

Bioinformatic Analysis Report

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Project title: Genome Sequence of Nannochloropsis
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Type of report: Sequence Trim Report
Date: May 25, 2011
Details: All Illumina singleton reads

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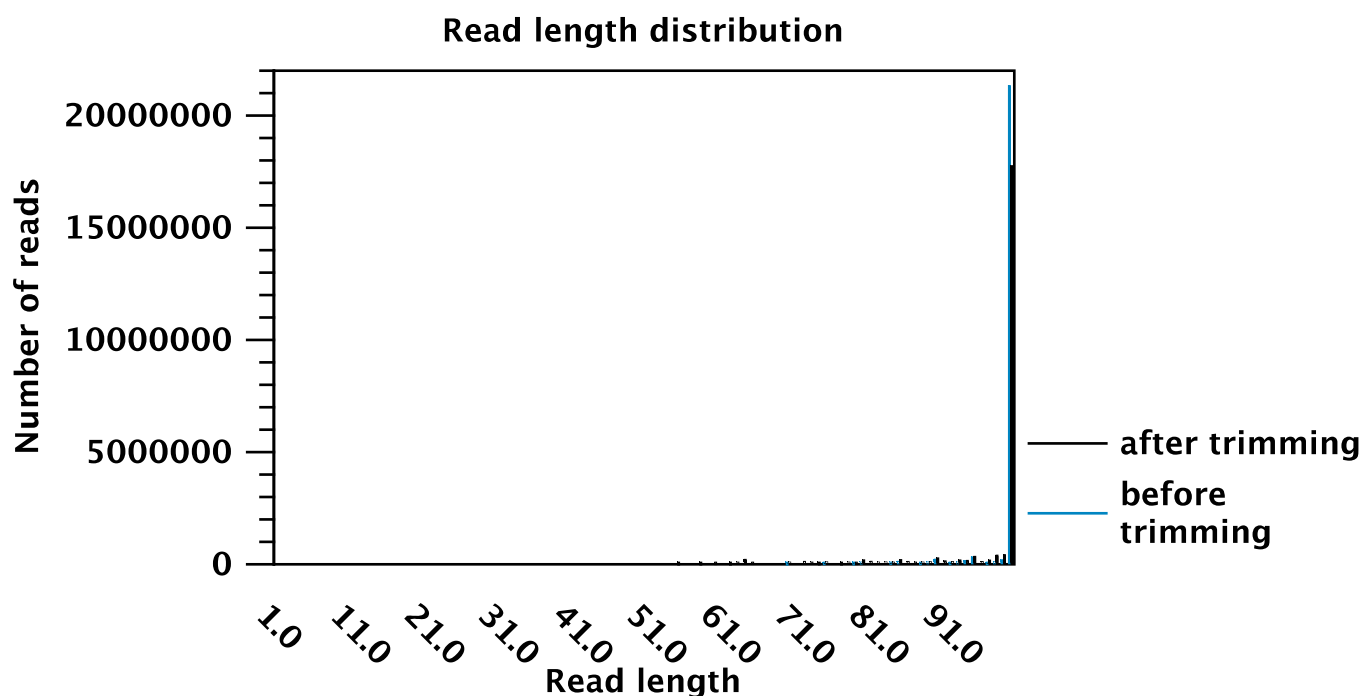
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1. Trim summary

Name	Number of reads	Avg.length	Number of reads after trim	Percentage trimmed
Nano_Eureka_gDNA	24,709,613	97.6	24,484,194	99.09%

Avg.length after trim
94.5

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 30 nucleotides.

4. Detailed trim results

Trim	Input reads	No trim	Trimmed	Nothing left or Discarded
Trim on quality	24,709,613	19,616,115	5,093,498	0
Ambiguity trim	24,709,613	24,123,879	571,722	14,012
Filter on length	24,695,601	24,484,194	0	211,407