

Supplementary materials

S1. Climate anomalies for monthly temperature and precipitation

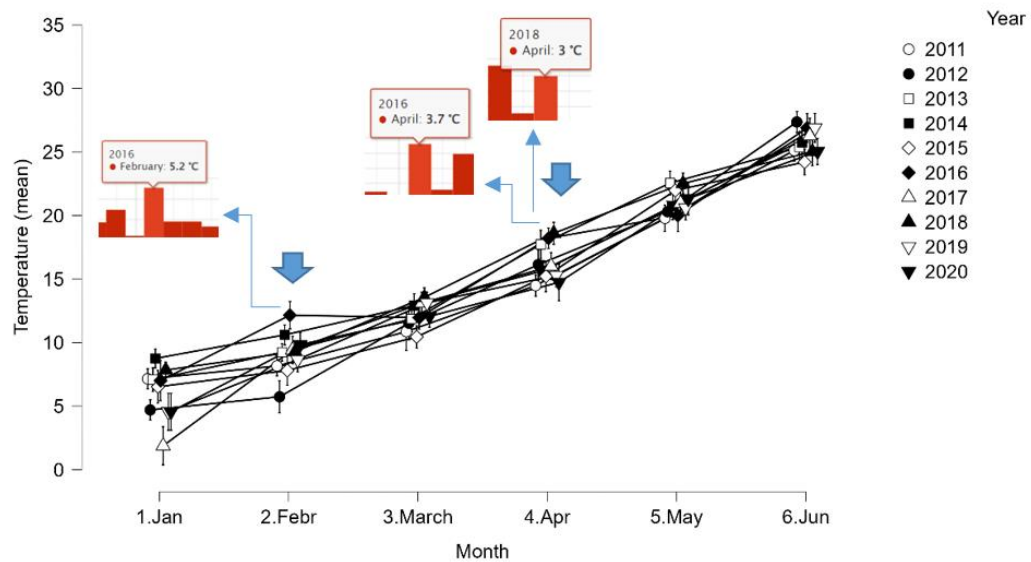


Figure S1. A descriptive plot of annual temperature change in the Larissa region. The blue arrows indicate the trend of climate change.

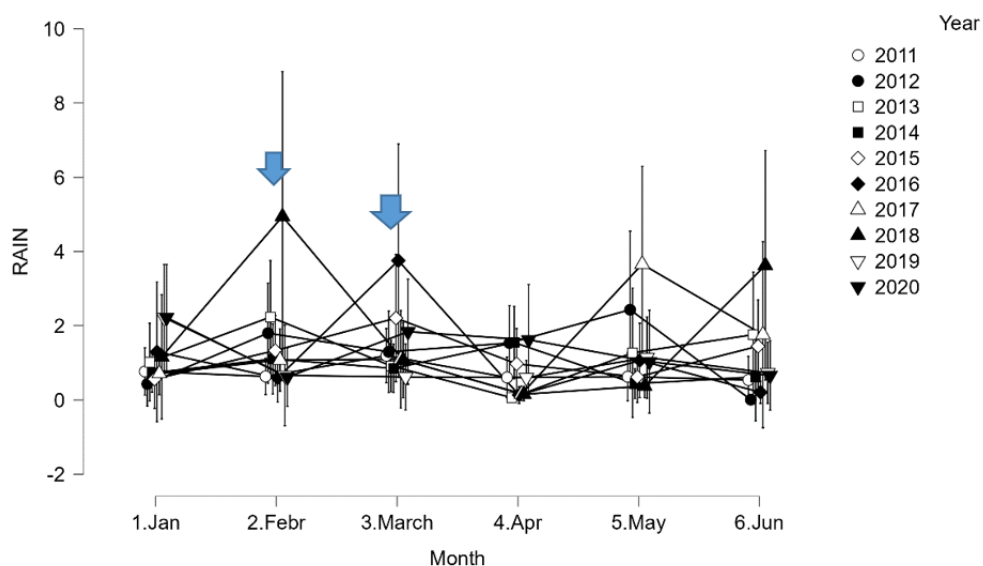


Figure S2 A descriptive plot of annual precipitation change in the Larissa region. The blue arrows indicate the trend of climate change.

