# Sequencing report

## Sample summary

245 samples were extracted for DNA from the 1, 5, 6 Nitrogen treatments (Table 1). Overall, 242 samples were included in the final mapping\_file\_taxonomy.csv. One sample was dropped from the mapping file because there was no corresponding qPCR data. Two samples were dropped because there was no corresponding sequencing file.

Table 1. Summary of samples sequenced for each date and treatment. 245 samples were extracted for DNA from the 1, 5, 6 Nitrogen treatments. One sample was dropped from the mapping file because there was no corresponding qPCR data. Two samples were dropped because there was no corresponding sequencing file.

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample date** | **Nitrogen** | **Water** | **Count** |
| 6/15/2021 | 1 | 1 | 6 |
| 6/15/2021 | 1 | 2 | 5 |
| 6/15/2021 | 5 | 1 | 6 |
| 6/15/2021 | 5 | 2 | 6 |
| 6/15/2021 | 6 | 1 | 6 |
| 6/15/2021 | 6 | 2 | 6 |
| 6/30/2021 | 1 | 1 | 5 |
| 6/30/2021 | 1 | 2 | 6 |
| 6/30/2021 | 5 | 1 | 4 |
| 6/30/2021 | 5 | 2 | 6 |
| 6/30/2021 | 6 | 1 | 6 |
| 6/30/2021 | 6 | 2 | 6 |
| 7/27/2021 | 1 | 1 | 6 |
| 7/27/2021 | 1 | 2 | 6 |
| 7/27/2021 | 5 | 1 | 6 |
| 7/27/2021 | 5 | 2 | 6 |
| 7/27/2021 | 6 | 1 | 6 |
| 7/27/2021 | 6 | 2 | 5 |
| 8/10/2021 | 1 | 1 | 6 |
| 8/10/2021 | 1 | 2 | 5 |
| 8/10/2021 | 5 | 1 | 6 |
| 8/10/2021 | 5 | 2 | 5 |
| 8/10/2021 | 6 | 1 | 6 |
| 8/10/2021 | 6 | 2 | 6 |
| 9/23/2021 | 1 | 1 | 3 |
| 9/23/2021 | 1 | 2 | 5 |
| 9/23/2021 | 5 | 1 | 6 |
| 9/23/2021 | 5 | 2 | 6 |
| 9/23/2021 | 6 | 1 | 6 |
| 9/23/2021 | 6 | 2 | 5 |
| 5/26/2022 | 1 | 1 | 3 |
| 5/26/2022 | 1 | 2 | 3 |
| 5/26/2022 | 5 | 1 | 3 |
| 5/26/2022 | 5 | 2 | 3 |
| 5/26/2022 | 6 | 1 | 3 |
| 5/26/2022 | 6 | 2 | 3 |
| 6/22/2022 | 1 | 1 | 3 |
| 6/22/2022 | 1 | 2 | 3 |
| 6/22/2022 | 5 | 1 | 3 |
| 6/22/2022 | 5 | 2 | 2 |
| 6/22/2022 | 6 | 1 | 3 |
| 6/22/2022 | 6 | 2 | 3 |
| 7/20/2022 | 1 | 1 | 3 |
| 7/20/2022 | 1 | 2 | 2 |
| 7/20/2022 | 5 | 1 | 3 |
| 7/20/2022 | 5 | 2 | 2 |
| 7/20/2022 | 6 | 1 | 3 |
| 7/20/2022 | 6 | 2 | 3 |
| 9/1/2022 | 1 | 1 | 3 |
| 9/1/2022 | 1 | 2 | 3 |
| 9/1/2022 | 5 | 1 | 3 |
| 9/1/2022 | 5 | 2 | 3 |
| 9/1/2022 | 6 | 1 | 3 |
| 9/1/2022 | 6 | 2 | 2 |
| 9/27/2022 | 1 | 2 | 3 |
| 9/27/2022 | 5 | 2 | 3 |
| 9/27/2022 | 6 | 2 | 3 |

## Sequencing quality

Bacterial sequencing quality was good according to the expected mock community (Figure 1). Most negative control had little to no total reads (Table 2). However, total reads from sequencing was much higher in the third sequencing run (Figure 2).

Chart

Description automatically generated

Figure 1. Actual versus expected mock community results for bacterial sequencing.

Table 2. Reads in negative controls.

|  |  |
| --- | --- |
| **Barcode** | **Total Reads** |
| barcode22C | 0 |
| barcode30B | 3423 |
| barcode93A | 159 |
| barcode94A | 0 |
| barcode93B | 18575 |
| barcode94B | 0 |
| barcode93C | 11 |
| barcode94C | 0 |

Chart, bar chart

Description automatically generated

Figure 2. Total reads for each sequencing run.