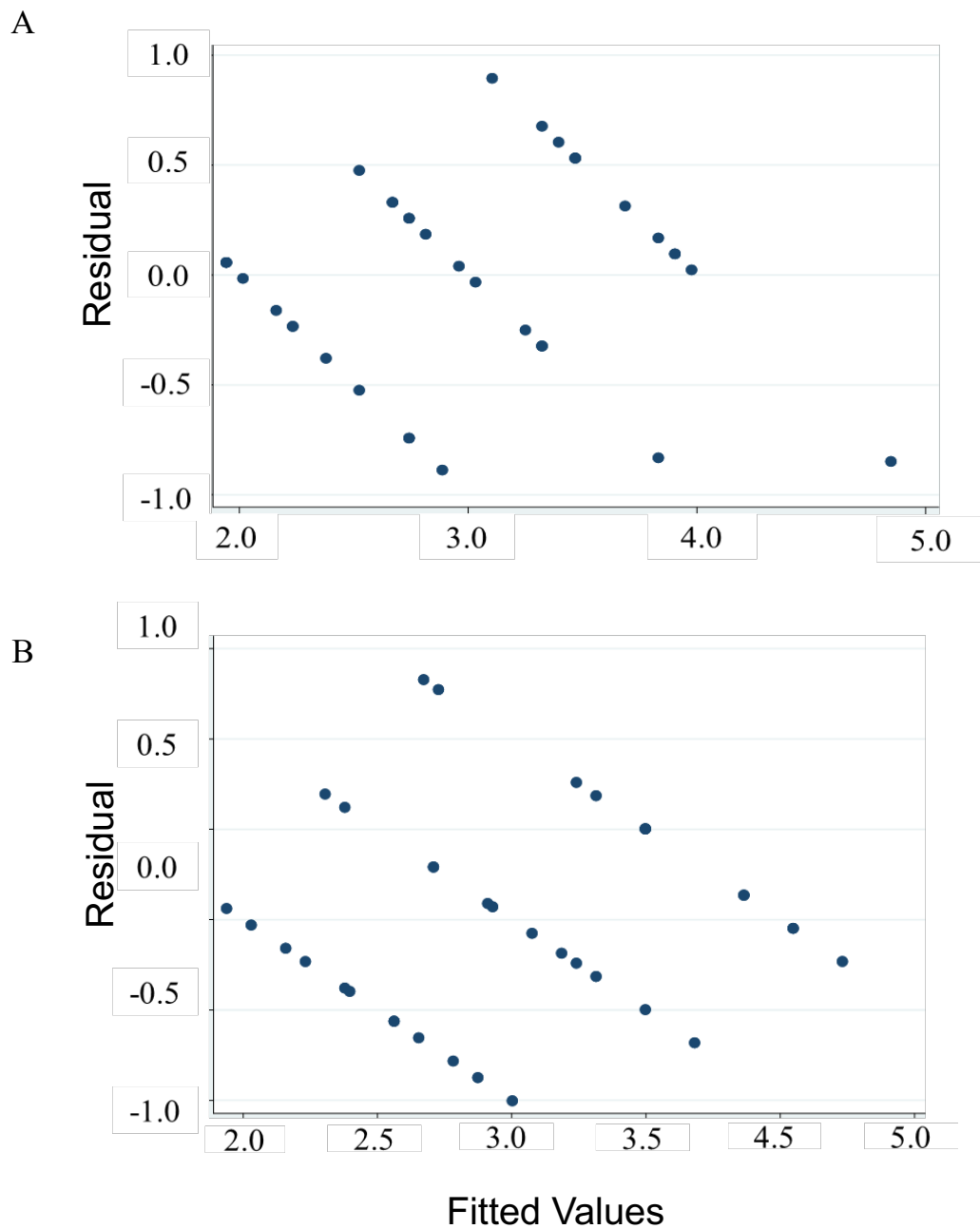


Figure S7. Linear regression model residuals for monochloramine inactivation of coxsakievirus (Figure 4B). Residuals are described as the different between observed and predicted values. Figures A and B represent the first (15° C) and second dataset (5° C) respectively.