S2. Visual Winter wheat infections

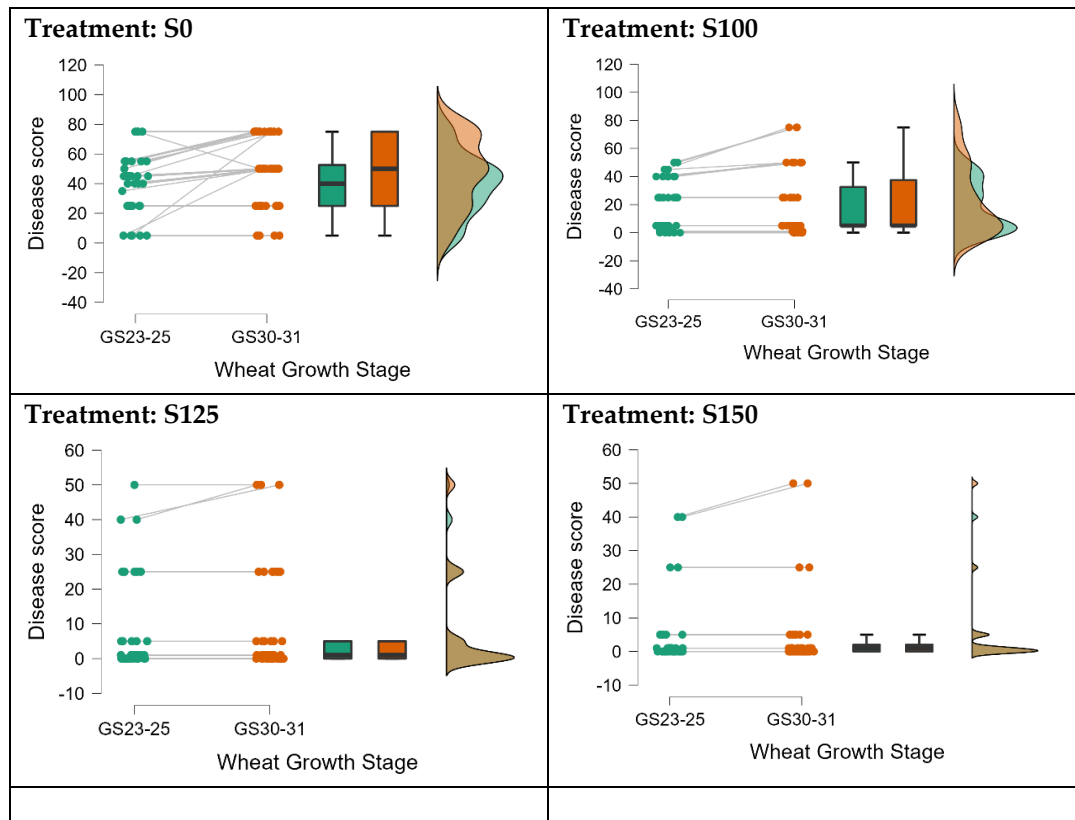


Figure S3. Raincloud plots for the Systiva® seed treatment fungicide effectivity among different application doses among GS23-25 and GS30-31 crop stages.

S3. Remote sensing results

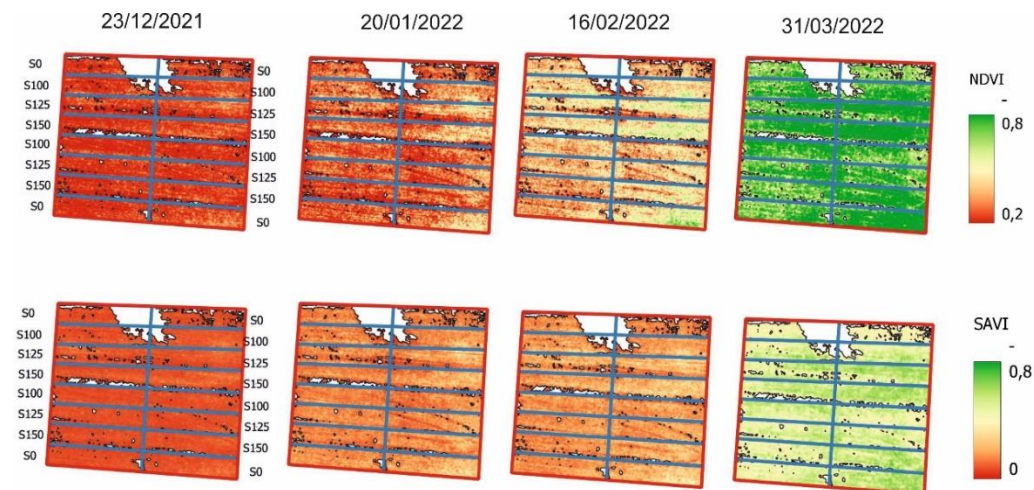


Figure S4. Images of NDVI (upper series) and SAVI (lower series) from the experimental field

