

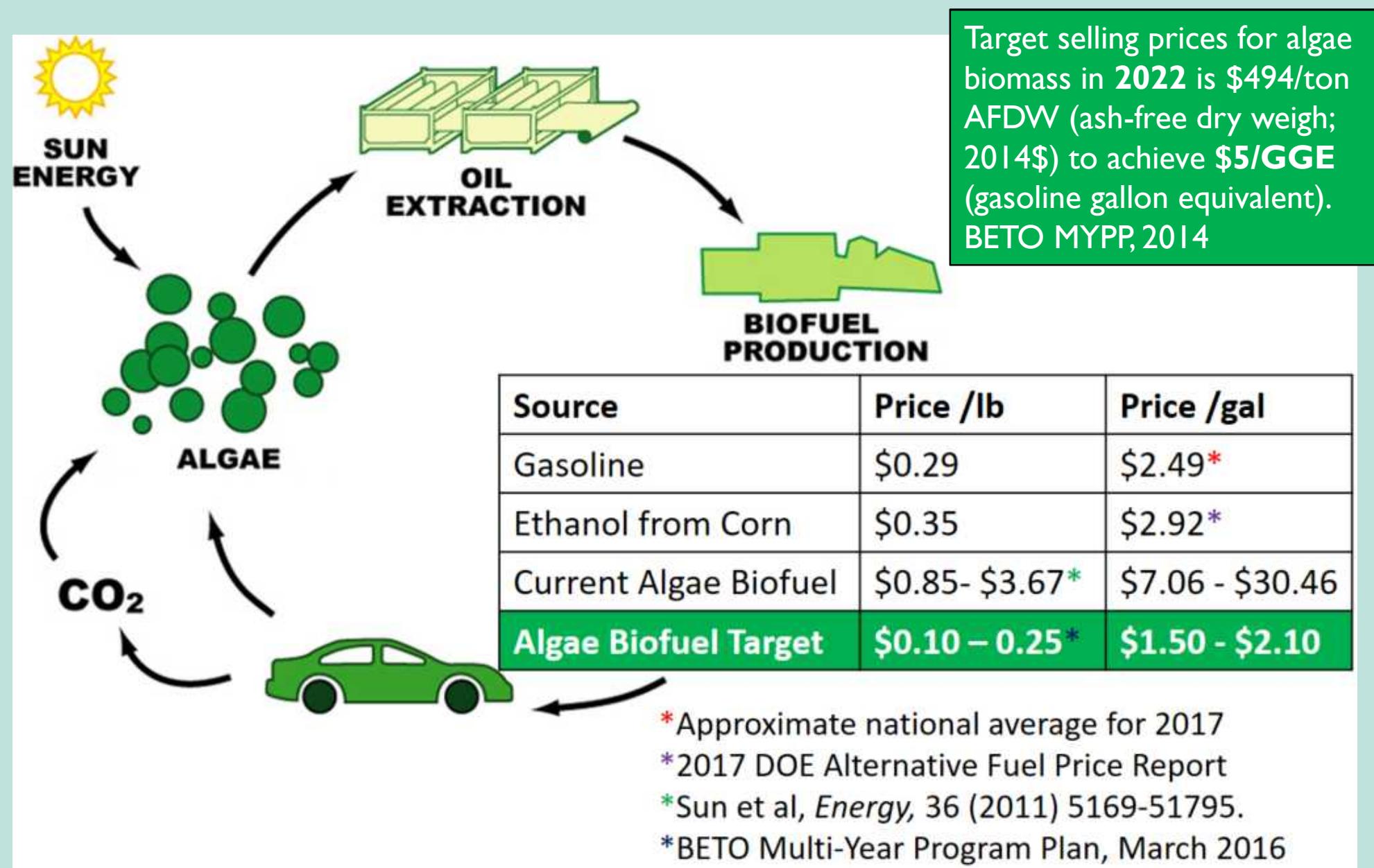


# Field Trials for Microalgae Cultures with Probiotic Bacteria

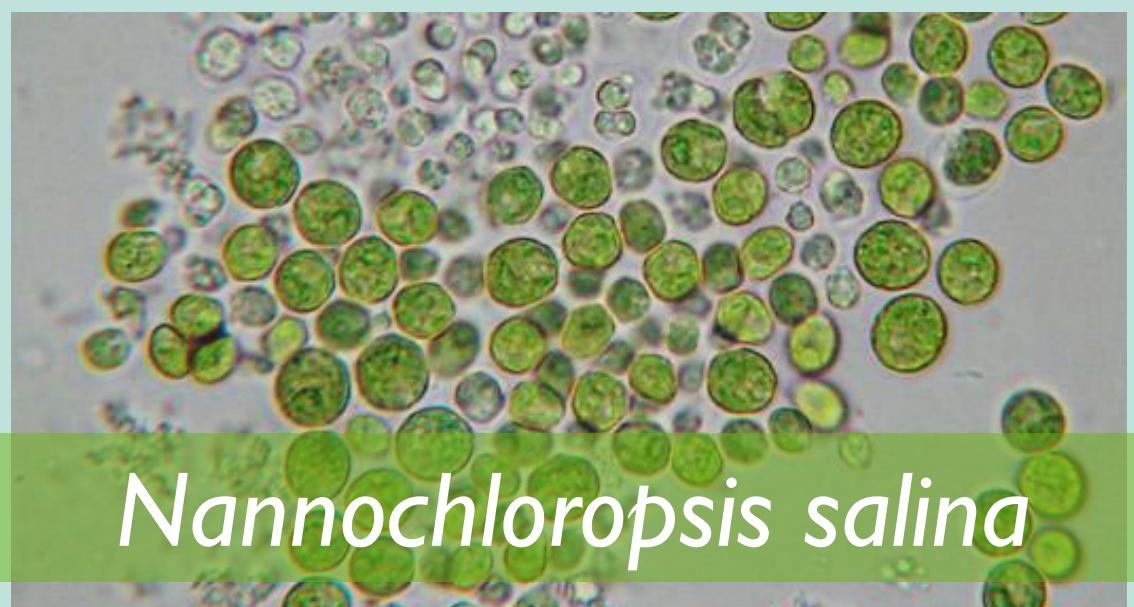
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## Introduction

The introduction of biofuels would create a drastic shift in both national and global policies towards an increasingly **environmentally aware future**. One of the main obstacles of mass microalgal biofuel production is the threat of pond crashes by foreign predators and bacteria. One way Sandia has tackled this problem is with the use of **probiotic consortium** that protect algae from foreign bacteria.