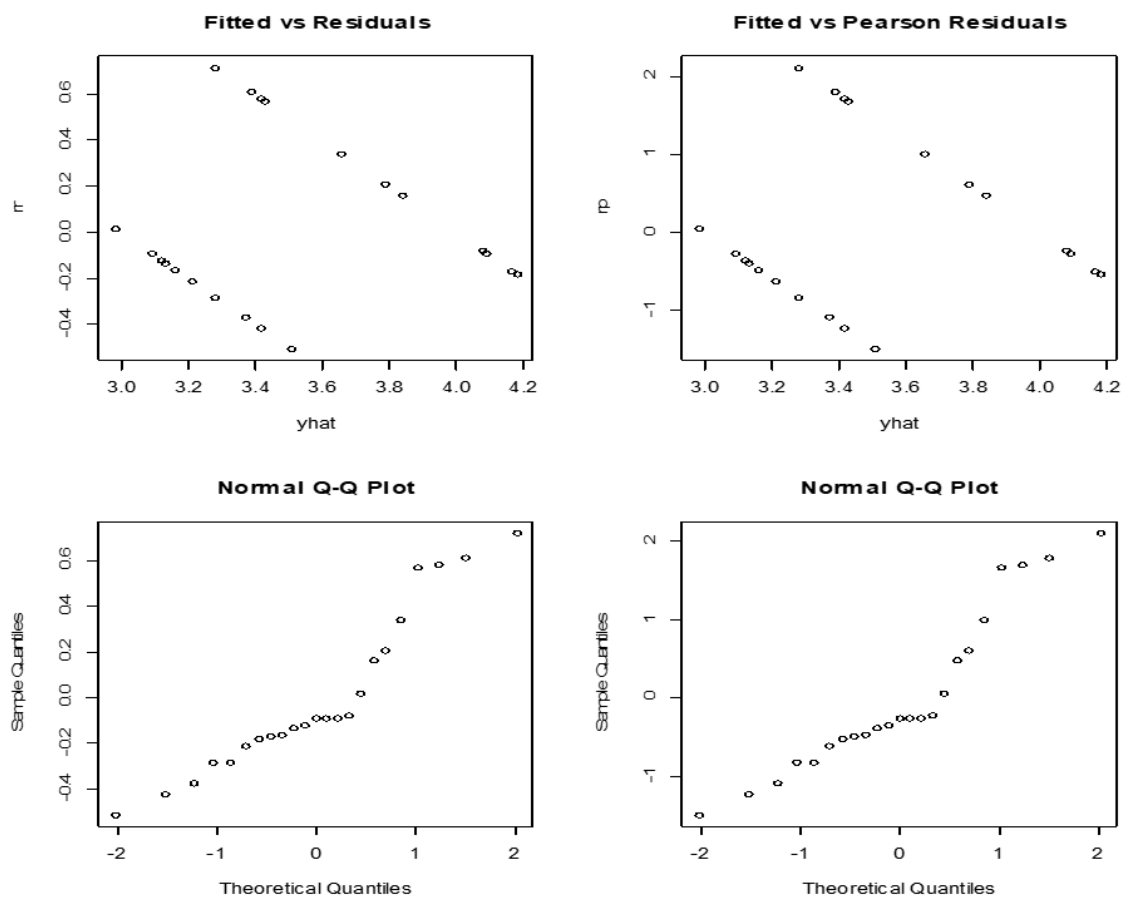


Figure S8. Linear regression model quantile – quantile plot of residuals and fitted value generated from MNV inactivation with free chlorine first data set (figure 1A).