S4. Quality control

S4.1 dada2: plotQualityProfile plot a visual summary of the quality scores

This function plots (Figures S5, S6), a visual summary of the distribution of quality scores as a function of sequence position for the input fastq datasets. The distribution of quality scores at each position is shown as a grey-scale heat map, with dark colors corresponding to higher

frequency. The plotted lines show positional summary statistics: green is the mean, orange is the median, and the dashed orange lines are the 25th and 75th quantiles. If the sequences vary in length, a red line will be plotted showing the percentage of reads that extend to at least that position.

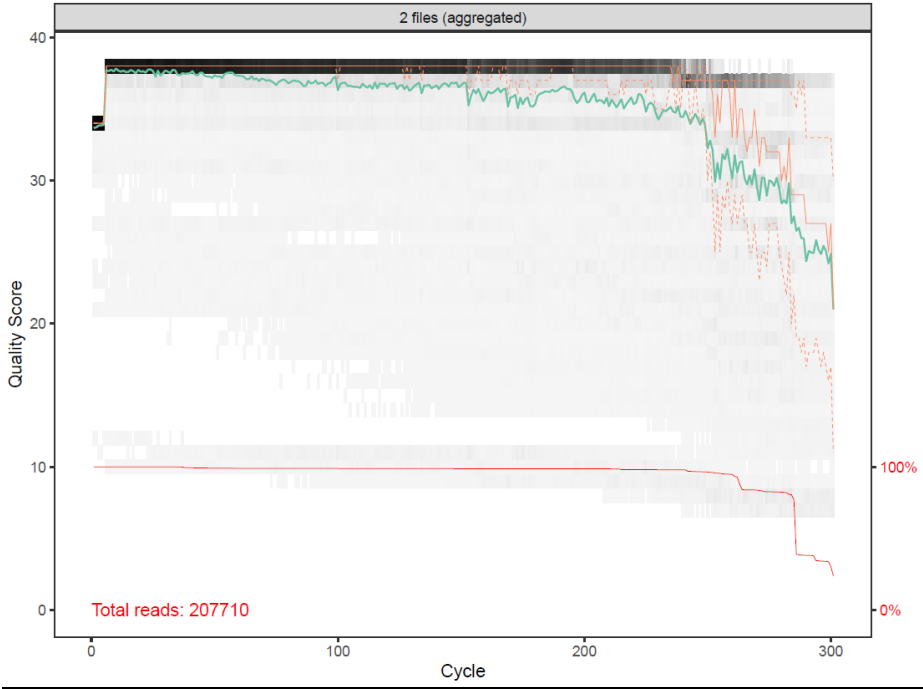


Figure S5. Quality scores forward reads



Figure S6. Quality scores reverse reads

S4.2. dada2: plotComplexity Plot sequence complexity profile

This function plots a histogram of the distribution of sequence complexities (Figures S7, S8), in the form of effective numbers of kmers as determined by seqComplexity. By default, kmers of size 2 are used, in which case a perfectly random sequences will approach an effective kmer number of $16 = 4 \text{ (nucleotides)}^2 \text{ (kmer size)}$. This function calculates the kmer complexity of input sequences. Complexity is quantified as the Shannon richness of kmers, which can be thought of as the effective number of kmers if they were all at equal frequencies. If a window size is provided, the minimum Shannon richness observed over sliding window along the sequence is returned.