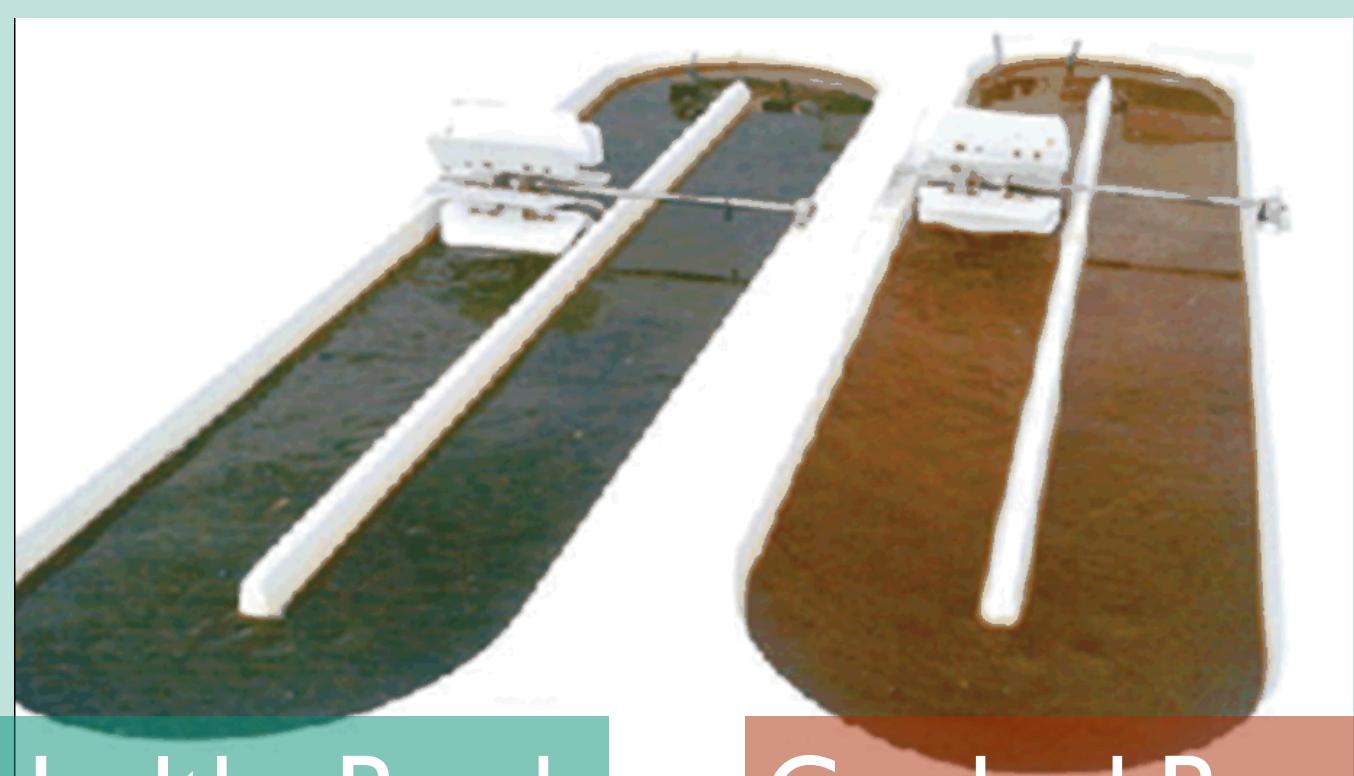
*Brachionus plicatilis*



*Nannochloropsis salina*

- Microalgae contain 25-60% lipids and do not require arable land, they not a source of food, and do not cause environmental harm
- Adaptable/ found in many systems: freshwater, marine, high pH, high salinity, and high nutrient municipal wastewater systems.