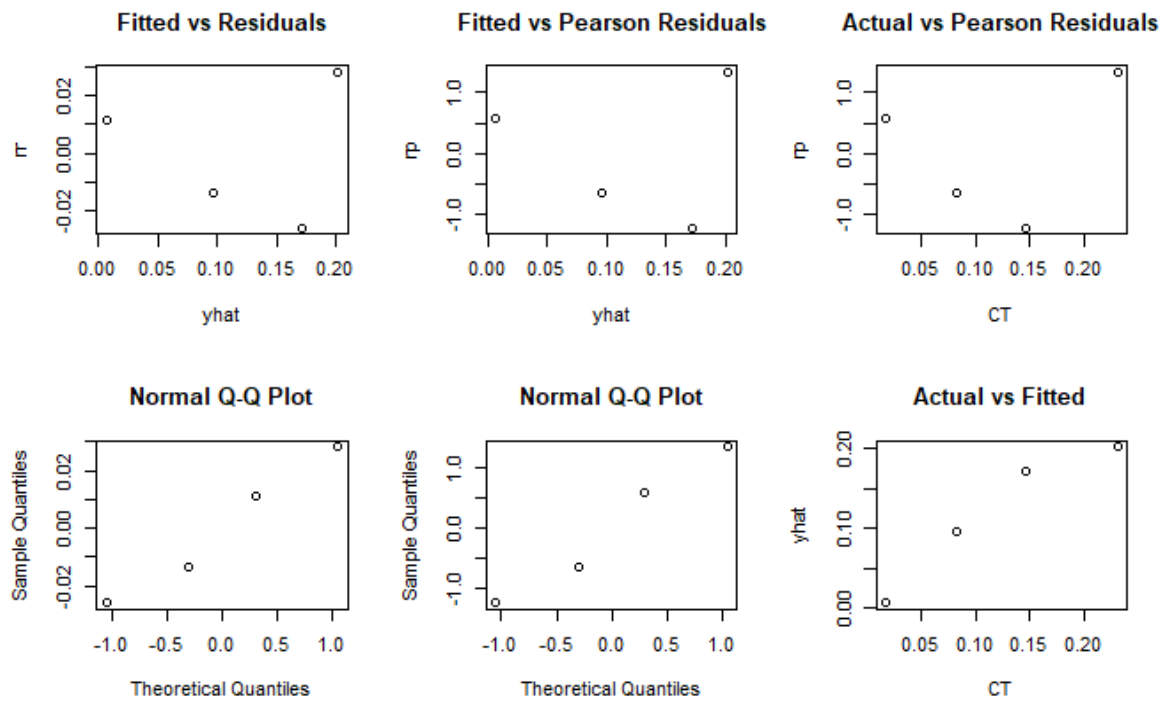


Figure S9. Tobit regression model quantile – quantile plot of residuals and fitted value generated from MNV inactivation with free chlorine second data set (figure 1A).

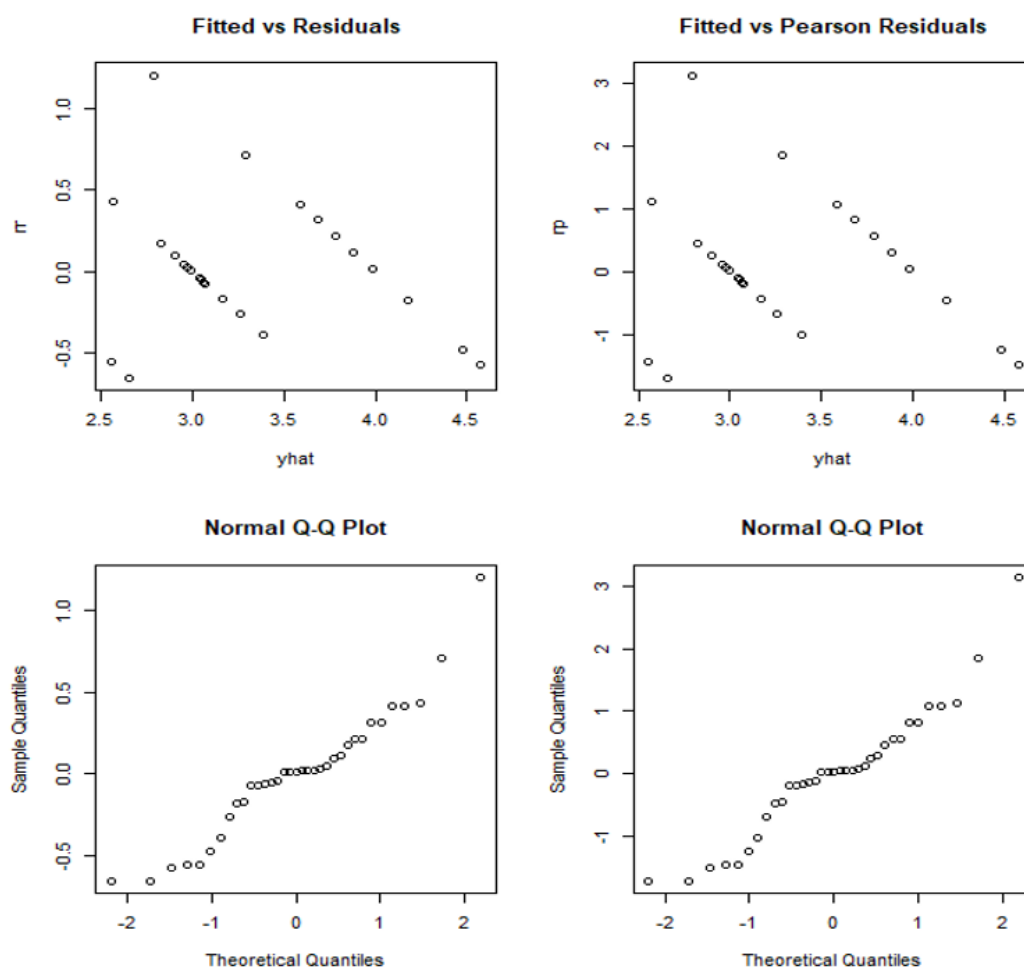


Figure S10. Linear regression model quantile – quantile plot of residuals and fitted value generated from MNV inactivation with monochloramine data set (5 C) from figure 1B

