

Bioinformatic Analysis Report

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Project title: Genome Sequence of Nannochloropsis
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Type of report: Sequence Trim Report
Date: September 1, 2011
Details: All Illumina paired-end (SIPES) reads
from the pooled cDNA sample

Table of contents

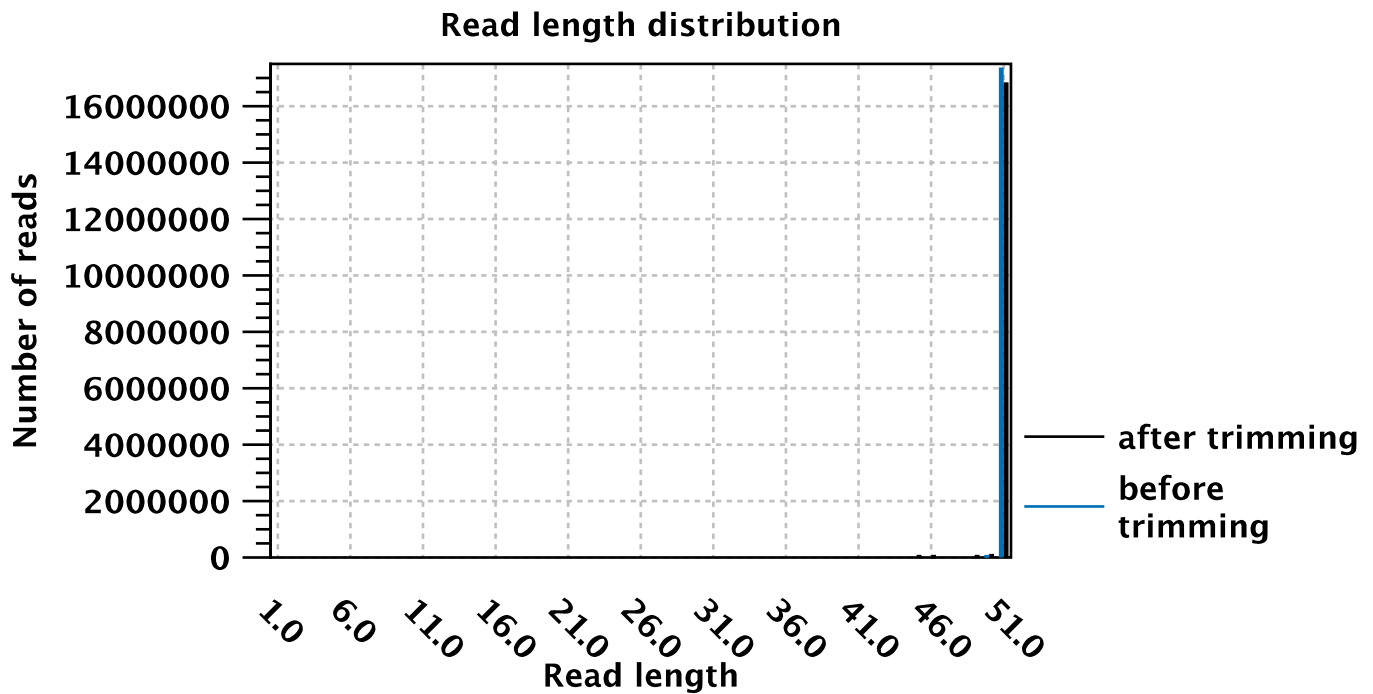
1. Trim summary	3
2. Read length before / after trimming	3
3. Trim settings	3
4. Detailed trim results	4

1. Trim summary

Name	Number of reads	Avg.length	Number of reads after trim	Percentage trimmed
pooled_NaGa_total_RNA_1 (paired)	17,823,072	50.7	17,723,662	99.44%

Avg.length after trim
50.5

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 20 nucleotides.

4. Detailed trim results

Trim	Input reads	No trim	Trimmed	Nothing left or Discarded
Trim on quality	17,823,072	17,101,784	721,288	0
Ambiguity trim	17,823,072	17,815,586	7,430	56
Filter on length	17,823,016	17,723,662	0	99,354