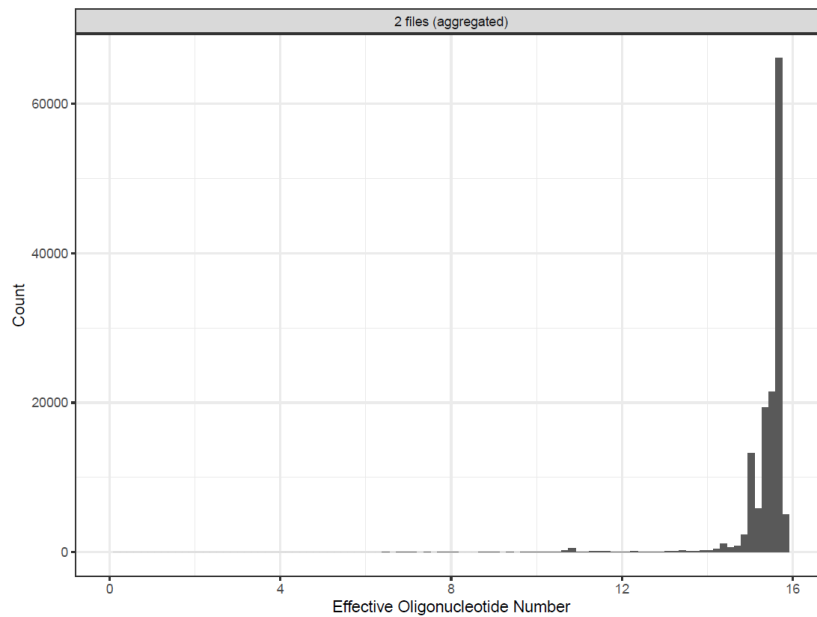


Figure S7. Distribution of sequence complexities, forward reads

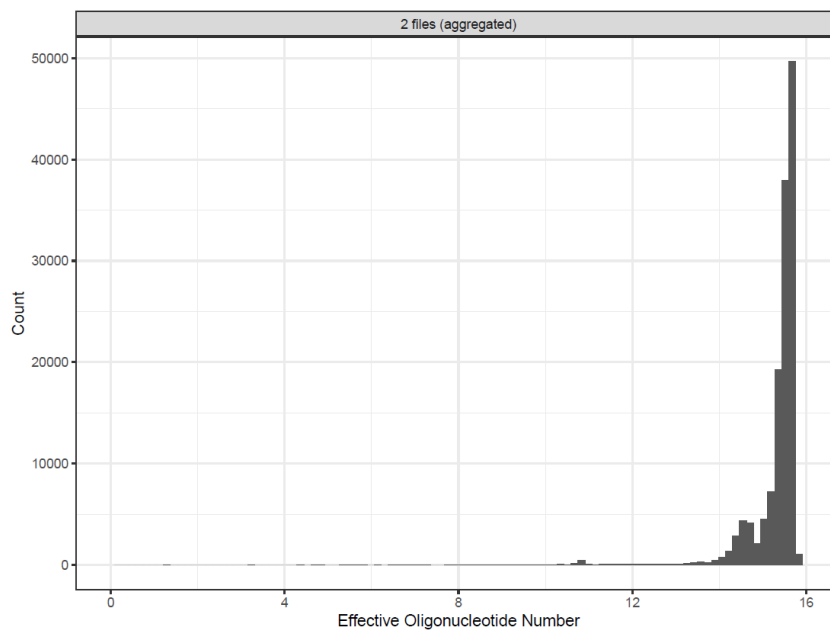


Figure S8. Distribution of sequence complexities, reverse reads

S4.3. dada2: learnErrors Learn Error rates

Error rates (Figure S9), are learned by alternating between sample inference and error rate estimation until convergence. Additionally, a plot is generated that shows the observed frequency of each transition (eg. A->C) as a function of the associated quality score, the final estimated error rates (if they exist), the initial input rates, and the expected error rates under the nominal definition of quality scores. In addition, a plot is generated (with plotErrors) that shows the observed frequency of each transition (eg. A->C) as a function of the associated quality score. Also, the final estimated error rates (if they exist) are shown.