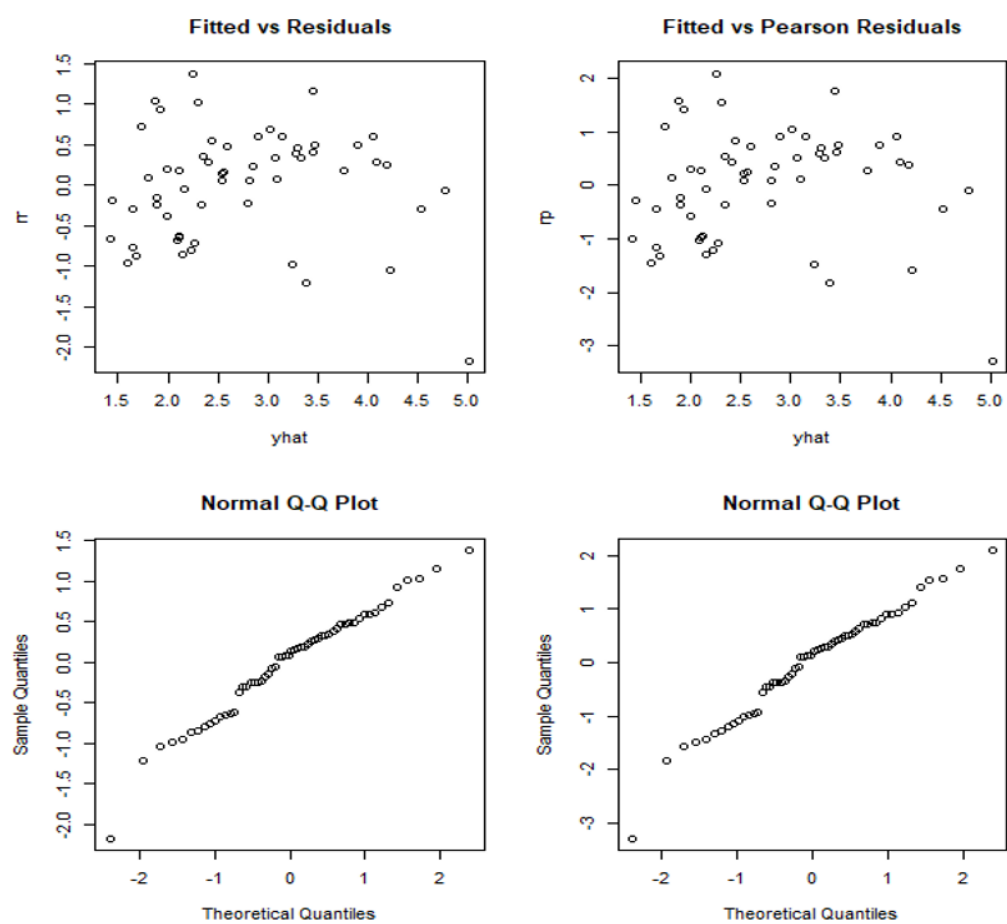


Figure S11. Linear regression model quantile – quantile plot of residuals and fitted value generated from AdV inactivation with free chlorine data set from figure 2A.

