Results

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##   
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':  
##   
## filter, lag

## The following objects are masked from 'package:base':  
##   
## intersect, setdiff, setequal, union

## New names:  
## Rows: 1352 Columns: 16  
## ── Column specification  
## ──────────────────────────────────────────────────────── Delimiter: "," chr  
## (4): Well, Fluor, Content, Sample dbl (8): Cq, Cq Mean, Cq Std. Dev, Starting  
## Quantity (SQ), Log Starting Quan... lgl (4): ...1, Target, Biological Set Name,  
## Well Note  
## ℹ Use `spec()` to retrieve the full column specification for this data. ℹ  
## Specify the column types or set `show\_col\_types = FALSE` to quiet this message.  
## New names:  
## Rows: 1030 Columns: 16  
## ── Column specification  
## ──────────────────────────────────────────────────────── Delimiter: "," chr  
## (4): Well, Fluor, Content, Sample dbl (8): Cq, Cq Mean, Cq Std. Dev, Starting  
## Quantity (SQ), Log Starting Quan... lgl (4): ...1, Target, Biological Set Name,  
## Well Note  
## ℹ Use `spec()` to retrieve the full column specification for this data. ℹ  
## Specify the column types or set `show\_col\_types = FALSE` to quiet this message.  
## Rows: 512 Columns: 7  
## ── Column specification  
## ──────────────────────────────────────────────────────── Delimiter: "," chr  
## (6): Well, Fluor, Content, Sample, Cq, Starting Quantity (SQ) lgl (1): Target  
## ℹ Use `spec()` to retrieve the full column specification for this data. ℹ  
## Specify the column types or set `show\_col\_types = FALSE` to quiet this message.  
## Rows: 133 Columns: 4  
## ── Column specification  
## ──────────────────────────────────────────────────────── Delimiter: "," chr  
## (3): pre\_post\_wet, cc\_treatment, drying\_treatment dbl (1): sample\_no  
## ℹ Use `spec()` to retrieve the full column specification for this data. ℹ  
## Specify the column types or set `show\_col\_types = FALSE` to quiet this message.  
## New names:  
## Rows: 116 Columns: 10  
## ── Column specification  
## ──────────────────────────────────────────────────────── Delimiter: "," chr  
## (3): sample\_no, qubit\_concentration, notes dbl (6): extraction\_date,  
## extraction\_soil\_wt\_mg, al\_pan\_wt, fresh\_soil\_mg, d... lgl (1): ...5  
## ℹ Use `spec()` to retrieve the full column specification for this data. ℹ  
## Specify the column types or set `show\_col\_types = FALSE` to quiet this message.  
## Joining, by = "sample\_no"  
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## Joining, by = "sample\_no"  
## `summarise()` has grouped output by 'drying\_treatment'. You can override using  
## the `.groups` argument.  
## Registering fonts with R  
## `summarise()` has grouped output by 'drying\_treatment'. You can override using  
## the `.groups` argument.  
## • `` -> `...1`

# How do microbes respond to drying and rewetting stress?

Both fungal and bacterial DNA quantities increased at each time point after rewetting as compared to pre-wetting DNA concentrations (Figure 3, Table 2). The effect of rewetting had a significant effect on both bacterial and fungal DNA quantities among samples without cover crops, with (p = 0.691828 χ² = 40.949, df = 1) for bacterial and p < 0.001 (χ² = 38.625, df = 1) for fungal (Kruskal-Wallis Rank Sum Test).