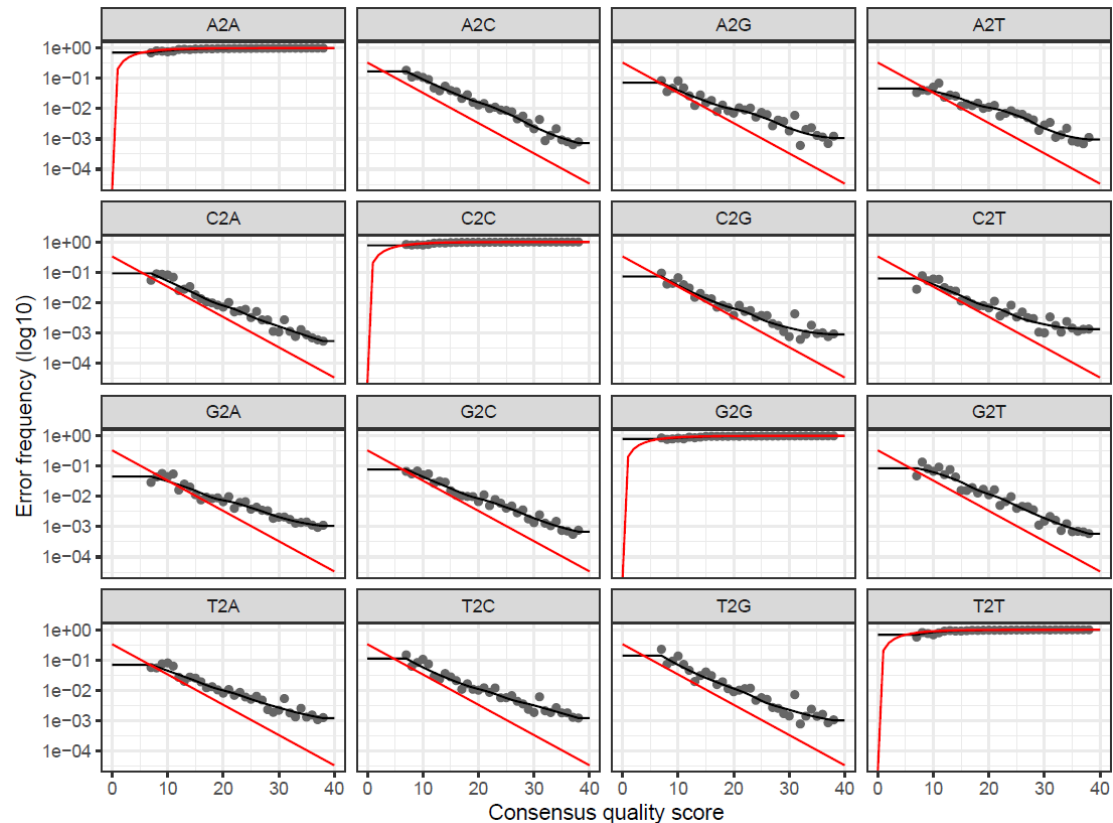


Figure S9. Sample inference and error rate estimation

S4.4. Counts

Comparison of representative Sequence length distribution, Abundance per sample, Abundance per sample/division (Phylum), Abundance per sample/Kingdom, and Abundance per sample are presented in Figures S10, S11, S12, S13, and S14 respectively.

