

## **Bioinformatic Analysis Report**

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Project title: Genome Sequence of Nannochloropsis  
Prepared for: Dr. Randor Radakovits and Dr. Matthew Posewitz  
Type of report: Sequence Trim Report  
Date: September 1, 2011  
Details: All Illumina paired-end (SIPES) reads  
from the plus and minus nitrogen cDNA samples

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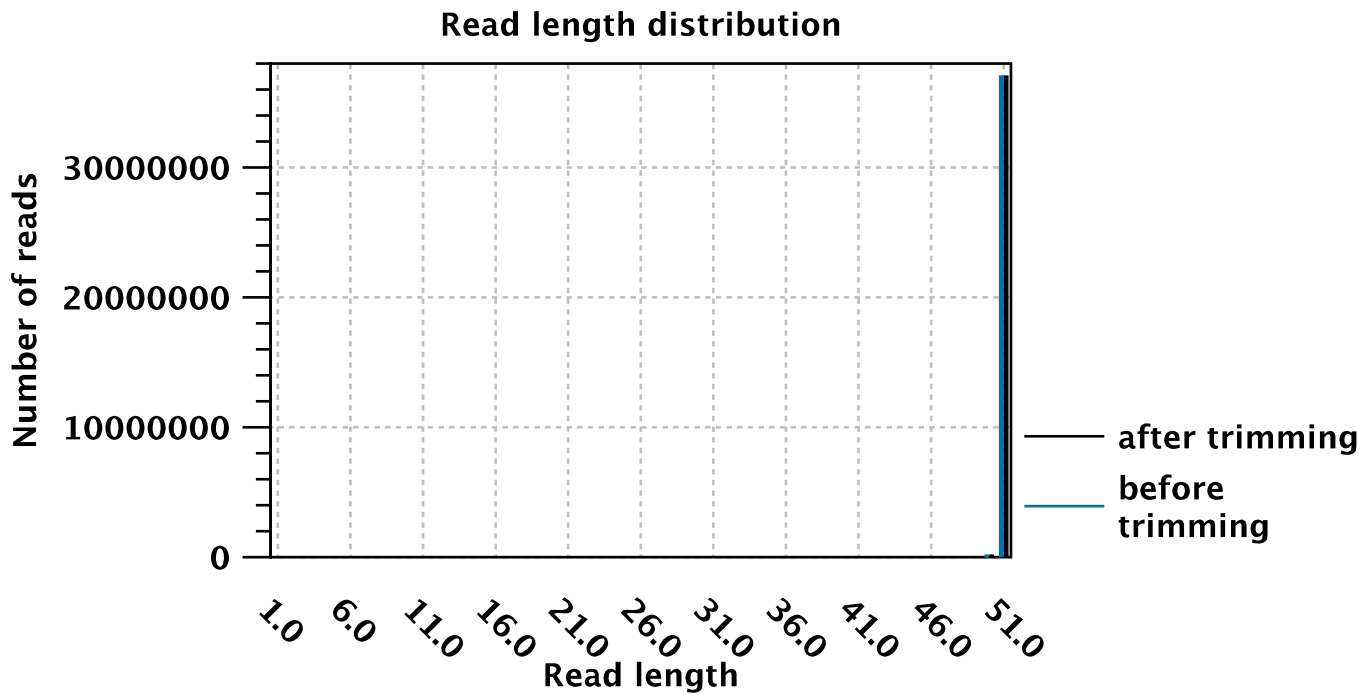
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# 1. Trim summary

Name	Number of reads	Avg.length	Number of reads after trim	Percentage trimmed
minus_N_NaGa_total_RNA (paired)	18,244,626	50.7	18,148,466	99.47%
plus_N_NaGa_total_RNA (paired)	19,736,016	50.7	19,646,689	99.55%

Avg.length after trim
50.9
50.9

# 2. Read length before / after trimming



# 3. Trim settings

- Removal of low quality sequence. (limit = 0.01).
- Removal of ambiguous nucleotides: No ambiguous nucleotides allowed.

- Removal of sequences on length: minimum length 30 nucleotides.

## 4. Detailed trim results

Trim	Input reads	No trim	Trimmed	Nothing left or Discarded
Trim on quality	37,980,642	37,980,642	0	0
Ambiguity trim	37,980,642	37,964,406	16,236	0
Filter on length	37,980,642	37,795,155	0	185,487