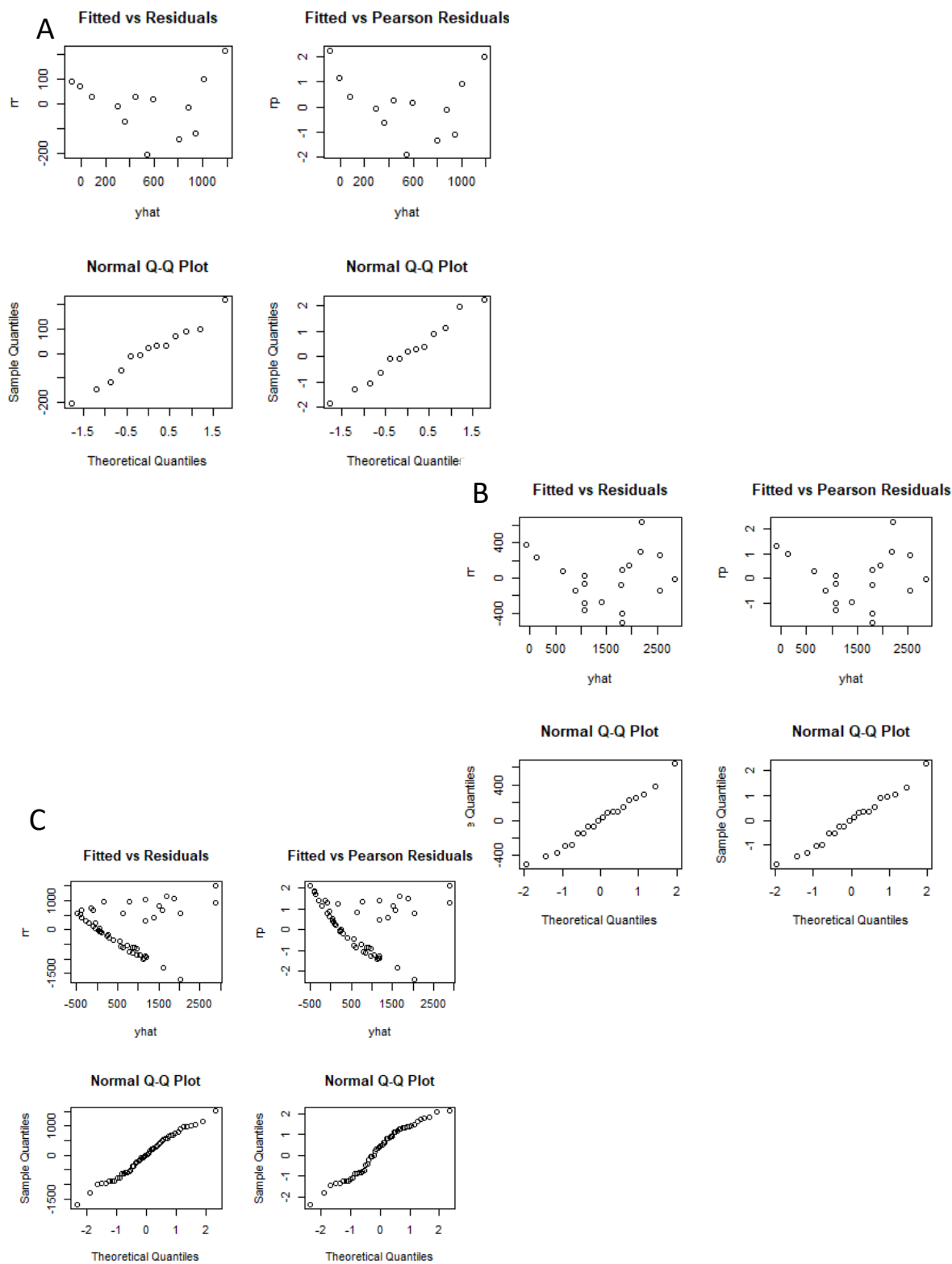


Figure S12. Linear regression model quantile – quantile plot of residuals and fitted value generated from AdV inactivation