- Microalgae utilize atmospheric CO<sub>2</sub> and are responsible for up to 40% carbon fixation worldwide, reducing harmful greenhouse gas.

Hannon et al, 2010; Douskova et al, 2009.

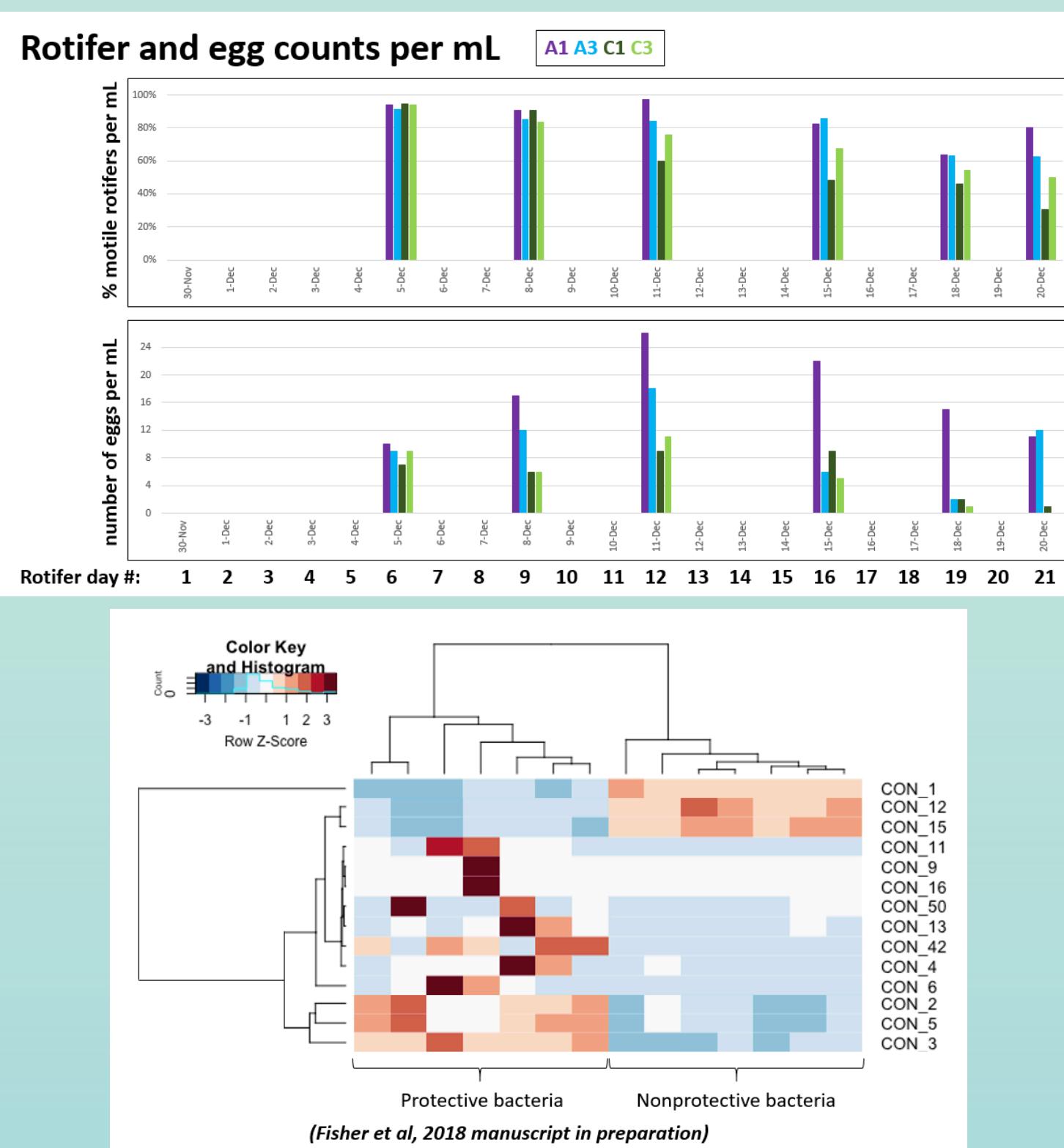


Healthy Pond

Crashed Pond

Algal population crashes cause losses of up to 30% of annual crop production from the typical open raceway system.  
Richardson et al, 2014.