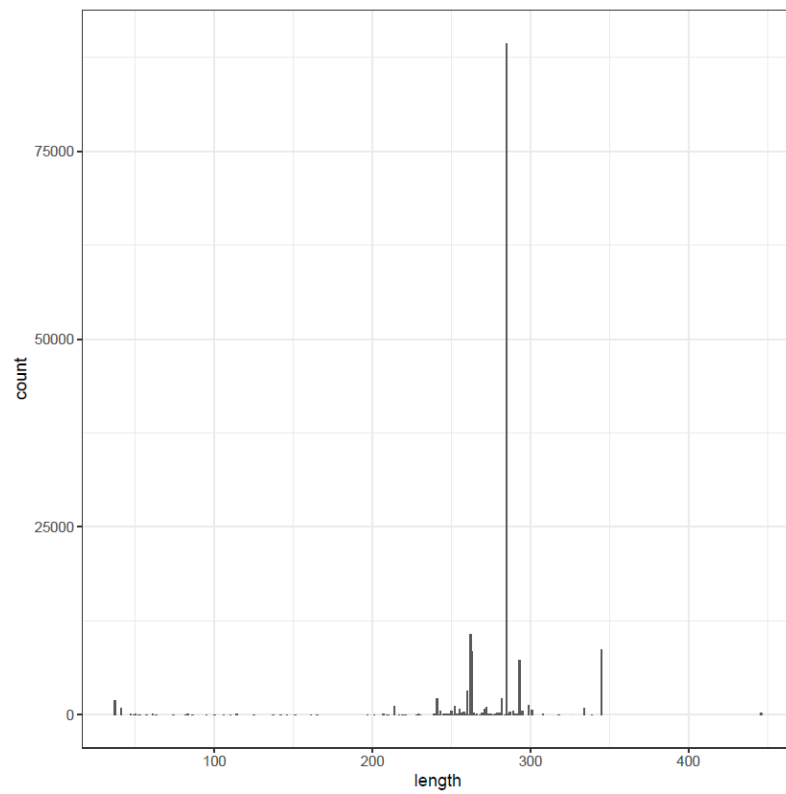


Figure S10. Sequence length distribution

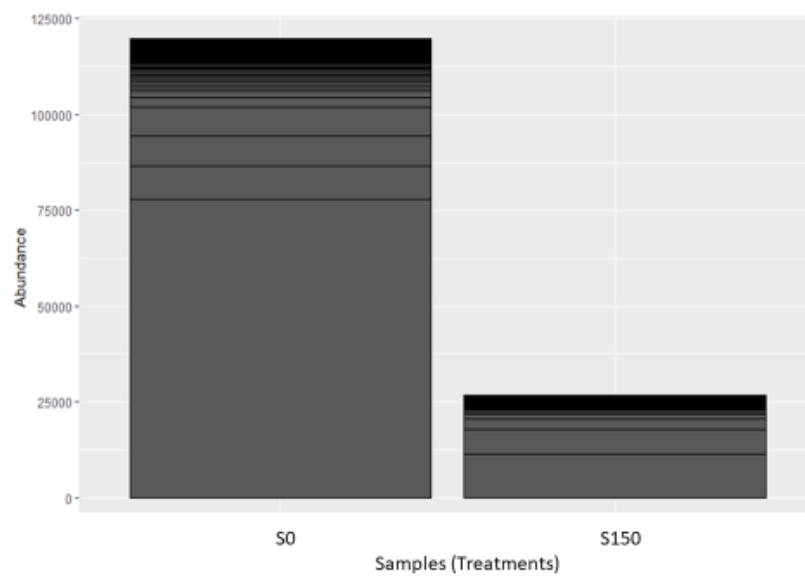


Figure S11. Abundance per sample

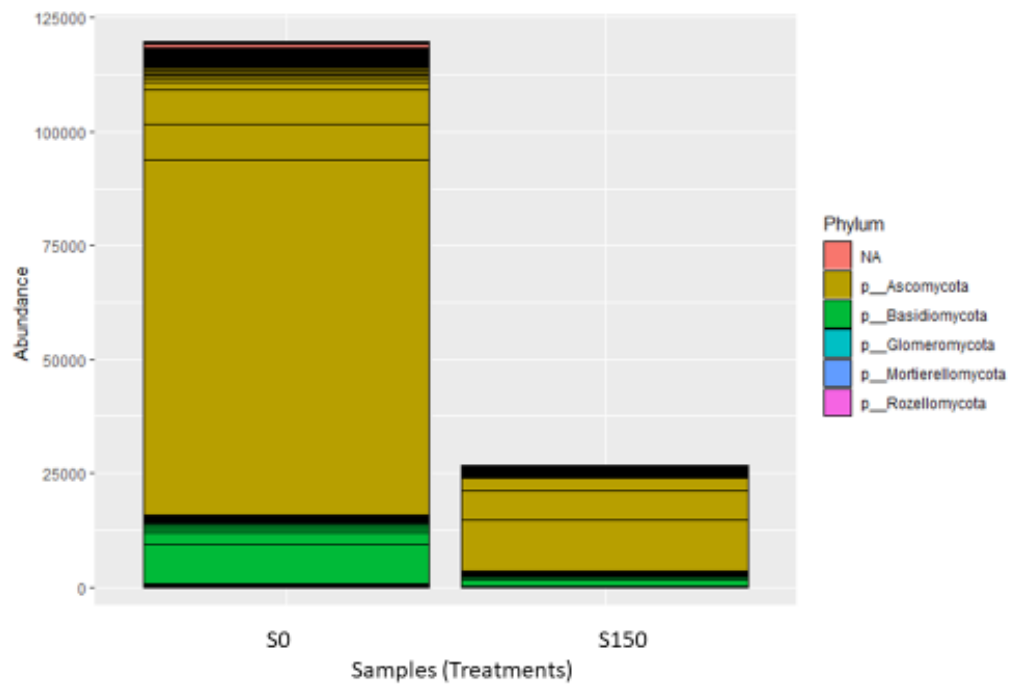


Figure S12. Abundance per sample/division (Phylum)