with monochloramine data set from figure 2B1 (A), B2 (B), and B3 (C).

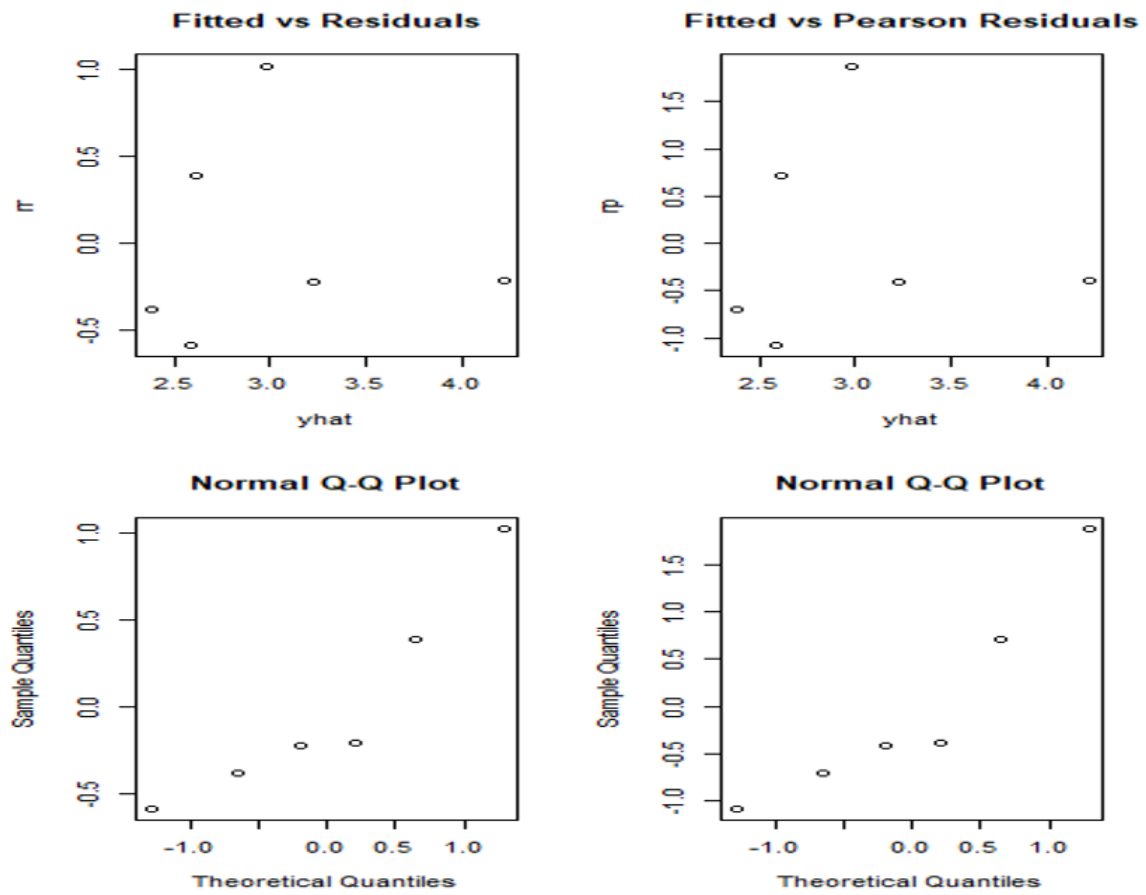
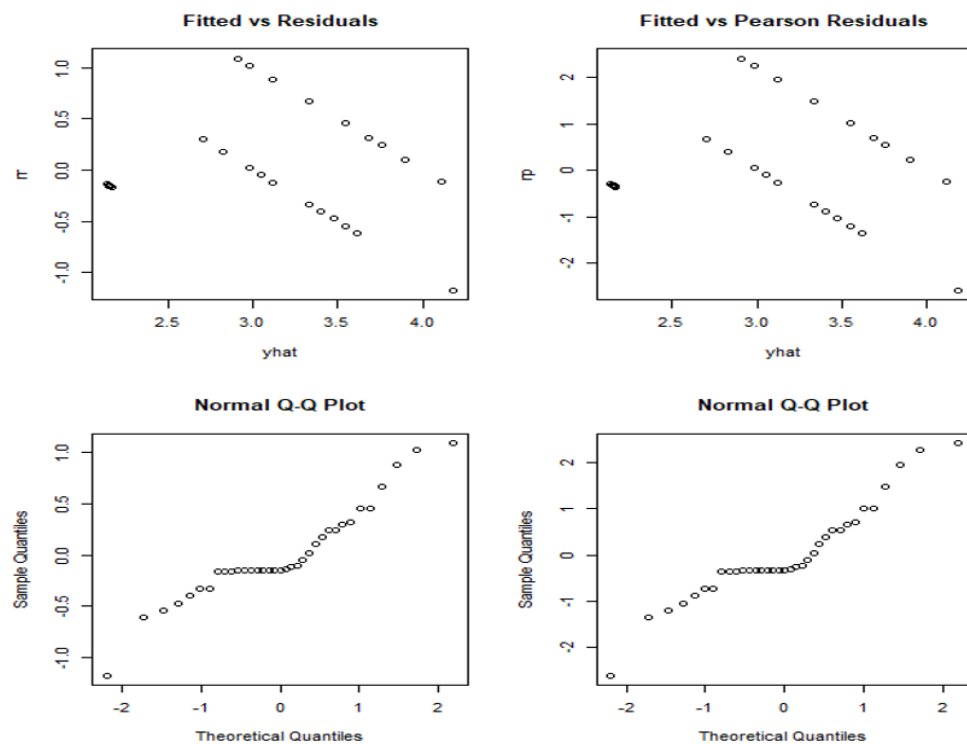