## Future Work

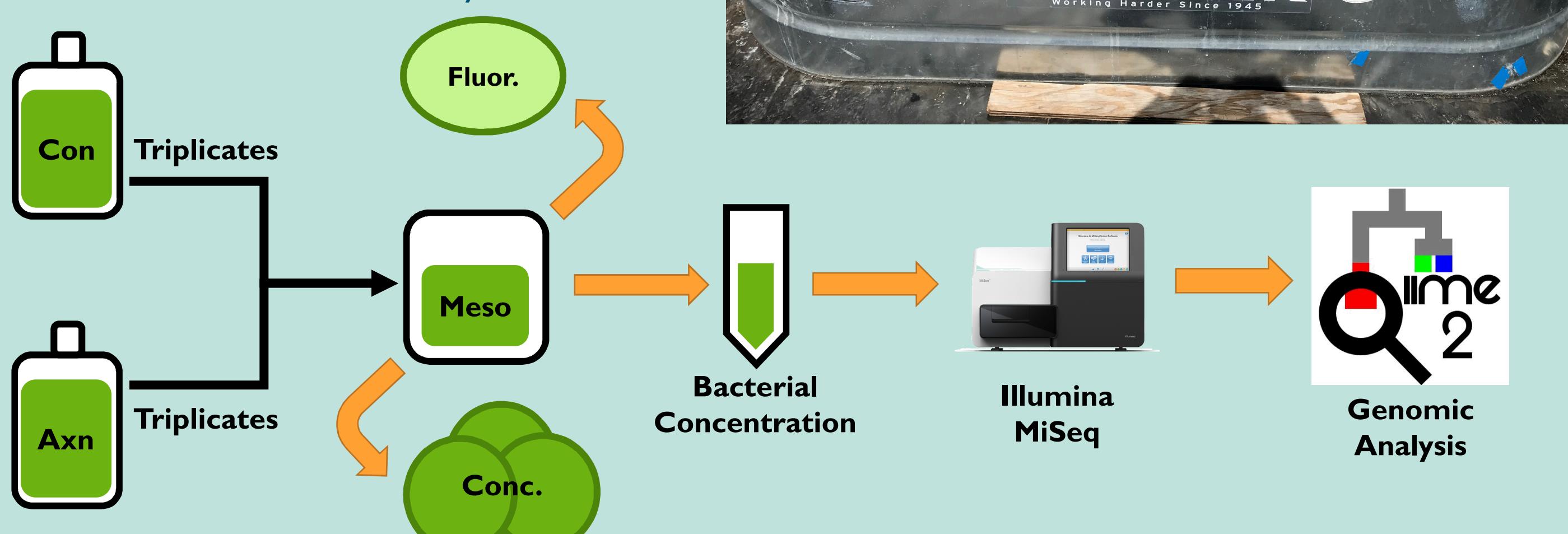


## Experimental Methods

3 sets of consortium algae culture and 3 sets of axenic algae culture were placed in outdoor mesocosms. Field trials of laboratory grown bacterial consortia test whether or not the consortia are still protective uncontrolled conditions.

Mesocosm data collection methods:

- Daily sampling of cell counts and fluorescence
- Nutrient and Sequence samples were collected every 3-4 days
- 90% harvests were done on
- Day 11 and Day 18**
- Mesocosm run lasted 25 days



## Results

Outdoor mesocosm trials were conducted to test the protectiveness of laboratory grown consortia samples in an environment similar to industry-wide outdoor alga raceways. These consortium mesocosms were compared with a set of axenic, non-bacterial algae culture. The DNA extracted from each mesocosm was amplified in the V3/V4 region of the 16s ribosome. Samples were sequenced using **Illumina MiSeq** and were further analyzed using **QIIME 2** microbiome bioinformatics platform.