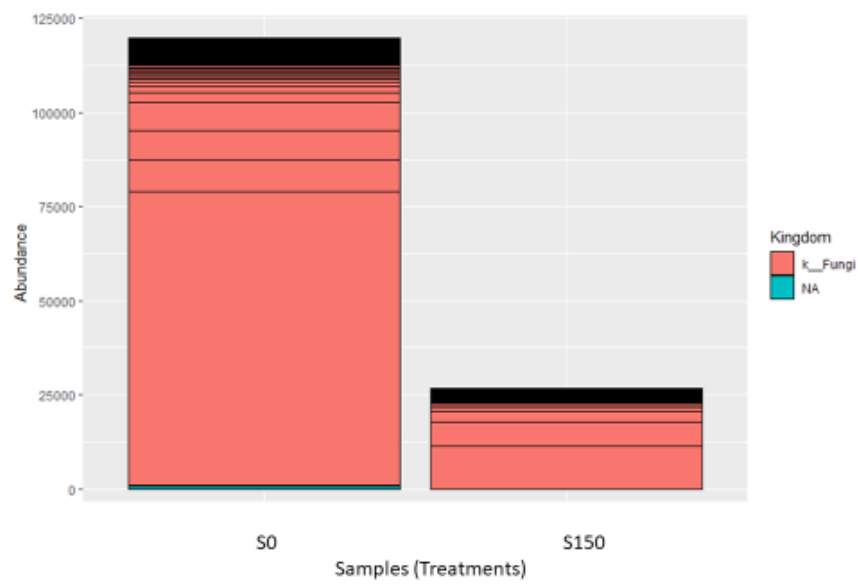


Figure S13. Abundance per sample/Kingdom

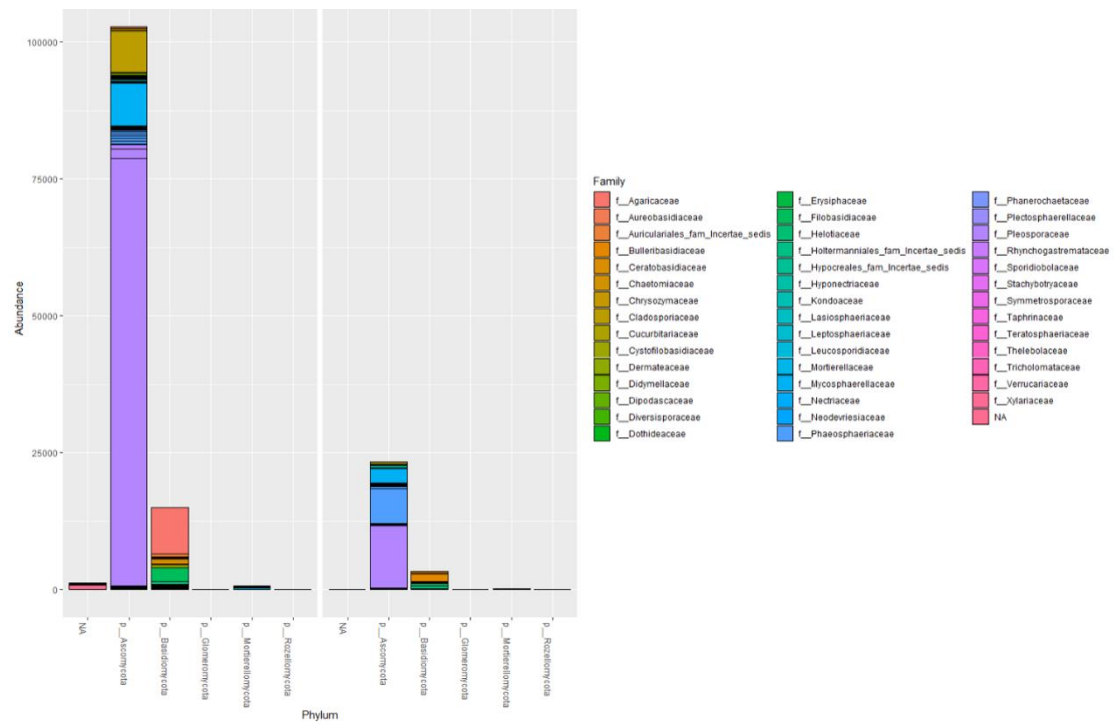


Figure S14. Abundance per sample/Family