Figure S13. Linear regression model quantile – quantile plot of residuals and fitted value generated from echovirus inactivation with free chlorine data set from figure 3A.

A



B

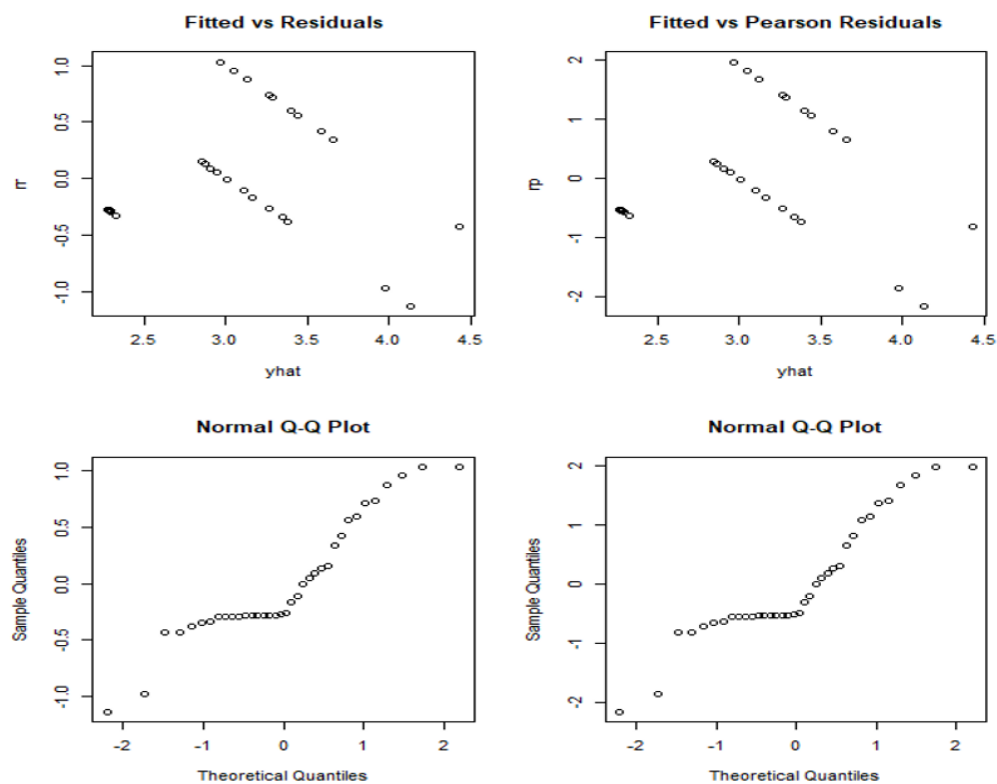
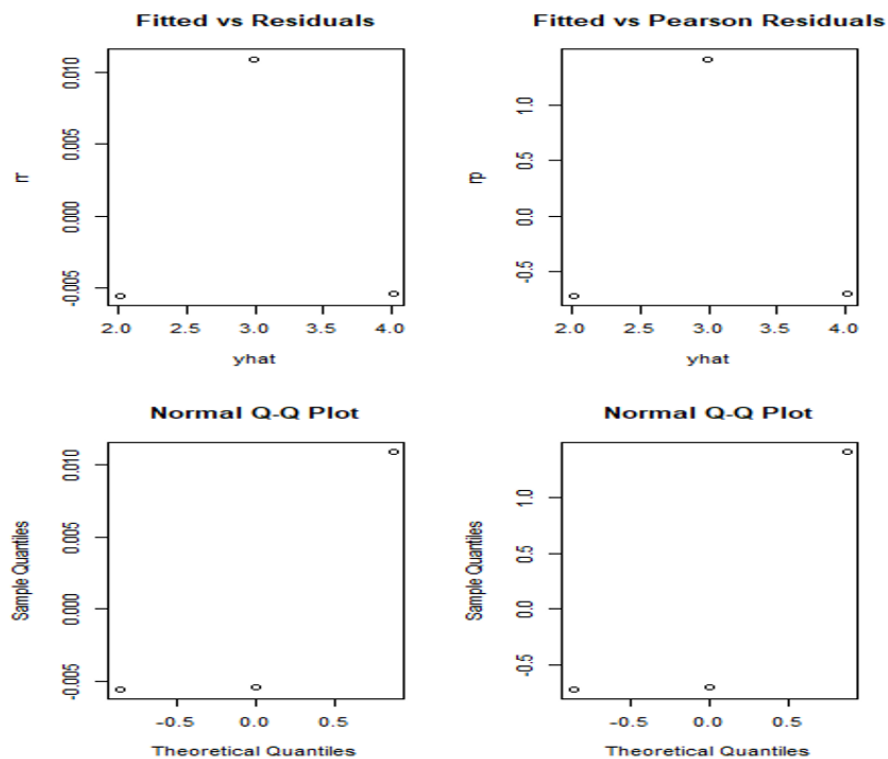


Figure S14. Linear regression model quantile – quantile plot of residuals and fitted value generated from echovirus inactivation with monochloramine data set from figure 3B at temperature of 5 °C (A) and 15°C (B).

A



B

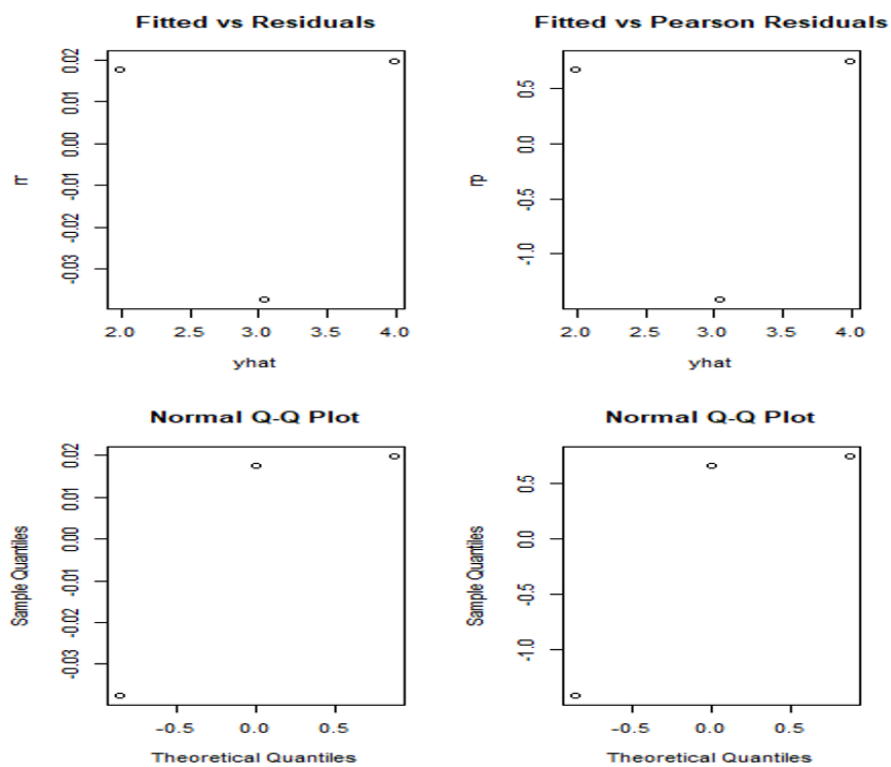


Figure S15. Linear regression model quantile – quantile plot of residuals and fitted value generated from coxsackievirus inactivation with free chlorine data set from figure 4A at pH 7.5 (A) and 9 (B).