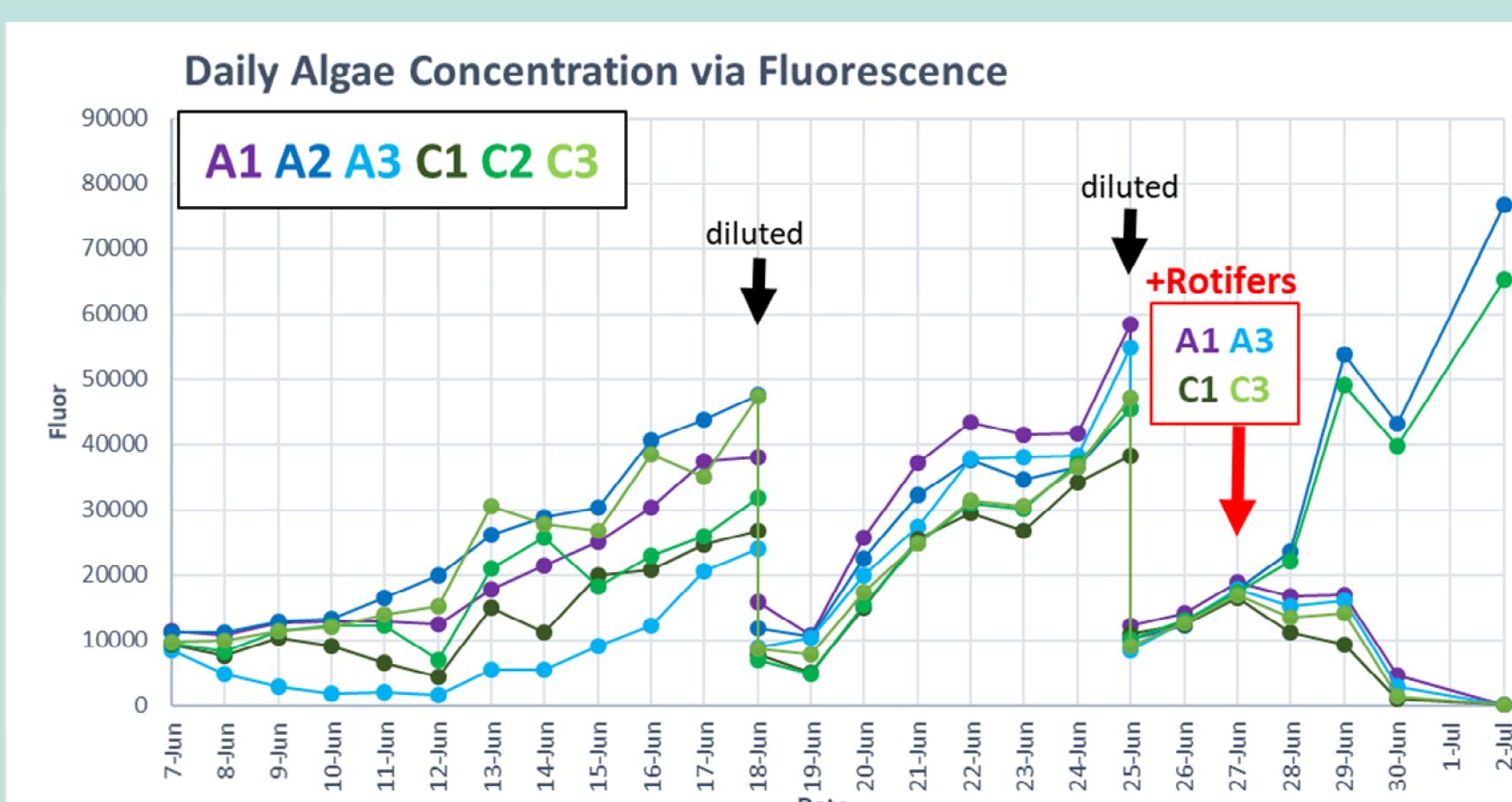


Fig. 1 Algae concentration via fluorescence illustrated the relative fluorescence unit of chlorophyll in algal cells.

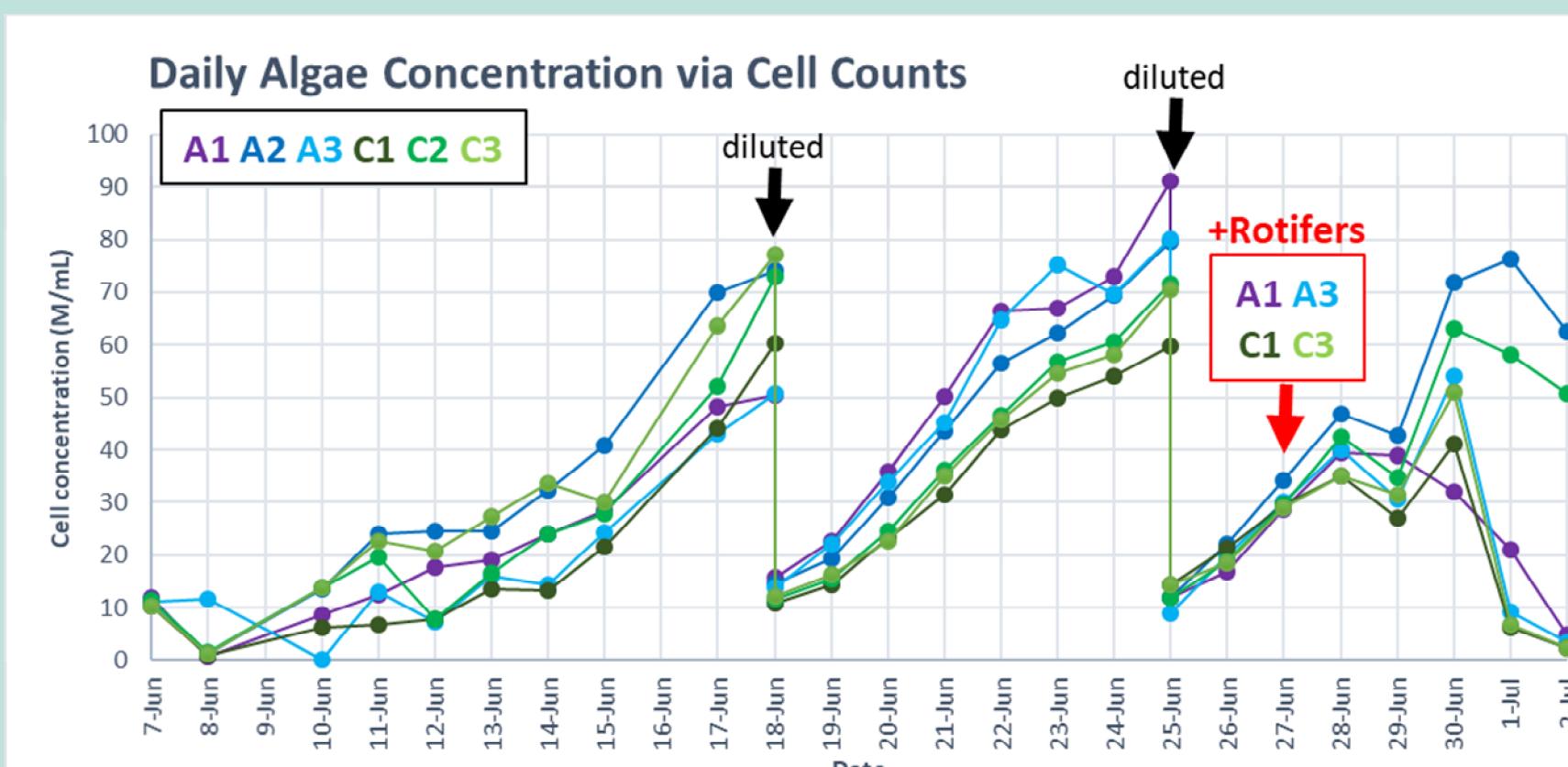


Fig. 2 Algae concentration via cell counts illustrated how many cells between 1.807-3.849 $\mu$ m were present in each mesocosm.