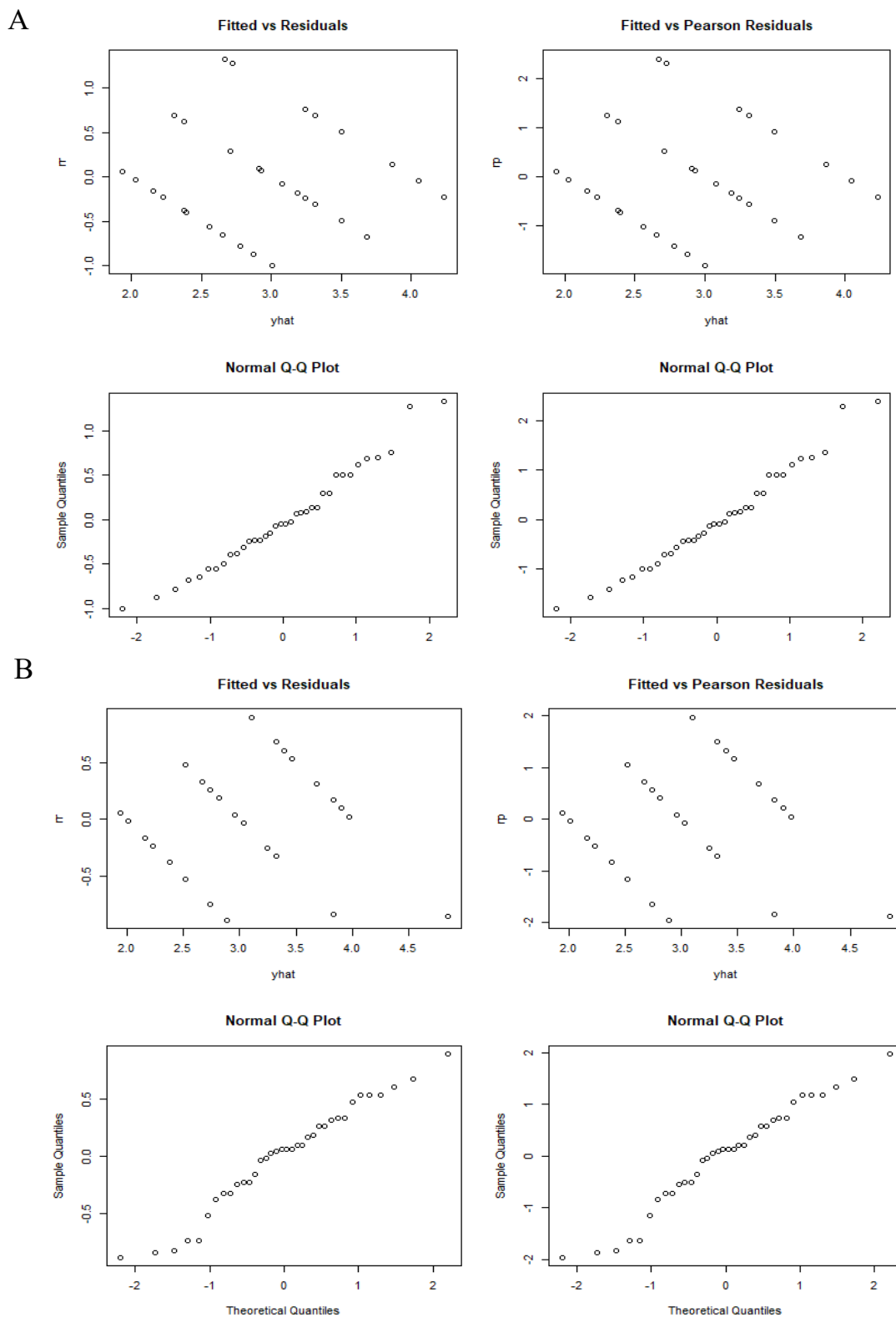


Figure S16. Linear regression model quantile – quantile plot of residuals and fitted value generated from coxsackievirus inactivation with free chlorine data set from figure 4B at temperature of 5°C (A) and 15°C (B).

SI17. R code for statistical analysis

R code for Tobit

Install the require packages:

- ggplot2
- GGally
- VGAM
- After the installment, add the data set and then insert the following codes
- `Summary(m <- vglm (dependent variable ~ independent variable 1 + ..., tobit , data="file name"))`

R code for Ancova

- `mod1 <- aov(log10~ Ct*buffer, data=mydata)`
- `mod2 <- aov(log10~ Ct+buffer, data=mydata)`
- `anova(mod1, mod2)`