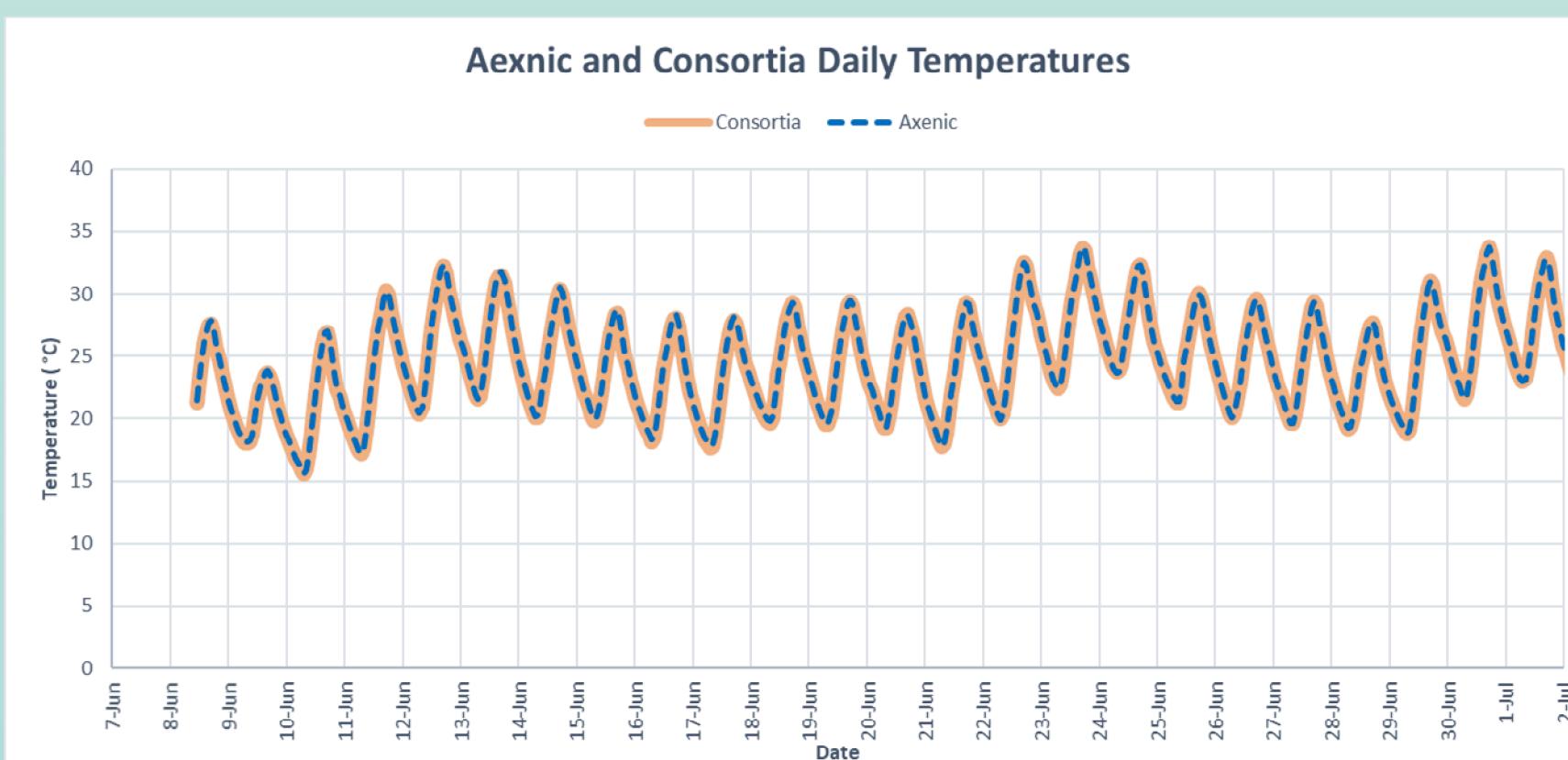


Fig. 3 HOBO temperature sensor data. Sensors were placed in mesocosm A2 to record axenic temperatures and in C2 to record consortia temperatures.

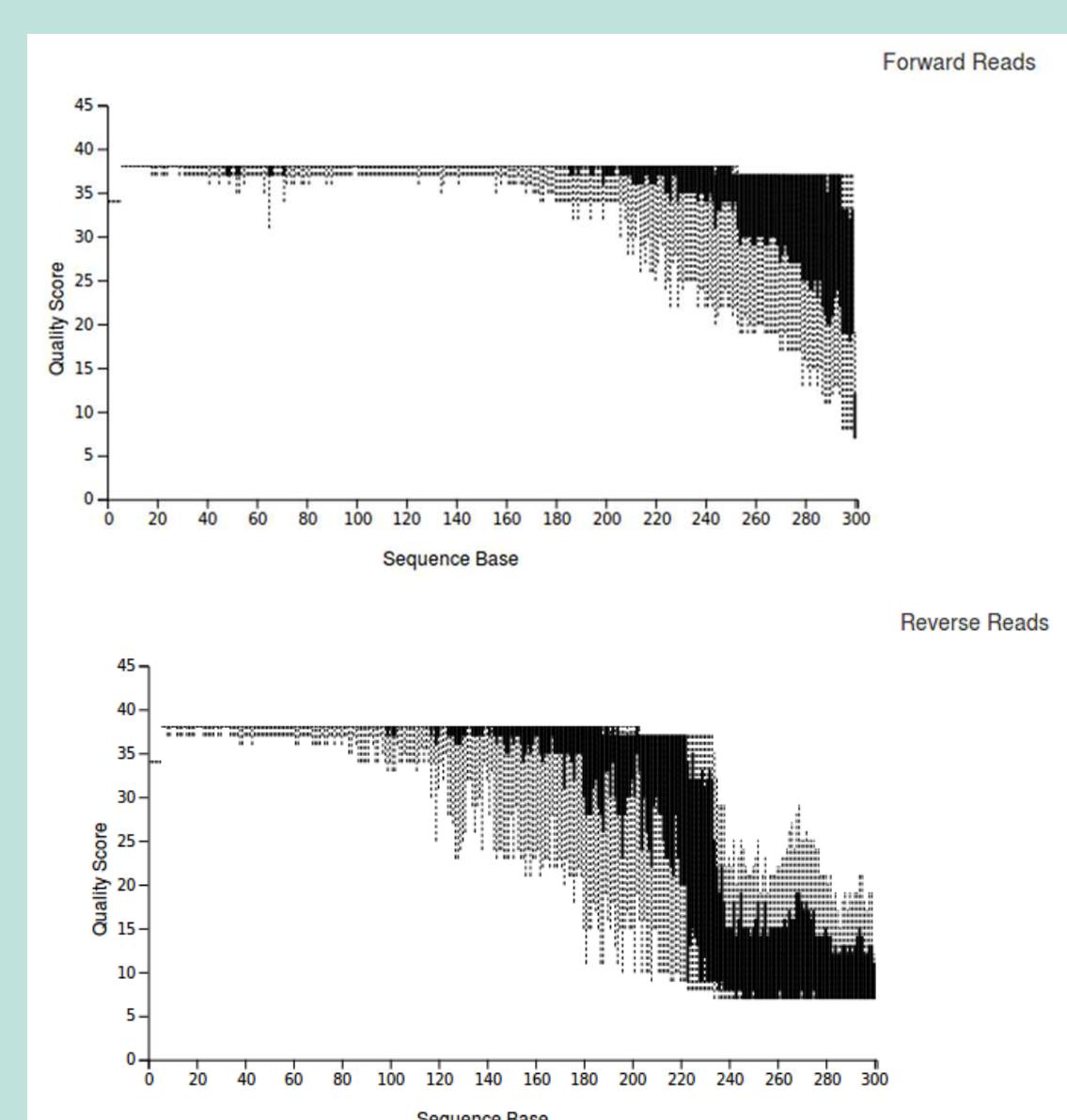


Fig. 4 Quality plots generated in QIIME 2 from Illumina MiSeq data for both forward and reverse sample reads.

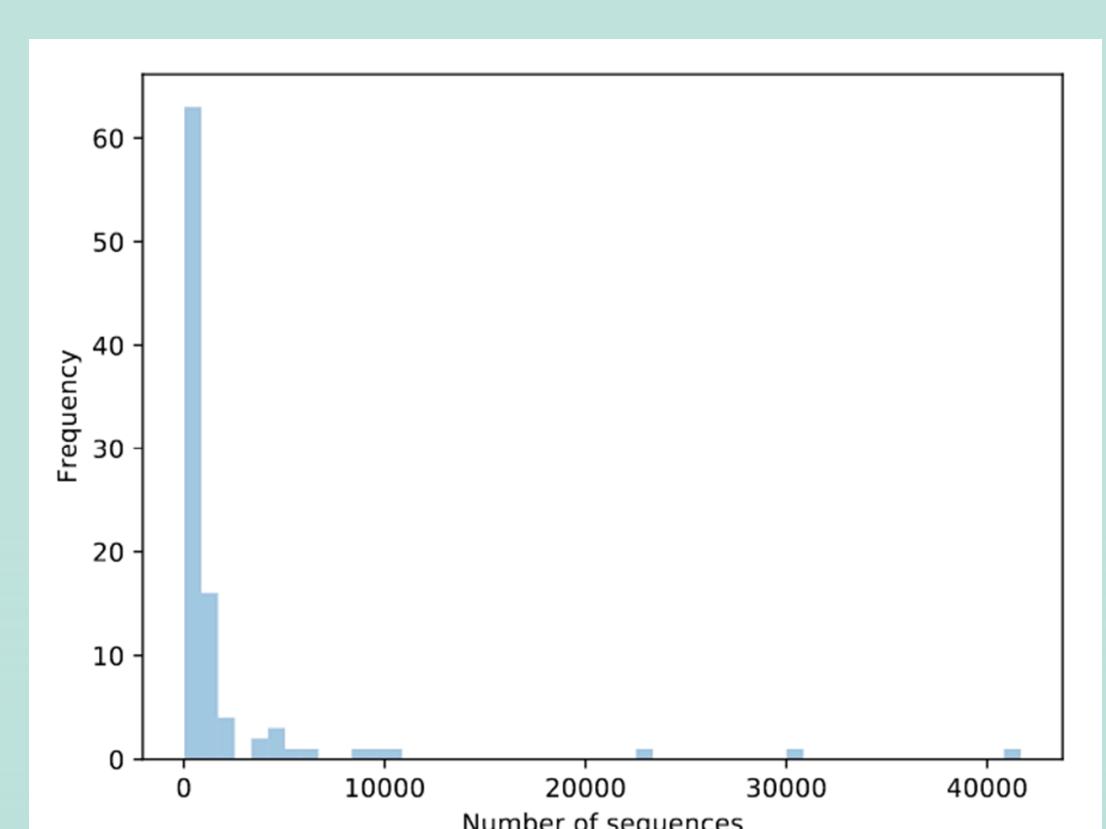


Fig. 5 Demultiplexed sequences generated in QIIME 2. Shows number and range of sequences generated across samples.